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(54) Title: *CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING PROTEINS INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE TRANSPORT

(57) Abstract: Isolated nucleic acid molecules, designated MCT nucleic acid molecules, which encode novel MCT proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing MCT nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated MCT proteins, mutated MCT proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of MCT genes in this organism.

CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE TRANSPORT

Related Applications

This application claims priority to prior filed U.S. Provisional Patent Application Serial No. 60/141031, filed June 25, 1999. This application also claims priority to German Patent Application No. 19931454.3, filed July 8, 1999, German Patent Application No. 19931478.0, filed July 8, 1999, German Patent Application No. 19931563.9, filed July 8, 1999, German Patent Application No. 19932122.1, filed July 9, 1999, German Patent Application No. 19932124.8, filed 99709, German Patent Application No. 19932125.6, filed July 9, 1999, German Patent Application No. 19932128.0, filed July 9, 1999, German Patent Application No. 19932180.9, filed July 9, 1999, German Patent Application No. 19932182.5, filed July 9, 1999, German Patent Application No. 19932190.6, filed July 9, 1999, German Patent Application No. 19932191.4, filed July 9, 1999, German Patent Application No. 19932209.0, filed July 9, 1999, German Patent Application No. 19932212.0, filed July 9, 1999, German Patent Application No. 19932227.9, filed July 9, 1999, German Patent Application No. 19932228.7, filed July 9, 1999, German Patent Application No. 19932229.5, filed 99070, German Patent Application No. 19932230.9, filed July 9, 1999, German Patent Application No. 19932927.3, filed July 14, 1999, German Patent Application No. 19933005.0, filed July 14, 1999, German Patent Application No. 19933006.9, filed July 14, 1999, German Patent Application No. 19940764.9, filed August 27, 1999, German Patent Application No. 19940765.7, filed August 27, 1999, German Patent Application No. 19940766.5, filed August 27, 1999, German Patent Application No. 19940830.0, filed August 27, 1999, German Patent Application No. 19940831.9, filed August 27, 1999, German Patent Application No. 19940832.7, filed August 27, 1999, German Patent Application No. 19940833.5, filed August 27, 1999, German Patent Application No. 19941378.9 filed August 31, 1999, German Patent Application No. 19941379.7, filed August 31, 1999, German Patent Application No. 19941395.9, filed August 31, 1999, German Patent Application No. 19942077.7, filed September 3, 1999, German Patent Application No. 19942078.5, filed September 3, 1999, German Patent

Application No. 19942079.3, filed September 3, 1999, and German Patent Application No. 19942088.2, filed September 3, 1999. The entire contents of all of the above referenced applications are hereby expressly incorporated herein by this reference.

Background of the Invention

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as membrane construction and membrane transport (MCT) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The MCT nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by

fermentation processes. Modulation of the expression of the MCT nucleic acids of the invention, or modification of the sequence of the MCT nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a Corynebacterium or Brevibacterium species).

The MCT nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The MCT nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered Corynebacterium or Brevibacterium species.

The MCT proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing a function involved in the metabolism (*e.g.*, the biosynthesis or degradation) of compounds necessary for membrane biosynthesis, or of assisting in the transmembrane transport of one or more compounds either into or out of the cell. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama et al, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals. This improved production or efficiency of

production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation.

There are a number of mechanisms by which the alteration of an MCT protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. Those MCT proteins involved in the export of fine chemical molecules from the cell may be increased in number or activity such that greater quantities of these compounds are secreted to the extracellular medium, from which they are more readily recovered. Similarly, those MCT proteins involved in the import of nutrients necessary for the biosynthesis of one or more fine chemicals (*e.g.*, phosphate, sulfate, nitrogen compounds, etc.) may be increased in number or activity such that these precursors, cofactors, or intermediate compounds are increased in concentration within the cell. Further, fatty acids and lipids themselves are desirable fine chemicals; by optimizing the activity or increasing the number of one or more MCT proteins of the invention which participate in the biosynthesis of these compounds, or by impairing the activity of one or more MCT proteins which are involved in the degradation of these compounds, it may be possible to increase the yield, production, and/or efficiency of production of fatty acid and lipid molecules from *C. glutamicum.*

The mutagenesis of one or more MCT genes of the invention may also result in MCT proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C .glutamicum*. For example, MCT proteins of the invention involved in the export of waste products may be increased in number or activity such that the normal metabolic wastes of the cell (possibly increased in quantity due to the overproduction of the desired fine chemical) are efficiently exported before they are able to damage nucleotides and proteins within the cell (which would decrease the viability of the cell) or to interfere with fine chemical biosynthetic pathways (which would decrease the yield, production, or efficiency of production of the desired fine chemical). Further, the relatively large intracellular quantities of the desired fine chemical may in itself be toxic to the cell, so by increasing the activity or number of transporters able to export this compound from the cell, one may increase the viability of the cell in culture, in turn leading to a greater number of cells in the culture producing the desired fine chemical. The MCT proteins of the invention may also be manipulated

such that the relative amounts of different lipid and fatty acid molecules are produced. This may have a profound effect on the lipid composition of the membrane of the cell. Since each type of lipid has different physical properties, an alteration in the lipid composition of a membrane may significantly alter membrane fluidity. Changes in membrane fluidity can impact the transport of molecules across the membrane, as well as the integrity of the cell, both of which have a profound effect on the production of fine chemicals from *C. glutamicum* in large-scale fermentative culture.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as MCT proteins, which are capable of, for example, participating in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. Nucleic acid molecules encoding an MCT protein are referred to herein as MCT nucleic acid molecules. In a preferred embodiment, the MCT protein participates in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an MCT protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of MCT-encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), forth as the odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or a portion

thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth as an even-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8...). The preferred MCT proteins of the present invention also preferably possess at least one of the MCT activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence having an even-numbered SEQ ID NO: in the Sequence Listing), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an MCT activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of the invention (*e.g.*, an entire amino acid sequence selected from those having an even-numbered SEQ ID NO in the Sequence Listing). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention (encoded by an open reading frame shown in the corresponding odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an MCT fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing) and is able to participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or has one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO in the Sequence Listing). Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* MCT protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an MCT protein by culturing the host cell in a suitable medium. The MCT protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an MCT gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated MCT sequence as a transgene. In another embodiment, an endogenous MCT gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered MCT gene. In another embodiment, an endogenous or introduced MCT gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MCT protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MCT gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MCT gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Cornyebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the

sequences set forth in the Sequence Listing as SEQ ID NOs 1 through 676) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated MCT protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated MCT protein or portion thereof can participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. In another preferred embodiment, the isolated MCT protein or portion thereof is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: in the Sequence Listing) such that the protein or portion thereof maintains the ability to participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes.

The invention also provides an isolated preparation of an MCT protein. In preferred embodiments, the MCT protein comprises an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the Sequence Listing A). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In other embodiments, the isolated MCT protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and is able to participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated MCT protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under

stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98,%, or 99% or more homologous, to a nucleotide sequence of one of the even-numbered SEQ ID NOs set forth in the Sequence Listing. It is also preferred that the preferred forms of MCT proteins also have one or more of the MCT bioactivities described herein.

The MCT polypeptide, or a biologically active portion thereof, can be operatively linked to a non-MCT polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the MCT protein alone. In other preferred embodiments, this fusion protein participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an MCT protein, either by interacting with the protein itself or a substrate or binding partner of the MCT protein, or by modulating the transcription or translation of an MCT nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an MCT nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an MCT nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates MCT protein activity or MCT nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum*

metabolic pathways for cell membrane components or is modulated for the transport of compounds across such membranes, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates MCT protein activity can be an agent which stimulates MCT protein activity or MCT nucleic acid expression. Examples of agents which stimulate MCT protein activity or MCT nucleic acid expression include small molecules, active MCT proteins, and nucleic acids encoding MCT proteins that have been introduced into the cell. Examples of agents which inhibit MCT activity or expression include small molecules and antisense MCT nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant MCT gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides MCT nucleic acid and protein molecules which are involved in the metabolism of cellular membrane components in C. glutamicum or in the transport of compounds across such membranes. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where overexpression or optimization of a fatty acid biosynthesis protein has a direct impact on the yield, production, and/or efficiency of production of the fatty acid from modified *C. glutamicum*), or may have an indirect impact which nonetheless results in an increase of yield, production, and/or efficiency of production of the desired compound (*e.g.*, where modulation of the metabolism of cell membrane components results in alterations in the yield, production,

and/or efficiency of production or the composition of the cell membrane, which in turn may impact the production of one or more fine chemicals). Aspects of the invention are further explicated below.

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. *Amino Acid Metabolism and Uses*

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in

proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino aids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial

amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α-ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β-carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. Biochemistry 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B_1) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B_2) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of

compounds collectively termed 'vitamin B_6' (*e.g.*, pyridoxine, pyridoxamine, pyridoxa-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)-β-alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β-alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β-alanine and for the condensation to panthotenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of panthothante, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B_5), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α-ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which is turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B_{12}) and porphyrines belong to a group of chemicals characterized by a tetrapyrole ring system. The biosynthesis of vitamin B_{12} is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B_6, pantothenate, and biotin. Only Vitamin B_{12} is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine,

folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) Nucleotides and Related Compounds in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: Progress in Nucleic Acid Research and Molecular Biology, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α, α-1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S.

Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) J. Japan 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Membrane Biosynthesis and Transmembrane Transport

Cellular membranes serve a variety of functions in a cell. First and foremost, a membrane differentiates the contents of a cell from the surrounding environment, thus giving integrity to the cell. Membranes may also serve as barriers to the influx of hazardous or unwanted compounds, and also to the efflux of desired compounds. Cellular membranes are by nature impervious to the unfacilitated diffusion of hydrophilic compounds such as proteins, water molecules and ions due to their structure: a bilayer of lipid molecules in which the polar head groups face outwards (towards the exterior and interior of the cell, respectively) and the nonpolar tails face inwards at the center of the bilayer, forming a hydrophobic core (for a general review of membrane structure and function, see Gennis, R.B. (1989) Biomembranes, Molecular Structure and Function, Springer: Heidelberg). This barrier enables cells to maintain a relatively higher concentration of desired compounds and a relatively lower concentration of undesired compounds than are contained within the surrounding medium, since the diffusion of these compounds is effectively blocked by the membrane. However, the membrane also presents an effective barrier to the import of desired compounds and the export of waste molecules. To overcome this difficulty, cellular membranes incorporate many kinds of transporter proteins which are able to facilitate the transmembrane transport of different kinds of compounds. There are two general classes of these transport proteins: pores or channels and transporters. The former are integral membrane proteins, sometimes complexes of proteins, which form a regulated hole through the membrane. This regulation, or 'gating' is generally specific to the molecules to be transported by the pore or channel, rendering these transmembrane constructs selectively permeable to a specific class of substrates; for example, a potassium channel is constructed such that only ions having a like charge and size to that of potassium may pass through. Channel and pore proteins tend to have discrete

hydrophobic and hydrophilic domains, such that the hydrophobic face of the protein may associate with the interior of the membrane while the hydrophilic face lines the interior of the channel, thus providing a sheltered hydrophilic environment through which the selected hydrophilic molecule may pass. Many such pores/channels are known in the art, including those for potassium, calcium, sodium, and chloride ions.

This pore and channel-mediated system of facilitated diffusion is limited to very small molecules, such as ions, because pores or channels large enough to permit the passage of whole proteins by facilitated diffusion would be unable to prevent the passage of smaller hydrophilic molecules as well. Transport of molecules by this process is sometimes termed 'facilitated diffusion' since the driving force of a concentration gradient is required for the transport to occur. Permeases also permit facilitated diffusion of larger molecules, such as glucose or other sugars, into the cell when the concentration of these molecules on one side of the membrane is greater than that on the other (also called 'uniport'). In contrast to pores or channels, these integral membrane proteins (often having between 6-14 membrane-spanning α-helices) do not form open channels through the membrane, but rather bind to the target molecule at the surface of the membrane and then undergo a conformational shift such that the target molecule is released on the opposite side of the membrane.

However, cells frequently require the import or export of molecules against the existing concentration gradient ('active transport'), a situation in which facilitated diffusion cannot occur. There are two general mechanisms used by cells for such membrane transport: symport or antiport, and energy-coupled transport such as that mediated by the ABC transporters. Symport and antiport systems couple the movement of two different molecules across the membrane (via permeases having two separate binding sites for the two different molecules); in symport, both molecules are transported in the same direction, while in antiport, one molecule is imported while the other is exported. This is possible energetically because one of the two molecules moves in accordance with a concentration gradient, and this energetically favorable event is permitted only upon concomitant movement of a desired compound against the prevailing concentration gradient. Single molecules may be transported across the membrane against the concentration gradient in an energy-driven process, such as that utilized by the ABC transporters. In this system, the transport protein located in the

membrane has an ATP-binding cassette; upon binding of the target molecule, the ATP is converted to ADP + Pi, and the resulting release of energy is used to drive the movement of the target molecule to the opposite face of the membrane, facilitated by the transporter. For more detailed descriptions of all of these transport systems, see: Bamberg, E. *et al.*, (1993) "Charge transport of ion pumps on lipid bilayer membranes", *Q. Rev. Biophys.* 26: 1-25; Findlay, J.B.C. (1991) "Structure and function in membrane transport systems", *Curr. Opin. Struct. Biol.* 1:804-810; Higgins, C.F. (1992) "ABC transporters from microorganisms to man", *Ann. Rev. Cell Biol.* 8: 67-113; Gennis, R.B. (1989) "Pores, Channels and Transporters", in: Biomembranes, Molecular Structure and Function, Springer: Heidelberg, p. 270-322; and Nikaido, H. and Saier, H. (1992) "Transport proteins in bacteria: common themes in their design", *Science* 258: 936-942, and references contained within each of these references.

The synthesis of membranes is a well-characterized process involving a number of components, the most important of which are lipid molecules. Lipid synthesis may be divided into two parts: the synthesis of fatty acids and their attachment to sn-glycerol-3-phosphate, and the addition or modification of a polar head group. Typical lipids utilized in bacterial membranes include phospholipids, glycolipids, sphingolipids, and phosphoglycerides. Fatty acid synthesis begins with the conversion of acetyl CoA either to malonyl CoA by acetyl CoA carboxylase, or to acetyl-ACP by acetyltransacylase. Following a condensation reaction, these two product molecules together form acetoacetyl-ACP, which is converted by a series of condensation, reduction and dehydration reactions to yield a saturated fatty acid molecule having a desired chain length. The production of unsaturated fatty acids from such molecules is catalyzed by specific desaturases either aerobically, with the help of molecular oxygen, or anaerobically (for reference on fatty acid synthesis, see F.C. Neidhardt *et al.* (1996) E. coli and Salmonella. ASM Press: Washington, D.C., p. 612-636 and references contained therein; Lengeler *et al.* (eds) (1999) Biology of Procaryotes. Thieme: Stuttgart, New York, and references contained therein; and Magnuson, K. *et al.*, (1993) *Microbiological Reviews* 57: 522-542, and references contained therein). The cyclopropane fatty acids (CFA) are synthesized by a specific CFA-synthase using SAM as a cosubstrate. Branched chain fatty acids are synthesized from branched chain amino acids that are deaminated to yield branched chain 2-oxo-acids (see Lengeler *et al.*, eds.

(1999) Biology of Procaryotes. Thieme: Stuttgart, New York, and references contained therein). Another essential step in lipid synthesis is the transfer of fatty acids onto the polar head groups by, for example, glycerol-phosphate-acyltransferases. The combination of various precursor molecules and biosynthetic enzymes results in the production of different fatty acid molecules, which has a profound effect on the composition of the membrane.

III. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as MCT nucleic acid and protein molecules, which control the production of cellular membranes in *C. glutamicum* and govern the movement of molecules across such membranes. In one embodiment, the MCT molecules participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. In a preferred embodiment, the activity of the MCT molecules of the present invention to regulate membrane component production and membrane transport has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the MCT molecules of the invention are modulated in activity, such that the *C. glutamicum* metabolic pathways which the MCT proteins of the invention regulate are modulated in yield, production, and/or efficiency of production and the transport of compounds through the membranes is altered in efficiency, which either directly or indirectly modulates the yield, production, and/or efficiency of production of a desired fine chemical by *C. glutamicum*.

The language, "MCT protein" or "MCT polypeptide" includes proteins which participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. Examples of MCT proteins include those encoded by the MCT genes set forth in Table 1 and by the odd-numbered SEQ ID NOs. The terms "MCT gene" or "MCT nucleic acid sequence" include nucleic acid sequences encoding an MCT protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of MCT genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation

product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound.

In another embodiment, the MCT molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. There are a number of mechanisms by which the alteration of an MCT protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. Those MCT proteins involved in the export of fine chemical molecules from the cell may be increased in number or activity such that greater quantities of these compounds are secreted to the extracellular medium, from which they are more readily recovered. Similarly, those MCT proteins involved in the import of nutrients necessary for the biosynthesis of one or more fine chemicals (*e.g.*, phosphate, sulfate, nitrogen compounds, etc.) may be increased in number or

activity such that these precursor , cofactor, or intermediate compounds are increased in concentration within the cell. Further, fatty acids and lipids themselves are desirable fine chemicals; by optimizing the activity or increasing the number of one or more MCT proteins of the invention which participate in the biosynthesis of these compounds, or by impairing the activity of one or more MCT proteins which are involved in the degradation of these compounds, it may be possible to increase the yield, production, and/or efficiency of production of fatty acid and lipid molecules from *C. glutamicum.*

The mutagenesis of one or more MCT genes of the invention may also result in MCT proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C .glutamicum.* For example, MCT proteins of the invention involved in the export of waste products may be increased in number or activity such that the normal metabolic wastes of the cell (possibly increased in quantity due to the overproduction of the desired fine chemical) are efficiently exported before they are able to damage nucleotides and proteins within the cell (which would decrease the viability of the cell) or to interfere with fine chemical biosynthetic pathways (which would decrease the yield, production, or efficiency of production of the desired fine chemical). Further, the relatively large intracellular quantities of the desired fine chemical may in itself be toxic to the cell, so by increasing the activity or number of transporters able to export this compound from the cell, one may increase the viability of the cell in culture, in turn leading to a greater number of cells in the culture producing the desired fine chemical. The MCT proteins of the invention may also be manipulated such that the relative amounts of different lipid and fatty acid molecules are produced. This may have a profound effect on the lipid composition of the membrane of the cell. Since each type of lipid has different physical properties, an alteration in the lipid composition of a membrane may significantly alter membrane fluidity. Changes in membrane fluidity can impact the transport of molecules across the membrane, as well as the integrity of the cell, both of which have a profound effect on the production of fine chemicals from *C. glutamicum* in large-scale fermentative culture.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* MCT DNAs and the predicted amino acid sequences of the *C.*

glutamicum MCT proteins are shown in the Sequence Listing as odd-numbered SEQ ID NOs and even-numbered SEQ ID NOs, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode proteins involved in the metabolism of cellular membrane components or proteins involved in the transport of compounds across such membranes.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of the invention (*e.g.*, the sequence of an even-numbered SEQ ID NO of the Sequence Listing).. As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

The MCT protein or a biologically active portion or fragment thereof of the invention can participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode MCT polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of MCT-encoding nucleic acid (*e.g.*, MCT DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about

20 nucleotides of sequence downstream from the 3'end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated MCT nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of an odd-numbered SEQ ID NO of the Sequence Listing, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* MCT DNA can be isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO:) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO of the Sequence Listing) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA

can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in the Sequence Listing. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an MCT nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in the Sequence Listing. The nucleic acid sequences of the invention, as set forth in the Sequence Listing correspond to the *Corynebacterium glutamicum* MCT DNAs of the invention. This DNA comprises sequences encoding MCT proteins (*i.e.*, the "coding region", indicated in each odd-numbered SEQ ID NO: in the Sequence Listing), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in each odd-numbered SEQ ID NO: in the Sequence Listing. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the nucleic acid sequences of the Sequence Listing.

For the purposes of this application, it will be understood that each of the nucleic acid and amino acid sequences set forth in the Sequence Listing has an identifying RXA, RXN, RXS, or RXC number having the designation "RXA", "RXN", "RXS" or "RXC" followed by 5 digits (*i.e.*, RXA02099, RXN03097, RXS00148, or RXC01748). Each of the nucleic acid sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, RXS, or RXC designation to eliminate confusion. The recitation "one of the odd-numbered sequences in of the Sequence Listing", then, refers to any of the nucleic acid sequences in the Sequence Listing, which may also be distinguished by their differing RXA, RXN, RXS, or RXC designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is also set forth in the Sequence Listing, as an even-numbered SEQ ID NO: immediately following

the corresponding nucleic acid sequence. For example, the coding region for RXA03097 is set forth in SEQ ID NO:1, while the amino acid sequence which it encodes is set forth as SEQ ID NO:2. The sequences of the nucleic acid molecules of the invention are identified by the same RXA, RXN, RXS, or RXC designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequences designated RXA02099, RXN03097, RXS00148, and RXC01748 are translations of the coding region of the nucleotide sequences of nucleic acid molecules RXA02099, RXN03097, RXS00148, and RXC01748, respectively. The correspondence between the RXA, RXN, RXS, and RXC nucleotide and amino acid sequences of the invention and their assigned SEQ ID NOs is set forth in Table 1. For example, as set forth in Table 1, the nucleotide sequence of RXA00104 is SEQ ID NO:5, and the amino acid sequence of RXA00104 is SEQ ID NO:6.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA, RXN, RXS, or RXC designation. For example, SEQ ID NO:11, designated, as indicated on Table 1, as "F RXA02581", is an F-designated gene, as are SEQ ID NOs: 31, 33, and 43 (designated on Table 1 as "F RXA02487", "F RXA02490", and "F RXA02809", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the dapD gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences shown in of the invention is one which is sufficiently complementary to one of the nucleotide sequences shown in the Sequence Listing (*e.g.*, the sequence of an odd-numbered SEQ ID NO:)such that it can

hybridize to one of the nucleotide sequences of the invention, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to one of the nucleotide sequences of the invention, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an MCT protein. The nucleotide sequences determined from the cloning of the MCT genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning MCT homologues in other cell types and organisms, as well as MCT homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the nucleotide sequences of the invention (*e.g.*, a sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing), an anti-sense sequence of one of these sequences, or naturally occurring mutants thereof. Primers based on a

nucleotide sequence of the invention can be used in PCR reactions to clone MCT homologues. Probes based on the MCT nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an MCT protein, such as by measuring a level of an MCT-encoding nucleic acid in a sample of cells, *e.g.*, detecting MCT mRNA levels or determining whether a genomic MCT gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO of the Sequence Listing) such that the protein or portion thereof maintains the ability to participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in a sequence of one of the even-numbered SEQ ID NOs of the Sequence Listing) amino acid residues to an amino acid sequence of the invention such that the protein or portion thereof is able to participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. Protein members of such membrane component metabolic pathways or membrane transport systems, as described herein, may play a role in the production and secretion of one or more fine chemicals. Examples of such activities are also described herein. Thus, "the function of an MCT protein" contributes either directly or indirectly to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of MCT protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino

acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing).

Portions of proteins encoded by the MCT nucleic acid molecules of the invention are preferably biologically active portions of one of the MCT proteins. As used herein, the term "biologically active portion of an MCT protein" is intended to include a portion, *e.g.*, a domain/motif, of an MCT protein that participates in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or has an activity as set forth in Table 1. To determine whether an MCT protein or a biologically active portion thereof can participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an MCT protein can be prepared by isolating a portion of one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing), expressing the encoded portion of the MCT protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the MCT protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing) (and portions thereof) due to degeneracy of the genetic code and thus encode the same MCT protein as that encoded by the nucleotide sequences of the invention. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in the Sequence Listing (*e.g.*, an even-numbered SEQ ID NO:). In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of the invention (encoded by an open reading frame shown in an odd-numbered SEQ ID NO: of the Sequence Listing).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 38% identical to the nucleotide sequence designated RXA01420 (SEQ ID NO:7), a nucleotide sequence which is greater than and/or at least 43% identical to the nucleotide sequence designated RXA00104 (SEQ ID NO:5), and a nucleotide sequence which is greater than and/or at least 45% identical to the nucleotide sequence designated RXA02173 (SEQ ID NO:25). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* MCT nucleotide sequences set forth in the Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by one of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of MCT proteins may exist within a population (*e.g.*, the *C. glutamicum* population). Such genetic polymorphism in the MCT gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an MCT protein, preferably a *C. glutamicum* MCT protein.

Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the MCT gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in MCT that are the result of natural variation and that do not alter the functional activity of MCT proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* MCT DNA of the invention can be isolated based on their homology to the *C. glutamicum* MCT nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of an odd-numbered SEQ ID NO: of the Sequence Listing. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a nucleotide sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* MCT protein.

In addition to naturally-occurring variants of the MCT sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be

introduced by mutation into a nucleotide sequence of the invention, thereby leading to changes in the amino acid sequence of the encoded MCT protein, without altering the functional ability of the MCT protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a nucleotide sequence of the invention. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the MCT proteins (*e.g.*, an even-numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said MCT protein, whereas an "essential" amino acid residue is required for MCT protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved in the domain having MCT activity) may not be essential for activity and thus are likely to be amenable to alteration without altering MCT activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding MCT proteins that contain changes in amino acid residues that are not essential for MCT activity. Such MCT proteins differ in amino acid sequence from a sequence of an even-numbered SEQ ID NO: of the Sequence Listing yet retain at least one of the MCT activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of the invention and is capable of participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to the amino acid sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing , more preferably at least about 60-70% homologous to one of these sequences, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of these sequences, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the amino acid sequences of the invention..

To determine the percent homology of two amino acid sequences (*e.g.*, one of the amino acid sequences of the invention and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding

amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the amino acid sequences of the invention) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the amino acid sequence), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an MCT protein homologous to a protein sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of the invention such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the nucleotide sequences of the invention by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an MCT protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an MCT coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an MCT activity described herein to identify mutants that retain MCT activity. Following mutagenesis of the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing,

the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding MCT proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire MCT coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an MCT protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO:5 (RXA00104) comprises nucleotides 1 to 756). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding MCT. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding MCT disclosed herein (*e.g.*, the sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of MCT mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of MCT mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of MCT mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized

using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5- oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MCT protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve

sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids. Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave MCT mRNA transcripts to thereby inhibit translation of MCT mRNA. A ribozyme having specificity for an MCT-encoding nucleic acid can be designed based upon the nucleotide sequence of an MCT DNA disclosed herein (*i.e.*, SEQ ID NO. 5 (RXA00104). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an MCT-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, MCT mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, MCT gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an MCT nucleotide sequence (*e.g.*, an MCT promoter and/or enhancers) to form triple helical structures that prevent transcription of an MCT gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an MCT protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185,

Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as cos-, tac-, trp-, tet-, trp-tet-, lpp-, lac-, lpp-lac-, $lacI^q$-, T7-, T5-, T3-, gal-, trc-, ara-, SP6-, arny, SPO2, λ-P_R- or λ P_L, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, MFα, AC, P-60, CYC1, GAPDH, TEF, rp28, ADH, promoters from plants such as CaMV/35S, SSU, OCS, lib4, usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by one of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, MCT proteins, mutant forms of MCT proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of MCT proteins in prokaryotic or eukaryotic cells. For example, MCT genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* –mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the MCT protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant MCT protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λgt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89 ; and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by

host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming Streptomyces, while plasmids pUB110, pC194, or pBD214 are suited for transformation of Bacillus species. Several plasmids of use in the transfer of genetic information into Corynebacterium include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018).

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the MCT protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ, pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York (IBSN 0 444 904018).

Alternatively, the MCT proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.*

(1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the MCT proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477),

pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α-fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to MCT mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an MCT protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other

suitable host cells are known to one of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", “conjugation” and “transduction” are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an MCT protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an MCT gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the MCT gene. Preferably, this MCT gene is a *Corynebacterium glutamicum* MCT gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous

recombination, the endogenous MCT gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous MCT gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous MCT protein). In the homologous recombination vector, the altered portion of the MCT gene is flanked at its 5' and 3' ends by additional nucleic acid of the MCT gene to allow for homologous recombination to occur between the exogenous MCT gene carried by the vector and an endogenous MCT gene in a microorganism. The additional flanking MCT nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced MCT gene has homologously recombined with the endogenous MCT gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an MCT gene on a vector placing it under control of the lac operon permits expression of the MCT gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous MCT gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced MCT gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MCT protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MCT gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MCT gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described MCT gene and protein modifications may be readily

produced using the methods of the invention, and are meant to be included in the present invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an MCT protein. Accordingly, the invention further provides methods for producing MCT proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an MCT protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered MCT protein) in a suitable medium until MCT protein is produced. In another embodiment, the method further comprises isolating MCT proteins from the medium or the host cell.

C. Isolated MCT Proteins

Another aspect of the invention pertains to isolated MCT proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of MCT protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of MCT protein having less than about 30% (by dry weight) of non-MCT protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-MCT protein, still more preferably less than about 10% of non-MCT protein, and most preferably less than about 5% non-MCT protein. When the MCT protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of MCT protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or

other chemicals" includes preparations of MCT protein having less than about 30% (by dry weight) of chemical precursors or non-MCT chemicals, more preferably less than about 20% chemical precursors or non-MCT chemicals, still more preferably less than about 10% chemical precursors or non-MCT chemicals, and most preferably less than about 5% chemical precursors or non-MCT chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the MCT protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* MCT protein in a microorganism such as *C. glutamicum.*

An isolated MCT protein or a portion thereof of the invention can participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) such that the protein or portion thereof maintains the ability participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an MCT protein of the invention has an amino acid sequence set forth as an even-numbered SEQ ID NO: of the Sequence Listing.. In yet another preferred embodiment, the MCT protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing). In still another preferred embodiment, the MCT protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of the invention, or a

portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred MCT proteins of the present invention also preferably possess at least one of the MCT activities described herein. For example, a preferred MCT protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention, and which can participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or which has one or more of the activities set forth in Table 1.

In other embodiments, the MCT protein is substantially homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and retains the functional activity of the protein of one of the amino acid sequences of the invention yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the MCT protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention and which has at least one of the MCT activities described herein. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention.

Biologically active portions of an MCT protein include peptides comprising amino acid sequences derived from the amino acid sequence of an MCT protein, *e.g.*, the an amino acid sequence of an even-numbered SEQ ID NO: of the Sequence Listing or the amino acid sequence of a protein homologous to an MCT protein, which include fewer amino acids than a full length MCT protein or the full length protein which is homologous to an MCT protein, and exhibit at least one activity of an MCT protein. Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an MCT protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an MCT protein include one or more selected domains/motifs or portions thereof having biological activity.

MCT proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the MCT protein is expressed in the host cell. The MCT protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an MCT protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native MCT protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-MCT antibody, which can be produced by standard techniques utilizing an MCT protein or fragment thereof of this invention.

The invention also provides MCT chimeric or fusion proteins. As used herein, an MCT "chimeric protein" or "fusion protein" comprises an MCT polypeptide operatively linked to a non-MCT polypeptide. An "MCT polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an MCT protein, whereas a "non-MCT polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the MCT protein, *e.g.*, a protein which is different from the MCT protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the MCT polypeptide and the non-MCT polypeptide are fused

in-frame to each other. The non-MCT polypeptide can be fused to the N-terminus or C-terminus of the MCT polypeptide. For example, in one embodiment the fusion protein is a GST-MCT fusion protein in which the MCT sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant MCT proteins. In another embodiment, the fusion protein is an MCT protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of an MCT protein can be increased through use of a heterologous signal sequence.

Preferably, an MCT chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An MCT-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the MCT protein.

Homologues of the MCT protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the MCT protein. As used herein, the term "homologue" refers to a variant form of the MCT protein which acts as an agonist or antagonist of the activity of the MCT protein. An agonist of the MCT protein can retain substantially the same, or a subset, of the biological activities of the MCT protein. An antagonist of the MCT protein can inhibit one or more of the activities of the naturally occurring form of the MCT protein, by, for example, competitively binding to a downstream or upstream member of the cell membrane component metabolic cascade which includes the MCT

protein, or by binding to an MCT protein which mediates transport of compounds across such membranes, thereby preventing translocation from taking place.

In an alternative embodiment, homologues of the MCT protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the MCT protein for MCT protein agonist or antagonist activity. In one embodiment, a variegated library of MCT variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of MCT variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential MCT sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of MCT sequences therein. There are a variety of methods which can be used to produce libraries of potential MCT homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential MCT sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the MCT protein coding can be used to generate a variegated population of MCT fragments for screening and subsequent selection of homologues of an MCT protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an MCT coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the MCT protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of MCT homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify MCT homologues (Arkin and Yourvan (1992) *PNAS* *89*:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated MCT library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of MCT protein regions required for function; modulation of an MCT protein activity; modulation of the metabolism of one or more cell membrane components; modulation of the transmembrane transport of one or more compounds; and modulation of cellular production of a desired compound, such as a fine chemical.

The MCT nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the

extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present.

Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

In one embodiment, the invention provides a method of identifying the presence or activity of *Cornyebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth as odd-numbered or even-numbered SEQ ID NOs, respectively, in the Sequence Listing) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in C. *glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the

localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The MCT nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic and transport processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the MCT nucleic acid molecules of the invention may result in the production of MCT proteins having functional differences from the wild-type MCT proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention provides methods for screening molecules which modulate the activity of an MCT protein, either by interacting with the protein itself or a substrate or binding partner of the MCT protein, or by modulating the transcription or translation of an MCT nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more MCT proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the MCT protein is assessed.

There are a number of mechanisms by which the alteration of an MCT protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. Recovery of fine chemical compounds from large-scale cultures of *C. glutamicum* is

significantly improved if *C. glutamicum* secretes the desired compounds, since such compounds may be readily purified from the culture medium (as opposed to extracted from the mass of *C. glutamicum* cells). By either increasing the number or the activity of transporter molecules which export fine chemicals from the cell, it may be possible to increase the amount of the produced fine chemical which is present in the extracellular medium, thus permitting greater ease of harvesting and purification. Conversely, in order to efficiently overproduce one or more fine chemicals, increased amounts of the cofactors, precursor molecules, and intermediate compounds for the appropriate biosynthetic pathways are required. Therefore, by increasing the number and/or activity of transporter proteins involved in the import of nutrients, such as carbon sources (*i.e.*, sugars), nitrogen sources (*i.e.*, amino acids, ammonium salts), phosphate, and sulfur, it may be possible to improve the production of a fine chemical, due to the removal of any nutrient supply limitations on the biosynthetic process. Further, fatty acids and lipids are themselves desirable fine chemicals, so by optimizing the activity or increasing the number of one or more MCT proteins of the invention which participate in the biosynthesis of these compounds, or by impairing the activity of one or more MCT proteins which are involved in the degradation of these compounds, it may be possible to increase the yield, production, and/or efficiency of production of fatty acid and lipid molecules from *C. glutamicum.*

The engineering of one or more MCT genes of the invention may also result in MCT proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C .glutamicum*. For example, the normal biochemical processes of metabolism result in the production of a variety of waste products (*e.g.*, hydrogen peroxide and other reactive oxygen species) which may actively interfere with these same metabolic processes (for example, peroxynitrite is known to nitrate tyrosine side chains, thereby inactivating some enzymes having tyrosine in the active site (Groves, J.T. (1999) *Curr. Opin. Chem. Biol.* 3(2): 226-235). While these waste products are typically excreted, the *C. glutamicum* strains utilized for large-scale fermentative production are optimized for the overproduction of one or more fine chemicals, and thus may produce more waste products than is typical for a wild-type *C. glutamicum*. By optimizing the activity of one or more MCT proteins of the invention which are involved in the export of waste molecules, it may be possible to improve the

viability of the cell and to maintain efficient metabolic activity. Also, the presence of high intracellular levels of the desired fine chemical may actually be toxic to the cell, so by increasing the ability of the cell to secrete these compounds, one may improve the viability of the cell.

Further, the MCT proteins of the invention may be manipulated such that the relative amounts of various lipid and fatty acid molecules produced are altered. This may have a profound effect on the lipid composition of the membrane of the cell. Since each type of lipid has different physical properties, an alteration in the lipid composition of a membrane may significantly alter membrane fluidity. Changes in membrane fluidity can impact the transport of molecules across the membrane, which, as previously explicated, may modify the export of waste products or the produced fine chemical or the import of necessary nutrients. Such membrane fluidity changes may also profoundly affect the integrity of the cell; cells with relatively weaker membranes are more vulnerable in the large-scale fermentor environment to mechanical stresses which may damage or kill the cell. By manipulating MCT proteins involved in the production of fatty acids and lipids for membrane construction such that the resulting membrane has a membrane composition more amenable to the environmental conditions extant in the cultures utilized to produce fine chemicals, a greater proportion of the *C. glutamicum* cells should survive and multiply. Greater numbers of *C. glutamicum* cells in a culture should translate into greater yields, production, or efficiency of production of the fine chemical from the culture.

The aforementioned mutagenesis strategies for MCT proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated MCT nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any natural product of *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do

not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, and the sequence listing cited throughout this application are hereby incorporated by reference.

TABLE 1: GENES IN THE APPLICATION

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1	2	RXN03097	VV0062	3	557	AMMONIUM TRANSPORT SYSTEM
3	4	RXA02099	GR00630	6198	6470	AMMONIUM TRANSPORT SYSTEM
5	6	RXA00104	GR00014	15895	16650	CYSQ PROTEIN, ammonium transport protein

Polyketide Synthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
7	8	RXA01420	GR00416	775	17	4"-MYCAROSYL ISOVALERYL-COA TRANSFERASE (EC 2.-.-.-)
9	10	RXN02581	VV0098	30482	28623	POLYKETIDE SYNTHASE
11	12	F RXA02581	GR00741	1	1527	POLYKETIDE SYNTHASE
13	14	RXA02582	GR00741	1890	6719	PROBABLE POLYKETIDE SYNTHASE CY338.20
15	16	RXA01138	GR00318	1656	2072	ACTINORHODIN POLYKETIDE DIMERASE (EC -.-.-.-)
17	18	RXA01980	GR00573	1470	838	POLYKETIDE CYCLASE
19	20	RXN01007	VV0021	2572	866	FRNA
21	22	RXN00784	VV0103	27531	28265	FRNE

Fatty acid and lipid synthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
23	24	RXA02335	GR00672	550	2322	BIOTIN CARBOXYLASE (EC 6.3.4.14)
25	26	RXA02173	GR00641	7473	8924	ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA (EC 6.4.1.2)
27	28	RXA01764	GR00500	2178	3110	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
29	30	RXN02487	VV0007	6367	4664	LONG-CHAIN-FATTY-ACID--COA LIGASE (EC 6.2.1.3)
31	32	F RXA02487	GR00718	4937	4650	LONG-CHAIN-FATTY-ACID--COA LIGASE (EC 6.2.1.3)
33	34	F RXA02490	GR00720	817	5	LONG-CHAIN-FATTY-ACID--COA LIGASE (EC 6.2.1.3)
35	36	RXA01467	GR00422	920	1210	ACYL CARRIER PROTEIN
37	38	RXA00796	GR00212	202	5	Acyl carrier protein phosphodiesterase
39	40	RXA01897	GR00544	617	1159	Acyl carrier protein phosphodiesterase
41	42	RXN02809	VV0342	380	6	Acyl carrier protein phosphodiesterase
43	44	F RXA02809	GR00790	277	5	Acyl carrier protein phosphodiesterase
45	46	RXN00113	VV0129	103	5724	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41;
47	48	F RXA00113	GR00017	2	3295	FATTY-ACID SYNTHASE (EC 2.3.1.85)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
49	50	RXN03111	VV0084	6040	5	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14]
51	52	F RXA00158	GR00024	2088	4	FATTY ACID SYNTHASE (EC 2.3.1.85)
53	54	F RXA00572	GR00155	2	3832	FATTY ACID SYNTHASE (EC 2.3.1.85)
55	56	RXA02582	GR00741	1890	6719	PROBABLE POLYKETIDE SYNTHASE CY338.20
57	58	RXA02691	GR00754	15347	14541	FATTY ACYL RESPONSIVE REGULATOR
59	60	RXA00880	GR00242	6213	8057	LONG-CHAIN-FATTY-ACID--COA LIGASE (EC 6.2.1.3)
61	62	RXA01060	GR00296	9566	10489	OMEGA-3 FATTY ACID DESATURASE (EC 1.14.99.-)
63	64	RXN01722	VV0036	2938	1214	MEDIUM-CHAIN-FATTY-ACID--COA LIGASE (EC 6.2.1.-)
65	66	F RXA01722	GR00488	5746	4022	MEDIUM-CHAIN-FATTY-ACID--COA LIGASE (EC 6.2.1.-)
67	68	RXA01644	GR00456	9854	8577	CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE (EC 2.1.1.79)
69	70	RXA02029	GR00618	356	1669	CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE (EC 2.1.1.79)
71	72	RXA01801	GR00509	3396	2380	ENOYL-COA HYDRATASE (EC 4.2.1.17)
73	74	RXN02512	VV0171	16147	15185	LIPID A BIOSYNTHESIS LAUROYL ACYLTRANSFERASE (EC 2.3.1.-)
75	76	F RXA02512	GR00721	3303	4259	LIPID A BIOSYNTHESIS LAUROYL ACYLTRANSFERASE (EC 2.3.1.-)
77	78	RXA00899	GR00245	1599	2864	CARDIOLIPIN SYNTHETASE (EC 2.7.8.-)
79	80	RXN00819	VV0054	18127	19455	ACYL-COA DEHYDROGENASE (EC 1.3.99.-)
81	82	F RXA00819	GR00221	18	1007	ACYL-COA DEHYDROGENASE (EC 1.3.99.-)
83	84	F RXA01766	GR00500	4081	4371	ACYL-COA DEHYDROGENASE (EC 1.3.99.-)
85	86	RXN01762	VV0054	15318	13783	LONG-CHAIN-FATTY-ACID--COA LIGASE (EC 6.2.1.3)
87	88	F RXA01762	GR00500	1272	10	LONG-CHAIN-FATTY-ACID--COA LIGASE (EC 6.2.1.3)
89	90	RXA00681	GR00179	3405	2662	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
91	92	RXA00802	GR00214	3803	4516	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
93	94	RXA02133	GR00639	3	308	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
95	96	RXN01114	VV0182	9118	10341	3-KETOACYL-COA THIOLASE (EC 2.3.1.16)
97	98	F RXA01114	GR00308	2	793	3-KETOACYL-COA THIOLASE (EC 2.3.1.16)
99	100	RXA01894	GR00542	1622	2476	PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41)
101	102	RXA02599	GR00742	3179	3655	PHOSPHATIDYLGLYCEROPHOSPHATASE B (EC 3.1.3.27)
103	104	RXN02638	VV0098	54531	53656	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.51)
105	106	F RXA02638	GR00749	8	511	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.51)
107	108	RXA00856	GR00232	720	1256	CDP-DIACYLGLYCEROL--GLYCEROL-3-PHOSPHATE 3-PHOSPHATIDYLTRANSFERASE (EC 2.7.8.5)
109	110	RXA02511	GR00721	2621	3277	CDP-DIACYLGLYCEROL--GLYCEROL-3-PHOSPHATE 3-PHOSPHATIDYLTRANSFERASE (EC 2.7.8.5)
111	112	RXN02836	VV0102	32818	33372	KETOACYL REDUCTASE HETN (EC 1.3.1.-)
113	114	F RXA02836	GR00827	106	411	KETOACYL REDUCTASE HETN (EC 1.3.1.-)
115	116	RXA02578	GR00740	2438	3541	PUTATIVE ACYLTRANSFERASE
117	118	RXA02150	GR00639	18858	19658	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.51)
119	120	RXA00607	GR00160	1869	2249	POLY(3-HYDROXYALKANOATE) POLYMERASE (EC 2.3.1.-)
121	122	RXA02397	GR00698	1688	2683	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (EC 2.3.1.-)
123	124	RXN03110	VV0083	16568	17929	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
125	126	F RXA00660	GR00171	1027	5	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
127	128	RXA00801	GR00214	3138	3770	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
129	130	RXA00821	GR00221	1469	2311	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
131	132	RXN02966	VV0143	12056	13462	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
133	134	F RXA01833	GR00517	1666	260	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
135	136	RXA01853	GR00525	5561	5010	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
137	138	RXN02424	VV0116	10570	11169	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
139	140	F RXA02424	GR00706	808	428	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
141	142	RXN00419	VV0112	1024	266	ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
143	144	F RXA00419	GR00095	3	464	ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
145	146	F RXA00421	GR00096	565	723	ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
147	148	RXN02923	VV0088	3301	2564	ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
149	150	RXN02922	VV0321	11407	10328	ACYL-COA DEHYDROGENASE, SHORT-CHAIN SPECIFIC (EC 1.3.99.2)
151	152	RXN03065	VV0038	6237	6629	HOLO-[ACYL-CARRIER PROTEIN] SYNTHASE (EC 2.7.8.7)
153	154	RXN03132	VV0127	39053	39472	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (EC 2.3.1.-)
155	156	RXN03157	VV0188	1607	1170	LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS PROTEIN KDTB
157	158	RXN00934	VV0171	15181	14099	(AE000805) LPS biosynthesis RfbU related protein [Methanobacterium thermoautotrophicum]
159	160	RXN00792	VV0321	10328	9132	ACYL-COA DEHYDROGENASE, SHORT-CHAIN SPECIFIC (EC 1.3.99.2)
161	162	RXN00931	VV0171	13011	12166	ACYL-COA THIOESTERASE II (EC 3.1.2.-)
163	164	F RXA00931	GR00253	4959	4114	thioesterase II
165	166	RXN01421	VV0122	16024	15638	ACYLTRANSFERASE (EC 2.3.1.-)
167	168	RXN02342	VV0078	3460	4266	BIOTIN--[ACETYL-COA-CARBOXYLASE] SYNTHETASE (EC 6.3.4.15)
169	170	RXN00563	VV0038	1	2739	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14]
171	172	RXN02168	VV0100	2894	81	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14]
173	174	RXN01090	VV0155	6483	5686	KETOACYL REDUCTASE HETN (EC 1.3.1.-)
175	176	RXN02062	VV0222	3159	1990	Lipopolysaccharide N-acetylglucosaminyltransferase
177	178	RXN02148	VV0300	16561	17703	Lipopolysaccharide N-acetylglucosaminyltransferase
179	180	RXN02595	VV0098	11098	9935	Lipopolysaccharide N-acetylglucosaminyltransferase
181	182	RXS00148	VV0167	9849	12059	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
183	184	RXS00149	VV0167	7995	9842	METHYLMALONYL-COA MUTASE BETA-SUBUNIT (EC 5.4.99.2)
185	186	RXS02106	VV0123	22649	21594	LIPOATE-PROTEIN LIGASE A (EC 6.-.-.-)
187	188	RXS01746	VV0185	934	1686	LIPOATE-PROTEIN LIGASE B (EC 6.-.-.-)
189	190	RXS01747	VV0185	1826	2869	LIPOIC ACID SYNTHETASE
191	192	RXC01748	VV0185	3001	3780	protein involved in lipid metabolism
193	194	RXC00354	VV0135	33604	32792	Cytosolic Protein involved in lipid metabolism
195	196	RXC01749	VV0185	3953	5569	Membrane Spanning Protein involved in lipid metabolism

Fatty acid degradation

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
197	198	RXA02268	GR00655	2182	3081	LIPASE (EC 3.1.1.3)
199	200	RXA02269	GR00655	3094	4065	LIPASE (EC 3.1.1.3)
201	202	RXA01614	GR00449	8219	7197	LYSOPHOSPHOLIPASE L2 (EC 3.1.1.5)
203	204	RXA01983	GR00573	3559	3053	LIPASE (EC 3.1.1.3)
205	206	RXN02947	VV0078	1319	6	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
207	208	F RXA02320	GR00667	593	6	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
209	210	F RXA02851	GR00851	524	6	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
211	212	RXN02321	VV0078	3291	1663	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
213	214	F RXA02321	GR00667	1380	937	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
215	216	F RXA02343	GR00675	1403	1816	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
217	218	F RXA02850	GR00850	2	493	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
219	220	RXA02583	GR00741	6743	8290	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
221	222	RXA00870	GR00239	809	2320	METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE (ACYLATING) (EC 1.2.1.27) 2-Methyl-3-oxopropanoate:NAD+ oxidoreductase (CoA-propanoylating)
223	224	RXA01260	GR00367	2381	1200	LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
225	226	RXA01261	GR00367	2607	2437	LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
227	228	RXA01136	GR00318	685	1116	ISOVALERYL-COA DEHYDROGENASE (EC 1.3.99.10)
229	230	RXN00559	VV0103	7568	6552	PROTEIN VDLD
231	232	F RXA00559	GR00149	218	6	PROTEIN VDLD
233	234	RXA01580	GR00440	707	6	Glycerophosphoryl diester phosphodiesterase
235	236	RXA02677	GR00754	3119	3877	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46)
237	238	RXS01166	VV0117	18142	16838	EXTRACELLULAR LIPASE PRECURSOR (EC 3.1.1.3)

Terpenoid biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
239	240	RXA00875	GR00241	2423	1857	ISOPENTENYL-DIPHOSPHATE DELTA-ISOMERASE (EC 5.3.3.2)
241	242	RXA01292	GR00373	1204	2388	PHYTOENE DEHYDROGENASE (EC 1.3.-.-)
243	244	RXA01293	GR00373	2370	2696	PHYTOENE DEHYDROGENASE (EC 1.3.-.-)
245	246	RXA02310	GR00665	1132	2394	GERANYLGERANYL HYDROGENASE
247	248	RXA02718	GR00758	18539	19585	GERANYLGERANYL PYROPHOSPHATE SYNTHASE (EC 2.5.1.1)
249	250	RXA01067	GR00298	1453	2181	undecaprenyl-diphosphate synthase (EC 2.5.1.31)
251	252	RXA01269	GR00367	20334	19894	UNDECAPRENYL-PHOSPHATE GALACTOSEPHOSPHOTRANSFERASE (EC 2.7.8.6)
253	254	RXA01205	GR00346	3	533	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
255	256	RXA01576	GR00438	8053	8811	DOLICHYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE (EC 2.4.1.117)
257	258	RXN02309	VV0025	28493	29542	OCTAPRENYL-DIPHOSPHATE SYNTHASE (EC 2.5.1.-)
259	260	F RXA02309	GR00665	978	4	OCTAPRENYL-DIPHOSPHATE SYNTHASE (EC 2.5.1.-)
261	262	RXN00477	VV0086	38905	37262	PHYTOENE DEHYDROGENASE (EC 1.3.-.-)
263	264	F RXA00477	GR00119	13187	11544	PHYTOENE DEHYDROGENASE (EC 1.3.-.-)
265	266	RXA00478	GR00119	14020	13190	PHYTOENE SYNTHASE (EC 2.5.1.-)
267	268	RXA01291	GR00373	345	1277	PHYTOENE SYNTHASE (EC 2.5.1.-)
269	270	RXA00480	GR00119	17444	16329	FARNESYL DIPHOSPHATE SYNTHASE (EC 2.5.1.1) (EC 2.5.1.10)
271	272	RXS01879	VV0105	1505	573	isopentenyl-phosphate kinase (EC 2.7.4.-)
273	274	RXS02023	VV0160	3234	4001	P450 cytochrome,isopentenyltransf, ferridox
275	276	RXS00948	VV0107	4266	5384	12-oxophytodienoate reductase (EC 1.3.1.42)
277	278	RXS02228	VV0068	1876	2778	TRNA DELTA(2)-ISOPENTENYLPYROPHOSPHATE TRANSFERASE (EC 2.5.1.8)
279	280	RXC01971	VV0105	4545	3715	Metal-Dependent Hydrolase involved in metabolism of terpenoids
281	282	RXC02697	VV0017	31257	32783	membrane protein involved in metabolism of terpenoids

Table 1 (continued)

ABC-Transporter

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
283	284	RXN01946	VV0228	2	1276	Hypothetical ABC Transporter ATP-Binding Protein
285	286	F RXA01946	GR00559	1849	575	(AL021184) ABC transporter ATP binding protein [Mycobacterium tuberculosis]
287	288	RXN00164	VV0232	1782	94	Hypothetical ABC Transporter ATP-Binding Protein
289	290	F RXA00164	GR00025	1782	94	, P, G, R ATPase subunits of ABC transporters
291	292	RXN00243	VV0057	28915	27899	, P, G, R ATPase subunits of ABC transporters
293	294	F RXA00243	GR00037	930	4	, P, G, R ATPase subunits of ABC transporters
295	296	RXA00259	GR00039	8469	6268	, P, G, R ATPase subunits of ABC transporters
297	298	RXN00410	VV0086	51988	51323	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
299	300	F RXA00410	GR00092	829	164	, P, G, R ATPase subunits of ABC transporters
301	302	RXN00456	VV0076	6780	8156	, P, G, R ATPase subunits of ABC transporters
303	304	F RXA00456	GR00114	316	5	, P, G, R ATPase subunits of ABC transporters
305	306	F RXA00459	GR00115	1231	245	, P, G, R ATPase subunits of ABC transporters
307	308	RXN01604	VV0137	8117	7470	, P, G, R ATPase subunits of ABC transporters
309	310	F RXA01604	GR00448	2	607	, P, G, R ATPase subunits of ABC transporters
311	312	RXN02547	VV0057	27726	25588	, P, G, R ATPase subunits of ABC transporters
313	314	F RXA02547	GR00726	22055	19932	, P, G, R ATPase subunits of ABC transporters
315	316	RXN02571	VV0101	12331	13359	MALTOSE/MALTODEXTRIN TRANSPORT ATP-BINDING PROTEIN MALK
317	318	F RXA02571	GR00736	1469	2497	, P, G, R ATPase subunits of ABC transporters
319	320	RXN02074	VV0318	12775	11153	TRANSPORT ATP-BINDING PROTEIN CYDD
321	322	F RXA02074	GR00628	5798	4176	, P, G, R ATPase subunits of ABC transporters
323	324	RXA02095	GR00629	14071	15474	, P, G, R ATPase subunits of ABC transporters
325	326	RXA02225	GR00652	3156	2275	, P, G, R ATPase subunits of ABC transporters
327	328	RXA02253	GR00654	20480	21406	, P, G, R ATPase subunits of ABC transporters
329	330	RXN01881	VV0105	529	95	Hypothetical ABC Transporter ATP-Binding Protein
331	332	F RXA01881	GR00537	3092	3532	ATPase components of ABC transporters with duplicated ATPase domains
333	334	RXA00526	GR00136	1353	664	Hypothetical ABC Transporter ATP-Binding Protein
335	336	RXN00733	VV0132	1647	2531	Hypothetical ABC Transporter ATP-Binding Protein
337	338	F RXA00733	GR00197	411	4	Hypothetical ABC Transporter ATP-Binding Protein
339	340	RXA00735	GR00198	849	181	Hypothetical ABC Transporter ATP-Binding Protein
341	342	RXA00878	GR00242	3733	1871	Hypothetical ABC Transporter ATP-Binding Protein
343	344	RXN01191	VV0169	10478	12067	Hypothetical ABC Transporter ATP-Binding Protein
345	346	F RXA01191	GR00341	1571	165	Hypothetical ABC Transporter ATP-Binding Protein
347	348	RXN01212	VV0169	3284	4207	Hypothetical ABC Transporter ATP-Binding Protein
349	350	F RXA01212	GR00350	1	813	Hypothetical ABC Transporter ATP-Binding Protein
351	352	RXA02749	GR00764	4153	5028	Hypothetical ABC Transporter ATP-Binding Protein
353	354	RXA02224	GR00652	2271	475	Hypothetical ABC Transporter ATP-Binding Protein
355	356	RXN01602	VV0229	1109	2638	Hypothetical ABC Transporter ATP-Binding Protein
357	358	RXN02515	VV0087	962	1717	Hypothetical ABC Transporter ATP-Binding Protein
359	360	RXN00525	VV0079	26304	27566	Hypothetical ABC Transporter Permease Protein
361	362	RXN02096	VV0126	20444	22135	Hypothetical ABC Transporter Permease Protein
363	364	RXN00412	VV0086	53923	52844	Hypothetical Amino Acid ABC Transporter ATP-Binding Protein
365	366	RXN00411	VV0086	52844	52170	Hypothetical Amino Acid ABC Transporter Permease Protein
367	368	RXN02614	VV0313	5964	5236	TAURINE TRANSPORT ATP-BINDING PROTEIN TAUB
369	370	RXN02613	VV0313	5223	4267	TAURINE-BINDING PERIPLASMIC PROTEIN PRECURSOR

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
371	372	RXN00368	VV0226	2300	726	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA
373	374	F RXA00368	GR00076	1	579	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA
375	376	F RXA00370	GR00077	6	803	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA
377	378	RXN01285	VV0215	1780	1055	FERRIC ENTEROBACTIN TRANSPORT ATP-BINDING PROTEIN FEPC
379	380	RXN00523	VV0194	1363	338	FERRIC ENTEROBACTIN TRANSPORT PROTEIN FEPG
381	382	RXN01142	VV0077	5805	6302	NITRATE TRANSPORT ATP-BINDING PROTEIN NRTD
383	384	RXN01141	VV0077	4644	5468	NITRATE TRANSPORT PROTEIN NRTA
385	386	RXN01002	VV0106	8858	8055	PHOSPHONATES TRANSPORT ATP-BINDING PROTEIN PHNC
387	388	RXN01000	VV0106	7252	6407	PHOSPHONATES TRANSPORT SYSTEM PERMEASE PROTEIN PHNE
389	390	RXN01732	VV0106	9944	8895	PHOSPHONATES-BINDING PERIPLASMIC PROTEIN PRECURSOR
391	392	RXN03080	VV0045	1670	2449	FERRIC ENTEROBACTIN TRANSPORT ATP-BINDING PROTEIN FEPC
393	394	RXN03081	VV0045	2476	2934	FERRIENTEROBACTIN-BINDING PERIPLASMIC PROTEIN PRECURSOR
395	396	RXN03082	VV0045	3131	3451	FERRIENTEROBACTIN-BINDING PERIPLASMIC PROTEIN PRECURSOR

Other transporters

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
397	398	RXA02261	GR00654	30936	32291	AMMONIUM TRANSPORT SYSTEM
399	400	RXA02020	GR00613	1015	5	AROMATIC AMINO ACID TRANSPORT PROTEIN AROP
401	402	RXA00281	GR00043	4721	5404	BACITRACIN TRANSPORT ATP-BINDING PROTEIN BCRA
403	404	RXN00570	VV0147	855	4	BENZOATE MEMBRANE TRANSPORT PROTEIN
405	406	F RXA00570	GR00153	1	498	BENZOATE MEMBRANE TRANSPORT PROTEIN
407	408	RXN00571	VV0173	1298	42	BENZOATE MEMBRANE TRANSPORT PROTEIN
409	410	F RXA00571	GR00154	2	1186	BENZOATE MEMBRANE TRANSPORT PROTEIN
411	412	RXA00962	GR00268	2	667	BENZOATE MEMBRANE TRANSPORT PROTEIN
413	414	RXA02811	GR00792	177	560	BENZOATE MEMBRANE TRANSPORT PROTEIN
415	416	RXA02115	GR00635	2	1198	BENZOATE MEMBRANE TRANSPORT PROTEIN
417	418	RXN00590	VV0178	5043	6230	BRANCHED CHAIN AMINO ACID TRANSPORT SYSTEM II CARRIER PROTEIN
419	420	F RXA00590	GR00157	178	564	BRANCHED CHAIN AMINO ACID TRANSPORT SYSTEM II CARRIER PROTEIN
421	422	F RXA01538	GR00427	5040	5429	BRANCHED CHAIN AMINO ACID TRANSPORT SYSTEM II CARRIER PROTEIN
423	424	RXA01727	GR00489	1471	194	BRANCHED-CHAIN AMINO ACID TRANSPORT SYSTEM CARRIER PROTEIN
425	426	RXA00623	GR00163	6525	7862	C4-DICARBOXYLATE TRANSPORT PROTEIN
427	428	RXA01584	GR00441	55	597	CHROMATE TRANSPORT PROTEIN
429	430	RXA00852	GR00231	3137	2448	COBALT TRANSPORT ATP-BINDING PROTEIN CBIO
431	432	RXA00690	GR00181	1213	68	COBALT TRANSPORT PROTEIN CBIQ
433	434	RXA00827	GR00223	1319	567	COBALT TRANSPORT PROTEIN CBIQ
435	436	RXA00851	GR00231	2448	1840	COBALT TRANSPORT PROTEIN CBIQ
437	438	RXS03220				D-XYLOSE-PROTON SYMPORT
439	440	F RXA02762	GR00768	346	630	D-XYLOSE PROTON-SYMPORTER
441	442	RXN00092	VV0129	27509	26844	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
443	444	F RXA00092	GR00014	1	204	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
445	446	RXN03060	VV0030	6227	5376	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
447	448	F RXA02618	GR00745	1914	2351	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
449	450	F RXA02900	GR10040	2979	2128	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
451	452	RXS03212				GLYCINE BETAINE TRANSPORTER BETP
453	454	F RXA01591	GR00446	3	947	GLYCINE BETAINE TRANSPORTER BETP
455	456	RXN00201	VV0096	197	6	HIGH AFFINITY RIBOSE TRANSPORT PROTEIN RBSD
457	458	F RXA00201	GR00032	191	6	HIGH AFFINITY RIBOSE TRANSPORT PROTEIN RBSD
459	460	RXA01221	GR00354	2108	2833	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT ATP-BINDING PROTEIN BRAG
461	462	RXA01222	GR00354	2844	3542	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT ATP-BINDING PROTEIN LIVF
463	464	RXA01219	GR00354	151	1032	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PERMEASE PROTEIN LIVH
465	466	RXA01220	GR00354	1032	2108	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PERMEASE PROTEIN LIVM
467	468	RXA00091	GR00013	7762	8514	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
469	470	RXA00228	GR00032	29232	28642	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
471	472	RXA00346	GR00064	1054	1743	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
473	474	RXA00524	GR00135	779	1111	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
475	476	RXA01823	GR00516	591	1367	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
477	478	RXA02767	GR00770	1032	1814	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
479	480	RXA02792	GR00777	8581	7829	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
481	482	RXN02929	VV0090	36837	37874	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
483	484	F RXA01235	GR00358	1165	194	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
485	486	RXN02794	VV0134	10625	9552	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
487	488	F RXA01419	GR00415	888	1151	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
489	490	F RXA02794	GR00777	10172	9552	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
491	492	RXN03079	VV0045	644	1660	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
493	494	F RXA02865	GR10007	3832	2816	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
495	496	RXA00181	GR00028	3954	2383	PROLINE TRANSPORT SYSTEM
497	498	RXA00591	GR00158	229	1581	PROLINE/BETAINE TRANSPORTER
499	500	RXA01629	GR00453	3476	1965	PROLINE/BETAINE TRANSPORTER
501	502	RXA02030	GR00618	3072	1687	PROLINE/BETAINE TRANSPORTER
503	504	RXA00186	GR00028	12242	12988	SHORT-CHAIN FATTY ACIDS TRANSPORTER
505	506	RXA00187	GR00028	13097	13447	SHORT-CHAIN FATTY ACIDS TRANSPORTER
507	508	RXA01667	GR00464	703	1908	SODIUM/GLUTAMATE SYMPORT CARRIER PROTEIN
509	510	RXA02171	GR00641	6571	4919	SODIUM/PROLINE SYMPORTER
511	512	RXA00902	GR00245	4643	5875	SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN
513	514	RXA00941	GR00257	1999	683	sodium-dependent phosphate transport protein
515	516	RXN00449	VV0112	30992	32572	Sodium-Dicarboxylate Symport Protein
517	518	F RXA00449	GR00109	2040	1036	Sodium-Dicarboxylate Symport Protein
519	520	F RXA01755	GR00498	352	5	Sodium-Dicarboxylate Symport Protein
521	522	RXA00269	GR00041	1826	1038	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA
523	524	RXA00369	GR00076	583	1299	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA
525	526	RXA02073	GR00628	4176	2647	TRANSPORT ATP-BINDING PROTEIN CYDC
527	528	RXA01399	GR00409	1	1119	TRANSPORT ATP-BINDING PROTEIN CYDD
529	530	RXA01339	GR00389	8408	7164	TYROSINE-SPECIFIC TRANSPORT PROTEIN
531	532	RXA02527	GR00725	5519	6847	2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR
533	534	RXN00298	VV0176	40228	42072	HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN
535	536	F RXA00298	GR00048	4459	6303	Ectoine/Proline/Glycine betaine carrier ectP

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
537	538	RXA00596	GR00159	335	787	potassium efflux system protein phaE
539	540	RXA02364	GR00686	841	215	C4-DICARBOXYLATE-BINDING PERIPLASMIC PROTEIN PRECURSOR, transport protein
541	542	RXN01411	VV0050	26015	26779	SHIKIMATE TRANSPORTER
543	544	RXN00960	VV0075	1139	105	PROTON/SODIUM-GLUTAMATE SYMPORT PROTEIN
545	546	RXN02447	VV0107	14297	13203	GALACTOSE-PROTON SYMPORT
547	548	RXN02395	VV0176	16747	14858	GLYCINE BETAINE TRANSPORTER BETP
549	550	RXN02348	VV0078	6027	7910	KUP SYSTEM POTASSIUM UPTAKE PROTEIN
551	552	RXN00297	VV0176	38630	39541	Hypothetical Malonate Transporter
553	554	RXN03103	VV0070	845	1087	GLUTAMATE-BINDING PROTEIN PRECURSOR
555	556	RXN02993	VV0071	736	65	GLUTAMINE-BINDING PROTEIN
557	558	RXN00349	VV0135	35187	36653	Hypothetical Trehalose Transport Protein
559	560	RXN03095	VV0057	4056	4424	CADMIUM EFFLUX SYSTEM ACCESSORY PROTEIN HOMOLOG
561	562	RXN03160	VV0189	5150	5617	CHROMATE TRANSPORT PROTEIN
563	564	RXN02955	VV0176	8666	9187	DICARBOXYLATE TRANSPORTER
565	566	RXN03109	VV0082	659	6	HEMIN TRANSPORT SYSTEM PERMEASE PROTEIN HMUU
567	568	RXN02979	VV0149	2150	2383	MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR
569	570	RXN02987	VV0234	527	294	MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR
571	572	RXN03084	VV0048	900	1817	IRON(III) DICITRATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
573	574	RXN03183	VV0372	1	417	TREHALOSE/MALTOSE BINDING PROTEIN
575	576	RXN01139	VV0077	2776	1823	CATION EFFLUX SYSTEM PROTEIN CZCD
577	578	RXN00378	VV0223	8027	5418	Cation transport ATPases
579	580	RXN01338	VV0032	2	1903	CATION-TRANSPORTING ATPASE PACS (EC 3.6.1.-)
581	582	RXN00980	VV0149	2635	4428	CATION-TRANSPORTING P-TYPE ATPASE B (EC 3.6.1.-)
583	584	RXN00099	VV0129	18876	17704	CYANATE TRANSPORT PROTEIN CYNX
585	586	RXN02662	VV0315	1461	1724	DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC
587	588	RXN02442	VV0217	5970	6818	zinc transport system membrane protein
589	590	RXN02443	VV0217	6818	7771	zinc-binding periplasmic protein precursor
591	592	RXN00842	VV0138	8686	7487	BRANCHED CHAIN AMINO ACID TRANSPORT SYSTEM II CARRIER PROTEIN
593	594	F RXA00842	GR00228	3208	2009	Permeases
595	596	RXN00832	VV0180	3133	4182	CALCIUM/PROTON ANTIPORTER
597	598	RXN00466	VV0086	63271	64266	Ferrichrome transport proteins
599	600	RXN01936	VV0127	40116	41387	MACROLIDE-EFFLUX PROTEIN
601	602	RXN01995	VV0182	2139	3476	PUTATIVE 3-(3-HYDROXYPHENYL) PROPIONATE TRANSPORT PROTEIN
603	604	RXN00661	VV0142	9718	9029	PNUC PROTEIN

Permeases

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
605	606	RXN02566	VV0154	11823	13031	NUCLEOSIDE PERMEASE NUPG
607	608	F RXA02561	GR00732	664	5	NUCLEOSIDE PERMEASE NUPG
609	610	F RXA02566	GR00733	782	345	NUCLEOSIDE PERMEASE NUPG
611	612	RXA00051	GR00008	5770	7173	PROLINE-SPECIFIC PERMEASE PROY
613	614	RXA01172	GR00334	2687	4141	SULFATE PERMEASE
615	616	RXA02128	GR00637	2906	4600	SULFATE PERMEASE

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
617	618	RXA02634	GR00748	6045	7655	SULFATE PERMEASE
619	620	RXN02233	VV0068	6856	8142	URACIL PERMEASE
621	622	F RXA02233	GR00653	6856	8067	URACIL PERMEASE
623	624	RXN02372	VV0213	9311	11197	XANTHINE PERMEASE
625	626	F RXA02372	GR00688	6	560	XANTHINE PERMEASE
627	628	F RXA02377	GR00689	3336	4526	XANTHINE PERMEASE
629	630	RXA02676	GR00754	2697	1309	GLUCONATE PERMEASE
631	632	RXN00432	VV0112	14751	13267	NA(+)-LINKED D-ALANINE GLYCINE PERMEASE
633	634	F RXA00432	GR00100	1	891	NA(+)-LINKED D-ALANINE GLYCINE PERMEASE
635	636	F RXA00436	GR00101	45	569	NA(+)-LINKED D-ALANINE GLYCINE PERMEASE
637	638	RXA00847	GR00230	1829	381	OLIGOPEPTIDE-BINDING PROTEIN APPA PRECURSOR (permease)
639	640	RXN01382	VV0119	8670	9761	OLIGOPEPTIDE-BINDING PROTEIN OPPA PRECURSOR
641	642	F RXA01382	GR00405	1067	6	OLIGOPEPTIDE-BINDING PROTEIN OPPA PRECURSOR (permease)
643	644	RXA02659	GR00753	2	313	OLIGOPEPTIDE-BINDING PROTEIN OPPA PRECURSOR (permease)
645	646	RXN02933	VV0176	30042	29233	DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC
647	648	RXN02991	VV0072	618	4	GLUTAMINE TRANSPORT SYSTEM PERMEASE PROTEIN GLNP
649	650	RXN02992	VV0072	842	621	GLUTAMINE TRANSPORT SYSTEM PERMEASE PROTEIN GLNP
651	652	RXN02996	VV0069	1980	2648	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PERMEASE PROTEIN LIVH
653	654	RXN03126	VV0112	9894	9001	TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN TAGG
655	656	RXN00443	VV0112	21572	20769	MOLYBDATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
657	658	RXN00444	VV0112	20785	19949	MOLYBDENUM TRANSPORT SYSTEM PERMEASE PROTEIN MODB
659	660	RXN00193	VV0371	1	594	POTENTIAL STARCH DEGRADATION PRODUCTS TRANSPORT SYSTEM PERMEASE PROTEIN AMYD
661	662	RXN01298	VV0116	2071	1142	POTENTIAL STARCH DEGRADATION PRODUCTS TRANSPORT SYSTEM PERMEASE PROTEIN AMYD

Channel Proteins

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
663	664	RXA01737	GR00493	2913	3971	POTASSIUM CHANNEL PROTEIN
665	666	RXN02348	VV0078	6027	7910	KUP SYSTEM POTASSIUM UPTAKE PROTEIN
667	668	RXA02426	GR00707	2165	633	PROBABLE NA(+)/H(+) ANTIPORTER
669	670	RXN03164	VV0277	1586	2455	POTASSIUM CHANNEL BETA SUBUNIT
671	672	RXN00024	VV0127	64219	63275	POTASSIUM CHANNEL BETA SUBUNIT

Lipoprotein and Lipopolysaccharide synthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
673	674	RXN01164	VV0117	15894	14260	DOLICHOL-PHOSPHATE MANNOSYLTRANSFERASE (EC 2.4.1.83) / APOLIPOPROTEIN N-ACYLTRANSFERASE (EC 2.3.1.-)
675	676	RXN01168	VV0117	14224	13415	DOLICHOL-PHOSPHATE MANNOSYLTRANSFERASE (EC 2.4.1.83) / APOLIPOPROTEIN N-ACYLTRANSFERASE (EC 2.3.1.-)

TABLE 2 – Excluded Genes

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvat corboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," *Biochem. Biophys. Res. Commun.*, 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," *Appl. Microbiol. Biotechnol.*, 51(2):223-228 (1999)
AB018530	dtsR		Kimura, E. et al. "Molecular cloning of a novel gene, dtsR, which rescues the detergent sensitivity of a mutant derived from *Brevibacterium lactofermentum*," *Biosci. Biotechnol. Biochem.*, 60(10):1565-1570 (1996)
AB018531	dtsR1; dtsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	gltB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamolytransferase	
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	

Table 2 (continued)

AF038651	dciAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," *Microbiology,* 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," *Mol. Cells.,* 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," *Appl. Environ. Microbiol.,* 65(4)1530-1539 (1999)
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinate synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		

Table 2 (continued)

AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.*, 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete[i])	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum," *J. Bacteriol.*, 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzmye); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in Corynebacterium glutamicum; Isolation of genes involved in biochemical characterization of corresponding proteins," *FEMS Microbiol.*, 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol aceteyl transferase	
AJ224946	mqo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from Corynebacterium glutamicum," *Eur. J. Biochem.*, 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of Corynebacterium glutamicum: The channel is formed by a low molecular mass polypeptide," *Biochemistry,* 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al."Isolation and characterization of IS31831, a transposable element from Corynebacterium glutamicum," *Mol. Microbiol.*, 11(4):739-746 (1994)
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," *Microbiology,* 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87

Table 2 (continued)

E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94

Table 2 (continued)

E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08649		Aspartase	Kohama, K. et al "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-trypophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97

Table 2 (continued)

E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," *J. Bacteriol.*, 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," *FEMS Microbiol. Lett.*, 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," *J. Bacteriol.*, 175(17):5595-5603 (1993)
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," *PNAS USA*, 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," *FEMS Microbiol. Lett.*, 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," *J. Microbiol. Biotechnol.*, 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," *Appl. Environ. Microbiol.*, 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxr	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," *J. Bacteriol.*, 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," *J. Bacteriol.*, 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," *J. Bacteriol.*, 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene*, 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3'end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene*, 52:191-200 (1987)

Table 2 (continued)

M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," *Gene,* 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.,* 138:1167-1175 (1992)
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.,* 138:1167-1175 (1992)
M89931	aecD; brnQ; yhbw	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbw	Rossol, I. et al. "The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," *J. Bacteriol.,* 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," *Arch. Microbiol.,* 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," *Appl. Environ. Microbiol.,* 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 tpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; clgIIR	Putative type II 5-cytosoine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," *J. Bacteriol.,* 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," *Gene,* 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.,* 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.,* 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?;gamma glutamyl kinase;similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.,* 178(15):4412-4419 (1996)

Table 2 (continued)

U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of Methylobacillus flagellatum and Corynebacterium glutamicum," *Gene,* 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A Corynebacterium glutamicum gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," *Arch. Microbiol.,* 166(2);76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A Corynebacterium glutamicum gene conferring multidrug resistance in the heterologous host Escherichia coli," *J. Bacteriol.,* 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5''-aminoglycoside phosphotransferase	
U89648		Corynebacterium glutamicum unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the Brevibacterium lactofermentum tryptophan operon," *Nucleic Acids Res.,* 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of Corynebacterium glutamicum and possible mechanisms for modulation of its expression," *Mol. Gen. Genet.,* 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of Corynebacterium glutamicum: Molecular cloning, nucleotide sequence, and expression," *Mol. Gen. Genet.,* 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," *Plant. Mol. Biol.,* 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the Corynebacterium glutamicum fda gene: structural comparison of C. glutamicum fructose-1, 6-biphosphate aldolase to class I and class II aldolases," *Mol. Microbiol.,*
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from Corynebacterium glutamicum," *Nucleic Acids Res.,* 18(21):6421 (1990)
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.,* 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," *Mol. Microbiol.,* 4(11):1819-1830 (1990)

Table 2 (continued)

X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," *Nucleic Acids Res.*, 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," *Mol. Microbiol.*, 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.*, 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," *Mol. Microbiol.*, 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspertate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," *Mol. Gen. Genet.*, 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomeras," *J. Bacteriol.*, 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," *Mol. Microbiol.*, 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," *Mol. Microbiol.*, 5(12):2995-3005 (1991)
X66078	cop1	Ps1 protein	Joliff, G. et al. "Cloning and nucleotide sequence of the csp1 gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," *Mol. Microbiol.*, 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," *Microbiol.*, 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," *Mol. Microbiol.*, 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," *Mol. Microbiol.*, 14(3):571-581 (1994)

Table 2 (continued)

X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," *Appl. Environ. Microbiol.*, 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," *J. Bacteriol.*, 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," *Biochem. Biophys. Res. Commun.*, 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," *Appl. Microbiol. Biotechnol.*, 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," *J. Bacteriol.*, 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek*, 64:285-305 (1993)
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek*, 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from Corynebacterium glutamicum," *DNA Seq.*, 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase: sequence analysis," *Microbiology*, 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera Rhodococcus and Norcardia and evidence for the evolutionary origin of the genus Norcardia from within the radiation of Rhodococcus species," *Microbiol.*, 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronemeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of Corynebacterium glutamicum," *J. Bacteriol.*, 177(5):1152-1158 (1995)
X81379	dapE	Succinyldiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of Corynebacterium glutamicum complementing dapE of Escherichia coli," *Microbiology*, 40:3349-56 (1994)

Table 2 (continued)

X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus Corynebacterium deduced from analyses of small-subunit ribosomal DNA sequences," *Int. J. Syst. Bacteriol.*, 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.*, 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.*, 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus Corynebacterium based on 16S rRNA gene sequences," *Int. J. Syst. Bacteriol.*, 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann et al. "Functional analysis of sequences adjacent to dapE of C. glutamicum proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," *J. Bacteriol.*, 177(20):5991-5993 (1995)
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in Corynebacterium glutamicum: enzyme evolution in the early steps of the arginine pathway," *Microbiology*, 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase and acetate kinase," *Microbiology*, 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," *J. Bacteriol.*, 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)

Table 2 (continued)

X90360		Promoter fragment F22	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from C. glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of Corynebacterium glutamicum," *J. Biol. Chem.*, 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the Corynebacterium glutamicum betP gene, encoding the transport system for the compatible solute glycine betaine," *J. Bacteriol.*, 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of Corynebacterium glutamicum, encoding two enzymes involved in L-lysine synthesis," *Biotechnol. Lett.*, 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from Corynebacterium glutamicum," *Mol. Microbiol.*, 22(5):815-826 (1996)

Table 2 (continued)

X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," *Appl. Environ. Microbiol.*, 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," *Gene,* 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.*, 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," *Nucleic Acids Res.*, 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.*, 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," *Mol. Microbiol.*, 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," *Mol. Gen. Genet.*, 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," *Arch. Microbiol.*, 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," *Microbiology,* 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," *Appl. Microbiol. Biotechnol.*, 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynephage Phi-16: The construction of an integration vector," *Microbiol.*, 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.*, 180(22):6005-6012 (1998)

Table 2 (continued)

Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of Corynebacterium glutamicum glnA gene encoding glutamine synthetase I," *FEMS Microbiol. Lett.*, 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynephage 304L	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," *Virology*, 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in Brevibacterium lactofermentum: Regulation of argS-lysA cluster expression by arginine," *J. Bacteriol.*, 175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," *J. Bacteriol.*, 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," *Appl. Environ. Microbiol.*, 60(7)2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.*, 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al "The galE gene encoding the UDP-galactose 4-epimerase of Brevibacterium lactofermentum is coupled transcriptionally to the dmdR gene," *Gene*, 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.*, 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of Brevibacterium lactofermentum ATCC 13869," *Gene*, 170(1):91-94 (1996)

[1] A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	ammoniagenes	21054							
Brevibacterium	ammoniagenes	19350							
Brevibacterium	ammoniagenes	19351							
Brevibacterium	ammoniagenes	19352							
Brevibacterium	ammoniagenes	19353							
Brevibacterium	ammoniagenes	19354							
Brevibacterium	ammoniagenes	19355							
Brevibacterium	ammoniagenes	19356							
Brevibacterium	ammoniagenes	21055							
Brevibacterium	ammoniagenes	21077							
Brevibacterium	ammoniagenes	21553							
Brevibacterium	ammoniagenes	21580							
Brevibacterium	ammoniagenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							
Brevibacterium	flavum			B11477					
Brevibacterium	flavum			B11478					
Brevibacterium	flavum	21127							
Brevibacterium	flavum			B11474					
Brevibacterium	healii	15527							
Brevibacterium	ketoglutamicum	21004							
Brevibacterium	ketoglutamicum	21089							
Brevibacterium	ketosoreductum	21914							
Brevibacterium	lactofermentum				70				
Brevibacterium	lactofermentum				74				
Brevibacterium	lactofermentum				77				
Brevibacterium	lactofermentum	21798							
Brevibacterium	lactofermentum	21799							
Brevibacterium	lactofermentum	21800							
Brevibacterium	lactofermentum	21801							
Brevibacterium	lactofermentum			B11470					
Brevibacterium	lactofermentum			B11471					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							
Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujiokense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							
Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							
Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japen.

Table 4: Alignment Results

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rxa00051	1527	GB_HTG3:AC009685	210031	AC009685	Homo sapiens chromosome 15 clone 91_E_13 map 15, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Homo sapiens	34,247	29-Sep-99
		GB_HTG3:AC009685	210031	AC009685	Homo sapiens chromosome 15 clone 91_E_13 map 15, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Homo sapiens	34,247	29-Sep-99
		GB_HTG7:AC009511	271896	AC009511	Homo sapiens clone RP11-860B13, *** SEQUENCING IN PROGRESS ***, 59 unordered pieces.	Homo sapiens	35,033	09-DEC-1999
rxa00091	876	GB_BA1:D50453	146191	D50453	Bacillus subtilis DNA for 25-36 degree region containing the amyE-srfA region, complete cds.	Bacillus subtilis	54,452	10-Feb-99
		GB_BA1:SCI51	40745	AL109848	Streptomyces coelicolor cosmid I51.	Streptomyces coelicolor A3(2)	36,806	16-Aug-99
		GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	38,642	17-Apr-96
rxa00092	789	GB_BA1:SCH35	45396	AL078610	Streptomyces coelicolor cosmid H35.	Streptomyces coelicolor	49,934	4-Jun-99
		GB_HTG3:AC011498_0	312343	AC011498	Homo sapiens chromosome 19 clone CIT978SKB_50L17, *** SEQUENCING IN PROGRESS ***, 190 unordered pieces.	Homo sapiens	37,117	13-Dec-99
		GB_HTG3:AC011498_0	312343	AC011498	Homo sapiens chromosome 19 clone CIT978SKB_50L17, *** SEQUENCING IN PROGRESS ***, 190 unordered pieces.	Homo sapiens	37,117	13-Dec-99
rxa00104	879	GB_BA1:MTCY270	37586	Z95388	Mycobacterium tuberculosis H37Rv complete genome; segment 96/162.	Mycobacterium tuberculosis	36,732	10-Feb-99
		GB_PL2:T24M8	68251	AF077409	Arabidopsis thaliana BAC T24M8.	Arabidopsis thaliana	37,150	3-Aug-98
		GB_BA1:MTCY270	37586	Z95388	Mycobacterium tuberculosis H37Rv complete genome; segment 96/162.	Mycobacterium tuberculosis	42,874	10-Feb-99
rxa00113	5745	GB_BA1:MAFASGEN	10520	X87822	B.ammoniagenes FAS gene.	Corynebacterium ammoniagenes	68,381	03-OCT-1996
		GB_BA1:BAFASAA	10549	X64795	B.ammoniagenes FAS gene.	Corynebacterium ammoniagenes	57,259	14-OCT-1997
		GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	39,870	17-Jun-98
rxa00164	1812	GB_HTG2:HSJ1153D9	118360	AL109806	Homo sapiens chromosome 20 clone RP5-1153D9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,714	03-DEC-1999
		GB_HTG2:HSJ1153D9	118360	AL109806	Homo sapiens chromosome 20 clone RP5-1153D9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,714	03-DEC-1999
		GB_HTG2:HSJ1153D9	118360	AL109806	Homo sapiens chromosome 20 clone RP5-1153D9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,334	03-DEC-1999
rxa00181	1695	GB_BA1:CGPUTP	3791	Y09163	C.glutamicum putP gene.	Corynebacterium glutamicum	100,000	8-Sep-97
		GB_BA2:U32814	10393	U32814	Haemophilus influenzae Rd section 129 of 163 of the complete genome.	Haemophilus influenzae Rd	36,347	29-MAY-1998
		GB_BA1:CGPUTP	3791	Y09163	C.glutamicum putP gene.	Corynebacterium glutamicum	37,454	8-Sep-97
rxa00186	870	GB_PR3:AC004843	136655	AC004843	Homo sapiens PAC clone DJ0612F12 from 7p12-p14, complete sequence.	Homo sapiens	37,315	5-Nov-98

Table 4 (continued)

		GB_HTG2:HS745I14	133309	AL033532	Homo sapiens chromosome 1 clone RP4-745I14 map q23.1-24.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	38,129	03-DEC-1999
		GB_HTG2:HS745I14	133309	AL033532	Homo sapiens chromosome 1 clone RP4-745I14 map q23.1-24.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	38,129	03-DEC-1999
rxa00187	474	GB_GSS10:AQ184082	506	AQ184082	HS_3216_A1_G08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3216 Col=15 Row=M, genomic survey sequence.	Homo sapiens	37,297	1-Nov-98
		GB_GSS1:CNS008ZZ	1101	AL052951	Drosophila melanogaster genome survey sequence T7 end of BAC # BACR18L01 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	Drosophila melanogaster	34,120	3-Jun-99
		GB_GSS10:AQ184082	506	AQ184082	HS_3216_A1_G08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3216 Col=15 Row=M, genomic survey sequence.	Homo sapiens	39,655	1-Nov-98
rxa00201	292	GB_PR3:HSJ824F16	139330	AL050325	Human DNA sequence from clone 824F16 on chromosome 20, complete sequence.	Homo sapiens	34,520	23-Nov-99
		GB_BA1:RCSECA	2724	X89411	R.capsulatus DNA for secA gene.	Rhodobacter capsulatus	38,163	6-Jan-96
		GB_EST34:AV122904	242	AV122904	AV122904 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone 2610529H07, mRNA sequence.	Mus musculus	38,889	1-Jul-99
rxa00228	714	GB_EST15:AA486042	515	AA486042	ab40c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:843278 5', mRNA sequence.	Homo sapiens	37,500	06-MAR-1998
		GB_EST15:AA486042	515	AA486042	ab40c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:843278 5', mRNA sequence.	Homo sapiens	38,816	06-MAR-1998
rxa00243	1140	GB_PR2:CNS01DS5	101584	AL121655	BAC sequence from the SPG4 candidate region at 2p21-2p22, complete	Homo sapiens	37,001	29-Sep-99
		GB_HTG3:AC011408	79332	AC011408	Homo sapiens clone CIT978SKB_65D22, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.	Homo sapiens	38,040	06-OCT-1999
		GB_HTG3:AC011408	79332	AC011408	Homo sapiens clone CIT978SKB_65D22, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.	Homo sapiens	38,040	06-OCT-1999
rxa00259	2325	GB_HTG1:CEY62E10	254217	AL031580	Caenorhabditis elegans chromosome IV clone Y62E10, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	36,776	6-Sep-99
		GB_HTG1:CEY62E10	254217	AL031580	Caenorhabditis elegans chromosome IV clone Y62E10, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	36,776	6-Sep-99
		GB_PL2:YSCCHROMI	41988	L22015	Saccharomyces cerevisiae chromosome I centromere and right arm sequence.	Saccharomyces cerevisiae	39,260	05-MAR-1998
rxa00269	912	GB_HTG4:AC009974	219565	AC009974	Homo sapiens chromosome unknown clone NH0459I19, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	37,358	29-OCT-1999
		GB_HTG4:AC009974	219565	AC009974	Homo sapiens chromosome unknown clone NH0459I19, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	37,358	29-OCT-1999
		GB_BA1:AB017508	32050	AB017508	Bacillus halodurans C-125 genomic DNA, 32 kb fragment, complete cds.	Bacillus halodurans	44,622	14-Apr-99
rxa00281	766	GB_BA1:SCE8	24700	AL035654	Streptomyces coelicolor cosmid E8.	Streptomyces coelicolor	36,328	11-MAR-1999
		GB_BA1:SCU51332	3216	U51332	Streptomyces coelicolor histidine kinase homolog (absA1) and response regulator homolog (absA2) genes, complete cds.	Streptomyces coelicolor	39,089	14-Sep-96
		GB_HTG4:AC011122	187123	AC011122	Homo sapiens chromosome 8 clone 23_D_19 map 8, *** SEQUENCING IN PROGRESS ***, 27 ordered pieces.	Homo sapiens	38,658	14-OCT-1999

Table 4 (continued)

rxa00298	1968	GB_BA1:CGECTP	2719	AJ001436	Corynebacterium glutamicum ectP gene.	Corynebacterium glutamicum	100,000	20-Nov-98
		GB_BA1:CGECTP	2719	AJ001436	Corynebacterium glutamicum ectP gene.	Corynebacterium glutamicum	100,000	20-Nov-98
		GB_EST24:AI234006	432	AI234006	EST230694 Normalized rat lung, Bento Soares Rattus sp. cDNA clone RLUCU01 3' end, mRNA sequence.	Rattus sp.	46,552	31-Jan-99
rxa00346	813	GB_BA1:SC2E9	20850	AL021530	Streptomyces coelicolor cosmid 2E9.	Streptomyces coelicolor	43,267	28-Jan-98
		GB_BA1:SC9B1	24800	AL049727	Streptomyces coelicolor cosmid 9B1.	Streptomyces coelicolor	44,613	27-Apr-99
		GB_BA1:ECU70214	123171	U70214	Escherichia coli chromosome minutes 4-6.	Escherichia coli	39,490	21-Sep-96
rxa00368	1698	GB_BA2:AF065159	35209	AF065159	Bradyrhizobium japonicum putative arylsulfatase (arsA), putative soluble lytic transglycosylase precursor (sltA), dihydrodipicolinate synthase (dapA), MscL (mscL), SmpB (smpB), BcpB (bcpB), RnpO (rnpO), RelA/SpoT homolog (relA), PdxJ (pdxJ), and acyl carrier protein synthase AcpS (acpS) genes, complete cds; prokaryotic type I signal peptidase SipF (sipF) gene, sipF-sipS allele, complete cds; RNase III (rnc) gene, complete cds; GTP-binding protein Era (era) gene, partial cds; and unknown genes.	Bradyrhizobium japonicum	40,409	27-OCT-1999
		GB_BA1:AEOCHIT1	6861	D63139	Aeromonas sp. gene for chitinase, complete and partial cds.	Aeromonas sp. 10S-24	38,577	13-Feb-99
		GB_EST4:D62996	314	D62996	HUM347G01B Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-347G01 5', mRNA sequence.	Homo sapiens	41,613	29-Aug-95
rxa00369	817	GB_BA1:YP102KB	119443	AL031866	Yersinia pestis 102 kbases unstable region: from 1 to 119443.	Yersinia pestis	35,396	4-Jan-99
		GB_GSS8:AQ012142	501	AQ012142	8750H1A037010398 Cosmid library of chromosome II Rhodobacter sphaeroides genomic clone 8750H1A037010398, genomic survey sequence.	Rhodobacter sphaeroides	54,800	4-Jun-98
		GB_HTG2:AC005081	180096	AC005081	Homo sapiens clone RG270D13, *** SEQUENCING IN PROGRESS ***, 18 unordered pieces.	Homo sapiens	45,786	12-Jun-98
rxa00410	789	GB_BA1:ATPLOCC	8870	Z30328	A.tumefaciens Ti plasmid pTiAch5 genes for OccR, OccQ, OccM, OccP, OccT, OoxB, OoxA and ornithine cyclodeaminase.	Agrobacterium tumefaciens	46,490	10-OCT-1994
		GB_BA2:U67591	9829	U67591	Methanococcus jannaschii section 133 of 150 of the complete genome.	Methanococcus jannaschii	45,677	28-Jan-98
		GB_BA1:TIPOCCQMPJ	4350	M80607	Plasmid pTiA6 (from Agribacterium tumefaciens) periplasmic-type octopine permease (occR, occQ, occM, occP, and occJ) and lysR-type regulatory protein (occR) genes, complete cds.	Plasmid pTiA6	46,490	24-Apr-96
rxa00419	882	GB_BA2:MSU46844	16951	U46844	Mycobacterium smegmatis catalase-peroxidase (katG), putative arabinosyl transferase (embC, embA, embB), genes complete cds and putative propionyl-coA carboxylase beta chain (pccB) genes, partial cds.	Mycobacterium smegmatis	57,029	12-MAY-1997
		GB_EST28:AI513245	471	AI513245	GH13311.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH13311 3prime, mRNA sequence.	Drosophila melanogaster	37,696	16-MAR-1999
		GB_HTG4:AC010066	187240	AC010066	Drosophila melanogaster chromosome 3L/72A4 clone RPCI98-25O1, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces.	Drosophila melanogaster	39,607	16-OCT-1999
rxa00432	1608	GB_BA1:BSUB0015	218410	Z99118	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540.	Bacillus subtilis	49,810	26-Nov-97
		GB_PL1:CAC35A5	42565	AL033396	C.albicans cosmid Ca35A5.	Candida albicans	35,041	5-Nov-98
		GB_EST13:AA336266	378	AA336266	EST40981 Endometrial tumor Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	39,733	21-Apr-97

Table 4 (continued)

rxa00449	1704	GB_HTG2:AC008199	124050	AC008199	Drosophila melanogaster chromosome 3 clone BACR01K08 (D756) RPCI-98 01.K.8 map 94D-94D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces.	Drosophila melanogaster	38,392	2-Aug-99
		GB_HTG2:AC008199	124050	AC008199	Drosophila melanogaster chromosome 3 clone BACR01K08 (D756) RPCI-98 01.K.8 map 94D-94D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces.	Drosophila melanogaster	38,392	2-Aug-99
		GB_RO:RATLNKP2	177	M22337	Rat link protein gene, exon 2.	Rattus sp.	40,678	27-Apr-93
rxa00456	1500	GB_GSS1:FR0030597	476	AL026966	Fugu rubripes GSS sequence, clone 091C22aF9, genomic survey sequence.	Fugu rubripes	47,407	25-Jun-98
		GB_GSS5:AQ786587	556	AQ786587	HS_3086_B1_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3086 Col=9 Row=P, genomic survey sequence.	Homo sapiens	38,406	3-Aug-99
		GB_GSS14:AQ526586	434	AQ526586	HS_5198_B1_B03_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=774 Col=5 Row=D, genomic survey sequence.	Homo sapiens	36,951	11-MAY-1999
rxa00477	1767	GB_EST17:AA610489	407	AA610489	np93e05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133888 similar to gb:M11353 HISTONE H3.3 (HUMAN);, mRNA sequence.	Homo sapiens	41,791	09-DEC-1997
		GB_PR1:HSH33G4	1015	X05857	Human H3.3 gene exon 4.	Homo sapiens	38,182	24-Jan-96
		GB_EST30:AI637667	579	AI637667	tt10g11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2240420 3', mRNA sequence.	Homo sapiens	35,417	27-Apr-99
rxa00478	954	GB_HTG3:AC008708	83932	AC008708	Homo sapiens chromosome 5 clone CIT978SKB_78F1, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces.	Homo sapiens	38,769	3-Aug-99
		GB_HTG3:AC008708	83932	AC008708	Homo sapiens chromosome 5 clone CIT978SKB_78F1, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces.	Homo sapiens	38,769	3-Aug-99
		GB_HTG3:AC008708	83932	AC008708	Homo sapiens chromosome 5 clone CIT978SKB_78F1, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces.	Homo sapiens	36,797	3-Aug-99
rxa00480	1239	GB_HTG1:HSJ575L21	94715	AL096841	Homo sapiens chromosome 1 clone RP4-575L21, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	38,138	23-Nov-99
		GB_HTG1:HSJ575L21	94715	AL096841	Homo sapiens chromosome 1 clone RP4-575L21, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	38,138	23-Nov-99
		GB_RO:AC005960	158414	AC005960	Mus musculus chromosome 17 BAC citb20h22 from the MHC region, complete sequence.	Mus musculus	38,712	01-DEC-1998
rxa00524	433	GB_BA1:SCI51	40745	AL109848	Streptomyces coelicolor cosmid I51.	Streptomyces coelicolor A3(2)	40,284	16-Aug-99
		GB_BA2:AF082879	3434	AF082879	Yersinia enterocolitica ABC transporter enterochelin/enterobactin gene cluster, complete sequence.	Yersinia enterocolitica	55,634	20-OCT-1999
		GB_BA1:BSP132617	5192	AJ132617	Burkholderia sp. P-transporter operon and flanking genes.	Burkholderia sp.	40,793	13-Jul-99
rxa00526	813	GB_BA1:BSUB0008	208230	Z99111	Bacillus subtilis complete genome (section 8 of 21): from 1394791 to 1603020.	Bacillus subtilis	54,534	26-Nov-97
		GB_BA2:AF012285	46864	AF012285	Bacillus subtilis mobA-nprE gene region.	Bacillus subtilis	54,534	1-Jul-98
		GB_BA1:D90725	13796	D90725	Escherichia coli genomic DNA. (19.7 - 20.0 min).	Escherichia coli	51,481	7-Feb-99
rxa00559	1140	GB_BA2:CAU77910	3385	U77910	Corynebacterium ammoniagenes sequence upstream of the 5-phosphoribosyl-1-pyrophosphate amidotransferase (purF) gene.	Corynebacterium ammoniagenes	39,007	1-Jan-98
		GB_EST4:H34952	382	H34952	EST108261 Rat PC-12 cells, untreated Rattus sp. cDNA clone RPCCK07 similar to NADH-ubiquinone oxidoreductase complex I 23 kDa precursor (iron-sulfur protein), mRNA sequence.	Rattus sp.	39,267	2-Apr-98
		GB_BA2:AE000963	22014	AE000963	Archaeoglobus fulgidus section 144 of 172 of the complete genome.	Archaeoglobus fulgidus	38,338	15-DEC-1997

Table 4 (continued)

rxa00570	852	GB_GSS12:AQ422451	563	AQ422451	RPCI-11-185C3.TV RPCI-11 Homo sapiens genomic clone RPCI-11-185C3, genomic survey sequence.	Homo sapiens	38,767	23-MAR-1999
		GB_EST28:AI504741	568	AI504741	vl16c01.x1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:972384 3' similar to gb:Z14044 M.musculus mRNA for valosin-containing protein (MOUSE);, mRNA sequence.	Mus musculus	37,900	11-MAR-1999
		GB_EST18:AA712043	68	AA712043	vu29f10.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1182091 5' similar to gb:L05093 60S RIBOSOMAL PROTEIN L18A (HUMAN);, mRNA sequence.	Mus musculus	42,647	24-DEC-1997
rxa00571	1280	GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	38,468	17-Jun-98
		GB_PR3:AC005788	36224	AC005788	Homo sapiens chromosome 19, cosmid R26652, complete sequence.	Homo sapiens	36,911	06-OCT-1998
		GB_PR3:AC005338	34541	AC005338	Homo sapiens chromosome 19, cosmid R31646, complete sequence.	Homo sapiens	36,911	30-Jul-98
rxa00590	1288	GB_HTG6:AC010932	203273	AC010932	Homo sapiens chromosome 15 clone RP11-296E22 map 15, *** SEQUENCING IN PROGRESS ***, 36 unordered pieces.	Homo sapiens	37,242	30-Nov-99
		GB_HTG6:AC010932	203273	AC010932	Homo sapiens chromosome 15 clone RP11-296E22 map 15, *** SEQUENCING IN PROGRESS ***, 36 unordered pieces.	Homo sapiens	36,485	30-Nov-99
		GB_BA1:MSGB26CS	37040	L78816	Mycobacterium leprae cosmid B26 DNA sequence.	Mycobacterium leprae	39,272	15-Jun-96
rxa00591	1476	GB_IN1:CEK09E9	30098	Z79602	Caenorhabditis elegans cosmid K09E9, complete sequence.	Caenorhabditis elegans	34,092	2-Sep-99
		GB_PR4:AF135802	4965	AF135802	Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170 mRNA, complete cds.	Homo sapiens	36,310	9-Apr-99
		GB_PR4:AF104256	4365	AF104256	Homo sapiens transcriptional co-activator CRSP150 (CRSP150) mRNA, complete cds.	Homo sapiens	36,617	4-Feb-99
rxa00596	576	GB_PR3:AC004659	129577	AC004659	Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete	Homo sapiens	34,321	02-MAY-1998
		GB_PR3:AC004659	129577	AC004659	Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete	Homo sapiens	35,739	02-MAY-1998
		GB_PR1:HUMCBP2	2047	D83174	Human mRNA for collagen binding protein 2, complete cds.	Homo sapiens	40,404	6-Feb-99
rxa00607	504	GB_BA1:MTV010	3400	AL021186	Mycobacterium tuberculosis H37Rv complete genome; segment 119/162.	Mycobacterium tuberculosis	40,862	23-Jun-99
		GB_BA1:MTV010	3400	AL021186	Mycobacterium tuberculosis H37Rv complete genome; segment 119/162.	Mycobacterium tuberculosis	38,833	23-Jun-99
rxa00623	1461	GB_BA1:MTCY428	26914	Z81451	Mycobacterium tuberculosis H37Rv complete genome; segment 107/162.	Mycobacterium tuberculosis	60,552	17-Jun-98
		GB_BA1:RSPNGR234	34010	Z68203	Rhizobium sp. plasmid NGR234a DNA.	Rhizobium sp.	51,992	8-Aug-96
		GB_BA2:AE000101	10057	AE000101	Rhizobium sp. NGR234 plasmid pNGR234a, section 38 of 46 of the complete plasmid sequence.	Rhizobium sp. NGR234	51,992	12-DEC-1997
rxa00681								
rxa00690	1269	GB_HTG5:AC008338	136685	AC008338	Drosophila melanogaster chromosome X clone BACR30J04 (D908) RPCI-98 30.J.4 map 19C-19E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 93 unordered pieces.	Drosophila melanogaster	35,341	15-Nov-99
		GB_HTG4:AC009766	170502	AC009766	Homo sapiens chromosome 11 clone 404_A_03 map 11, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Homo sapiens	37,984	19-OCT-1999

Table 4 (continued)

		GB_HTG4:AC009766	170502	AC009766	Homo sapiens chromosome 11 clone 404_A_03 map 11, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Homo sapiens	37,984	19-OCT-1999
rxa00733	1008	GB_EST30:AU054038	245	AU054038	AU054038 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium discoideum cDNA clone SLK472, mRNA sequence.	Dictyostelium discoideum	43,265	28-Apr-99
		GB_EST30:AU054038	245	AU054038	AU054038 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium discoideum cDNA clone SLK472, mRNA sequence.	Dictyostelium discoideum	43,265	28-Apr-99
rxa00735	692	GB_BA1:MTCY50	36030	Z77137	Mycobacterium tuberculosis H37Rv complete genome; segment 55/162.	Mycobacterium tuberculosis	36,819	17-Jun-98
		GB_BA1:D90904	150894	D90904	Synechocystis sp. PCC6803 complete genome, 6/27, 630555-781448.	Synechocystis sp.	52,585	7-Feb-99
		GB_BA1:D90904	150894	D90904	Synechocystis sp. PCC6803 complete genome, 6/27, 630555-781448.	Synechocystis sp.	39,699	7-Feb-99
rxa00796	298	GB_GSS14:AQ579838	651	AQ579838	T135342b shotgun sub-library of BAC clone 31P06 Medicago truncatula genomic clone 31-P-06-C-054, genomic survey sequence.	Medicago truncatula	37,153	27-Sep-99
		GB_PR4:AC007625	174701	AC007625	Genomic sequence of Homo sapiens clone 2314F2 from chromosome 18, complete sequence.	Homo sapiens	38,014	30-Jun-99
		GB_EST14:AA427576	580	AA427576	zw54b04.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773839 3' similar to gb:M86852 PEROXISOME ASSEMBLY FACTOR-1 (HUMAN);, mRNA sequence.	Homo sapiens	42,731	16-OCT-1997
rxa00801	756	GB_BA1:MTV022	13025	AL021925	Mycobacterium tuberculosis H37Rv complete genome; segment 100/162.	Mycobacterium tuberculosis	59,350	17-Jun-98
		GB_RO:AC002109	160048	AC002109	Genomic sequence from Mouse 9, complete sequence.	Mus musculus	39,398	9-Sep-97
		GB_BA1:MTV022	13025	AL021925	Mycobacterium tuberculosis H37Rv complete genome; segment 100/162.	Mycobacterium tuberculosis	36,842	17-Jun-98
rxa00802	837	GB_GSS14:AQ563349	642	AQ563349	HS_5335_B2_A09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=911 Col=18 Row=B, genomic survey sequence.	Homo sapiens	37,649	29-MAY-1999
		GB_BA1:DIHCLPBA	2441	M32229	B.nodosus clpB gene encoding a regulatory subunit of ATP-dependent protease.	Dichelobacter nodosus	41,140	26-Apr-93
		GB_GSS3:B61538	698	B61538	T17M17TR TAMU Arabidopsis thaliana genomic clone T17M17, genomic survey sequence.	Arabidopsis thaliana	36,946	21-Nov-97
rxa00819	1452	GB_HTG3:AC008691_1	110000	AC008691	Homo sapiens chromosome 5 clone CIT978SKB_63A22, *** SEQUENCING IN PROGRESS ***, 253 unordered pieces.	Homo sapiens	38,270	3-Aug-99
		GB_HTG3:AC008691_1	110000	AC008691	Homo sapiens chromosome 5 clone CIT978SKB_63A22, *** SEQUENCING IN PROGRESS ***, 253 unordered pieces.	Homo sapiens	38,270	3-Aug-99
		GB_HTG3:AC009127	186591	AC009127	Homo sapiens chromosome 16 clone RPCI-11_498D10, *** SEQUENCING IN PROGRESS ***, 49 unordered pieces.	Homo sapiens	38,947	3-Aug-99
rxa00821	966	GB_HTG1:HS32B1	271488	AL023693	Homo sapiens chromosome 6 clone RP1-32B1, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,565	23-Nov-99
		GB_HTG1:HS32B1	271488	AL023693	Homo sapiens chromosome 6 clone RP1-32B1, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,565	23-Nov-99
		GB_PR3:AC004919	75547	AC004919	Homo sapiens PAC clone DJ0895B23 from UL, complete sequence.	Homo sapiens	34,346	19-Sep-98
rxa00827	876	GB_EST6:W06539	300	W06539	T2367 MVAT4 bloodstream form of serodeme WRATat1.1 Trypanosoma brucei rhodesiense cDNA 5', mRNA sequence.	Trypanosoma brucei rhodesiense	40,000	12-Aug-96
		GB_PR4:AC008179	181745	AC008179	Homo sapiens clone NH0576F01, complete sequence.	Homo sapiens	35,903	28-Sep-99

Table 4 (continued)

		GB_EST18:AA710415	533	AA710415	vt53f08.r1 Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone IMAGE:1166823 5', mRNA sequence.	Mus musculus	41,562	24-DEC-1997
rxa00842	1323	GB_PR2:AC002379	118595	AC002379	Human BAC clone GS165I04 from 7q21, complete sequence.	Homo sapiens	36,321	23-Jul-97
		GB_PR2:AC002379	118595	AC002379	Human BAC clone GS165I04 from 7q21, complete sequence.	Homo sapiens	37,284	23-Jul-97
		GB_IN1:CEF02D8	31624	Z78411	Caenorhabditis elegans cosmid F02D8, complete sequence.	Caenorhabditis elegans	38,163	23-Nov-98
rxa00847	1572	GB_OV:XELRDS38A	1209	L79915	Xenopus laevis rds/peripherin (rds38) mRNA, complete cds.	Xenopus laevis	36,044	30-Jul-97
		GB_HTG4:AC007920	234529	AC007920	Homo sapiens chromosome 3q27 clone RPCI11-208N14, *** SEQUENCING IN PROGRESS ***, 51 unordered pieces.	Homo sapiens	33,742	21-OCT-1999
		GB_HTG4:AC007920	234529	AC007920	Homo sapiens chromosome 3q27 clone RPCI11-208N14, *** SEQUENCING IN PROGRESS ***, 51 unordered pieces.	Homo sapiens	33,742	21-OCT-1999
rxa00851	732	GB_HTG2:AC004064	185000	AC004064	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.	Homo sapiens	39,833	9-Jul-98
		GB_HTG2:AC004064	185000	AC004064	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.	Homo sapiens	39,833	9-Jul-98
		GB_PR3:HSJ824F16	139330	AL050325	Human DNA sequence from clone 824F16 on chromosome 20, complete sequence.	Homo sapiens	39,833	23-Nov-99
rxa00852	813	GB_HTG3:AC010120	121582	AC010120	Drosophila melanogaster chromosome 3 clone BACR22N13 (D1061) RPCI-98 22.N.13 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces.	Drosophila melanogaster	36,855	24-Sep-99
		GB_HTG3:AC010120	121582	AC010120	Drosophila melanogaster chromosome 3 clone BACR22N13 (D1061) RPCI-98 22.N.13 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces.	Drosophila melanogaster	36,855	24-Sep-99
		GB_HTG2:AC006898	299308	AC006898	Caenorhabditis elegans clone Y73B6x, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces.	Caenorhabditis elegans	36,768	24-Feb-99
rxa00856								
rxa00870	1635	GB_BA1:STMMSDA	3986	L48550	Streptomyces coelicolor methylmalonic acid semialdehyde dehydrogenase (msdA) gene, complete cds.	Streptomyces coelicolor	63,743	09-MAY-1996
		GB_PAT:I92043	713	I92043	Sequence 10 from patent US 5726299.	Unknown.	38,850	01-DEC-1998
		GB_PAT:I78754	713	I78754	Sequence 10 from patent US 5693781.	Unknown.	38,850	3-Apr-98
rxa00875	690	GB_BA2:AF119715	549	AF119715	Escherichia coli isopentyl diphosphate isomerase (idi) gene, complete cds.	Escherichia coli	54,827	22-Apr-99
		GB_BA2:AE000372	12144	AE000372	Escherichia coli K-12 MG1655 section 262 of 400 of the complete genome.	Escherichia coli	51,416	12-Nov-98
		GB_BA1:ECU28375	55175	U28375	Escherichia coli K-12 genome; approximately 64 to 65 minutes.	Escherichia coli	51,416	08-DEC-1995
rxa00878	1986	GB_HTG2:AC007472	114003	AC007472	Drosophila melanogaster chromosome 2 clone BACR30D19 (D587) RPCI-98 30.D.19 map 49E-49F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 79 unordered pieces.	Drosophila melanogaster	36,592	2-Aug-99
		GB_HTG2:AC007472	114003	AC007472	Drosophila melanogaster chromosome 2 clone BACR30D19 (D587) RPCI-98 30.D.19 map 49E-49F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 79 unordered pieces.	Drosophila melanogaster	36,592	2-Aug-99
		GB_HTG2:AC006798	207370	AC006798	Caenorhabditis elegans clone Y51F8, *** SEQUENCING IN PROGRESS ***, 30 unordered pieces.	Caenorhabditis elegans	36,699	25-Feb-99

Table 4 (continued)

rxa00880	1968	GB_EST4:H22888	468	H22888	ym54e12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52158 5', mRNA sequence.	Homo sapiens	37,179	6-Jul-95
		GB_GSS13:AQ426858	516	AQ426858	CITBI-E1-2578F1.TF CITBI-E1 Homo sapiens genomic clone 2578F1, genomic survey sequence.	Homo sapiens	38,447	24-MAR-1999
		GB_PR1:AB002335	6289	AB002335	Human mRNA for KIAA0337 gene, complete cds.	Homo sapiens	35,799	13-Feb-99
rxa00899	1389	GB_BA1:NGU58849	2401	U58849	Neisseria gonorrhoeae pilS6 silent pilus locus.	Neisseria gonorrhoeae	40,623	20-Jun-96
		GB_BA1:PLPDHOS	3119	L06822	Plasmid pSa (from Escherichia coli) dihydropteroate synthase gene, 3' end.	Plasmid pSa	38,966	20-MAR-1996
		GB_BA1:PDGINTORF	6747	L06418	Integron In7 (from Plasmid pDGO100 from Escherichia coli) integrase (int), aminoglycoside adenylyltransferase (aad), quaternary ammonium compound-resistance protein, dihydrofolate reductase (dhfrX), and dihydropteroate synthase (sulI) genes.	Plasmid pDGO100	38,966	20-MAR-1996
rxa00902	1333	GB_GSS15:AQ606873	581	AQ606873	HS_5404_B2_H05_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=980 Col=10 Row=P, genomic survey sequence.	Homo sapiens	37,900	10-Jun-99
		GB_GSS9:AQ163442	658	AQ163442	nbxb0007A07f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0007A07f, genomic survey sequence.	Oryza sativa	41,885	12-Sep-98
		GB_PL1:PSST70	4974	X69213	P.sativum Psst70 gene for heat-shock protein.	Pisum sativum	36,866	3-Jul-96
rxa00931	969	GB_GSS1:FR0025208	612	AL018047	F.rubripes GSS sequence, clone 145D10aA8, genomic survey sequence.	Fugu rubripes	37,815	10-DEC-1997
		GB_GSS1:FR0021844	252	AL014715	F.rubripes GSS sequence, clone 069K22aG5, genomic survey sequence.	Fugu rubripes	37,698	10-DEC-1997
		GB_GSS12:AQ403344	593	AQ403344	HS_2257_B1_B03_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2257 Col=5 Row=D, genomic survey sequence.	Homo sapiens	31,552	13-MAR-1999
rxa00941	1440	GB_BA1:MTCY180	44201	Z97193	Mycobacterium tuberculosis H37Rv complete genome; segment 85/162.	Mycobacterium tuberculosis	37,902	17-Jun-98
		GB_BA1:MTCY180	44201	Z97193	Mycobacterium tuberculosis H37Rv complete genome; segment 85/162.	Mycobacterium tuberculosis	39,140	17-Jun-98
		GB_BA2:MSGKATG	1745	L14268	Mycobacterium tuberculosis ethyl methane sulphonate resistance protein (katG) gene, 3'end.	Mycobacterium tuberculosis	42,517	26-Aug-99
rxa00962	689	GB_HTG6:AC010998	144338	AC010998	Homo sapiens clone RP11-95I16, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.	Homo sapiens	39,497	08-DEC-1999
		GB_GSS1:GGA340111	990	AJ232089	Gallus gallus anonymous sequence from Cosmid mapping to chromosome 2 (Cosmid 34 - Contig 15), genomic survey sequence.	Gallus gallus	37,970	25-Aug-98
		GB_HTG6:AC010998	144338	AC010998	Homo sapiens clone RP11-95I16, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.	Homo sapiens	38,226	08-DEC-1999
rxa01060	1047	GB_BA1:ECTTN7	2280	AJ001816	Escherichia coli left end of transposon Tn7 including type 2 integron.	Escherichia coli	38,822	4-Nov-97
		GB_IN2:AF176377	8220	AF176377	Caenorhabditis briggsae CES-1 (ces-1) gene, complete cds; and CPN-1 (cpn-1) gene, partial cds.	Caenorhabditis briggsae	39,921	09-DEC-1999
		GB_GSS10:AQ196728	429	AQ196728	CIT-HSP-2381F4.TR CIT-HSP Homo sapiens genomic clone 2381F4, genomic survey sequence.	Homo sapiens	39,019	16-Sep-98
rxa01067	852	GB_BA1:U00016	42931	U00016	Mycobacterium leprae cosmid B1937.	Mycobacterium leprae	58,303	01-MAR-1994
		GB_BA1:SYCGROESL	3256	D12677	Synechocystis sp. groES and groEL genes.	Synechocystis sp.	34,593	3-Feb-99
		GB_BA1:D90905	139467	D90905	Synechocystis sp. PCC6803 complete genome, 7/27, 781449-920915.	Synechocystis sp.	34,593	7-Feb-99
rxa01114	1347	GB_BA1:PSEFAOAB	3480	D10390	P. fragi faoA and faoB genes, complete cds.	Pseudomonas fragi	51,919	2-Feb-99

Table 4 (continued)

		GB_BA1:AB014757	6057	AB014757	Pseudomonas sp. 61-3 genes for PhbR, acetoacetyl-CoA reductase, beta-ketothiolase and PHB synthase, complete cds.	Pseudomonas sp. 61-3	50,573	26-DEC-1998
		GB_BA1:SC8D9	38681	AL035569	Streptomyces coelicolor cosmid 8D9.	Streptomyces coelicolor	42,200	26-Feb-99
rxa01136	555	GB_EST11:AA244557	379	AA244557	mx07a01.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:679464 5', mRNA sequence.	Mus musculus	39,050	10-MAR-1997
		GB_EST14:AA407673	306	AA407673	EST01834 Mouse 7.5 dpc embryo ectoplacental cone cDNA library Mus musculus cDNA clone C0014F02 3', mRNA sequence.	Mus musculus	38,562	26-Aug-98
		GB_EST26:AI390328	604	AI390328	mx07a01.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:679464 5', mRNA sequence.	Mus musculus	33,136	2-Feb-99
rxa01138	540	GB_OV:XLXINT1	1278	X13138	Xenopus laevis int-1 mRNA for int-1 protein.	Xenopus laevis	40,038	31-MAR-1995
		GB_PR4:AC006054	143738	AC006054	Homo sapiens Xq28 BAC RPCI11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	37,996	1-Apr-99
		GB_PR4:AC006054	143738	AC006054	Homo sapiens Xq28 BAC RPCI11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	36,053	1-Apr-99
rxa01172	1578	GB_BA1:SCE39	23550	AL049573	Streptomyces coelicolor cosmid E39.	Streptomyces coelicolor	62,357	31-MAR-1999
		GB_BA1:MSU50335	5193	U50335	Mycobacterium smegmatis phage resistance (mpr) gene, complete cds.	Mycobacterium smegmatis	37,853	1-Feb-97
		GB_BA1:BACTHRTRNA	15467	D84213	Bacillus subtilis genome, trnl-feuABC region.	Bacillus subtilis	53,807	6-Feb-99
rxa01191	1713	GB_PR2:HS1191B2	60828	AL022237	Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribososmal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.	Homo sapiens	38,366	23-Nov-99
		GB_PR2:HS1191B2	60828	AL022237	Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribososmal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.	Homo sapiens	39,595	23-Nov-99
rxa01205	554	GB_BA1:MTCY373	35516	Z73419	Mycobacterium tuberculosis H37Rv complete genome; segment 57/162.	Mycobacterium tuberculosis	57,762	17-Jun-98
		GB_PL1:ATY12776	38483	Y12776	Arabidopsis thaliana DNA, 40 kb surrounding ACS1 locus.	Arabidopsis thaliana	32,971	7-Sep-98
		GB_PL2:ATT6K21	99643	AL021889	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSA project).	Arabidopsis thaliana	35,273	16-Aug-99
rxa01212	1047	GB_BA2:SCD25	41622	AL118514	Streptomyces coelicolor cosmid D25.	Streptomyces coelicolor A3(2)	39,654	21-Sep-99
		GB_BA1:SLGLYUB	2576	X65556	S.lividans tRNA-GlyU beta gene.	Streptomyces lividans	54,493	20-DEC-1993
		GB_BA1:SCH10	39524	AL049754	Streptomyces coelicolor cosmid H10.	Streptomyces coelicolor	44,638	04-MAY-1999
rxa01219	1005	GB_PAT:A68024	520	A68024	Sequence 19 from Patent WO9743409.	unidentified	42,553	05-MAY-1999
		GB_PAT:A68025	193	A68025	Sequence 20 from Patent WO9743409.	unidentified	43,229	05-MAY-1999
		GB_PAT:A68027	193	A68027	Sequence 22 from Patent WO9743409.	unidentified	38,342	05-MAY-1999

Table 4 (continued)

rxa01220	1200	GB_PR3:HS512B11	64356	AL031058	Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin I (DPI) gene, ESTs, STSs and GSSs, complete sequence.	Homo sapiens	35,478	23-Nov-99
		GB_EST6:N99239	424	N99239	zb76h11.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:309573 3', mRNA sequence.	Homo sapiens	39,623	20-Aug-96
		GB_EST16:AA554268	400	AA554268	nk36c09.s1 NCI_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1015600 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);, mRNA sequence.	Homo sapiens	36,111	8-Sep-97
rxa01221	849	GB_PR4:AF179633	96371	AF179633	Homo sapiens chromosome 16 map 16q23.3-q24.1 sequence.	Homo sapiens	40,199	5-Sep-99
		GB_VI:EHVU20824	184427	U20824	Equine herpesvirus 2, complete genome.	Equine herpesvirus 2	37,001	2-Feb-96
		GB_BA2:AE000407	10601	AE000407	Escherichia coli K-12 MG1655 section 297 of 400 of the complete genome.	Escherichia coli	39,471	12-Nov-98
rxa01222	822	GB_PAT:AR068625	28804	AR068625	Sequence 1 from patent US 5854034.	Unknown.	40,574	29-Sep-99
		GB_BA2:SSU51197	28804	U51197	Sphingomonas S88 sphingan polysaccharide synthesis (spsG), (spsS), (spsR), glycosyl transferase (spsQ), (spsI), glycosyl transferase (spsK), glycosyl transferase (spsL), (spsJ), (spsF), (spsD), (spsC), (spsE), Urf 32, Urf 26, ATP-binding cassette transporter (atrD), ATP-binding cassette transporter (atrB), glucosyl-isoprenylphosphate transferase (spsB), glucose-1-phosphate thymidylyltransferase (rhsA), dTDP-6-deoxy-D-glucose -3,5-epimerase (rhsC) dTDP-D-glucose-4,6-dehydratase (rhsB), dTDP-6-deoxy-L-mannose-dehydrogenase (rhsD), Urf 31, and Urf 34 genes, complete cds.	Sphingomonas sp. S88	40,574	16-MAY-1996
		GB_IN1:BBU44918	2791	U44918	Babesia bovis ATP-binding protein (babc) mRNA, complete cds.	Babesia bovis	39,228	9-Aug-97
rxa01260	1305	GB_BA1:CGLPD	1800	Y16642	Corynebacterium glutamicum lpd gene, complete CDS.	Corynebacterium glutamicum	99,923	1-Feb-99
		GB_BA1:MTV038	16094	AL021933	Mycobacterium tuberculosis H37Rv complete genome; segment 24/162.	Mycobacterium tuberculosis	59,056	17-Jun-98
		GB_PR3:AC005618	176714	AC005618	Homo sapiens chromosome 5, BAC clone 249h5 (LBNL H149), complete sequence.	Homo sapiens	36,270	5-Sep-98
rxa01261	294	GB_BA1:CGLPD	1800	Y16642	Corynebacterium glutamicum lpd gene, complete CDS.	Corynebacterium glutamicum	100,000	1-Feb-99
		GB_HTG4:AC010045	164829	AC010045	Drosophila melanogaster chromosome 3L/75A1 clone RPCI98-17C17, *** SEQUENCING IN PROGRESS ***, 50 unordered pieces.	Drosophila melanogaster	50,512	16-OCT-1999
		GB_HTG4:AC010045	164829	AC010045	Drosophila melanogaster chromosome 3L/75A1 clone RPCI98-17C17, *** SEQUENCING IN PROGRESS ***, 50 unordered pieces.	Drosophila melanogaster	50,512	16-OCT-1999
rxa01269	564	GB_BA2:AF125164	26443	AF125164	Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.	Bacteroides fragilis	56,071	01-DEC-1999
		GB_BA1:AB002668	24907	AB002668	Actinobacillus actinomycetemcomitans DNA for glycosyltransferase, lytic transglycosylase, dTDP-4-rhamnose reductase, complete cds.	Actinobacillus actinomycetemcomitans	46,679	21-Feb-98
		GB_BA1:AB010415	23112	AB010415	Actinobacillus actinomycetemcomitans gene cluster for 6-deoxy-L-talan synthesis, complete cds.	Actinobacillus actinomycetemcomitans	46,679	13-Feb-99
rxa01291	1056	GB_STS:AU027820	238	AU027820	Rattus norvegicus, OTSUKA clone, OT78.02/918b07, microsatellite sequence, sequence tagged site.	Rattus norvegicus	34,874	02-MAR-1999
		GB_STS:AU027820	238	AU027820	Rattus norvegicus, OTSUKA clone, OT78.02/918b07, microsatellite sequence, sequence tagged site.	Rattus norvegicus	34,874	02-MAR-1999

Table 4 (continued)

		GB_HTG3:AC006445	174547	AC006445	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	34,812	15-Sep-99
rxa01292	1308	GB_BA1:BSUB0017	217420	Z99120	Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.	Bacillus subtilis	37,802	26-Nov-97
		GB_HTG3:AC010580	121119	AC010580	Drosophila melanogaster chromosome 3 clone BACR48J06 (D1102) RPCI-98 48.J.6 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 71 unordered pieces.	Drosophila melanogaster	35,637	01-OCT-1999
		GB_HTG3:AC010580	121119	AC010580	Drosophila melanogaster chromosome 3 clone BACR48J06 (D1102) RPCI-98 48.J.6 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 71 unordered pieces.	Drosophila melanogaster	35,637	01-OCT-1999
rxa01293	450	GB_GSS8:AQ001809	705	AQ001809	CIT-HSP-2290D17.TF CIT-HSP Homo sapiens genomic clone 2290D17, genomic survey sequence.	Homo sapiens	42,021	26-Jun-98
		GB_GSS8:AQ001809	705	AQ001809	CIT-HSP-2290D17.TF CIT-HSP Homo sapiens genomic clone 2290D17, genomic survey sequence.	Homo sapiens	40,323	26-Jun-98
rxa01339	1111	GB_PL1:MGU60290	4614	U60290	Magnaporthe grisea nitrogen regulatory protein (NUT1) gene, complete cds.	Magnaporthe grisea	38,707	3-Jul-96
		GB_HTG3:AC011371	189187	AC011371	Homo sapiens chromosome 5 clone CIT978SKB_107C20, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces.	Homo sapiens	39,741	06-OCT-1999
		GB_HTG3:AC011371	189187	AC011371	Homo sapiens chromosome 5 clone CIT978SKB_107C20, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces.	Homo sapiens	39,741	06-OCT-1999
rxa01382	1192	GB_HTG4:AC009892	138122	AC009892	Homo sapiens chromosome 19 clone CIT978SKB_83J4, *** SEQUENCING IN PROGRESS ***, 6 ordered pieces.	Homo sapiens	40,154	31-OCT-1999
		GB_HTG4:AC009892	138122	AC009892	Homo sapiens chromosome 19 clone CIT978SKB_83J4, *** SEQUENCING IN PROGRESS ***, 6 ordered pieces.	Homo sapiens	40,154	31-OCT-1999
		GB_PR3:AC002416	128915	AC002416	Human Chromosome X, complete sequence.	Homo sapiens	37,521	29-Jan-98
rxa01399	1142	GB_EST9:AA096601	524	AA096601	mo03b09.r1 Stratagene mouse lung 937302 Mus musculus cDNA clone IMAGE:552473 5' similar to gb:L06505 60S RIBOSOMAL PROTEIN L12 (HUMAN); gb:L04280 Mus musculus ribosomal protein (MOUSE);, mRNA	Mus musculus	40,525	15-Feb-97
		GB_EST37:AI982114	626	AI982114	pat.pk0074.e9.f chicken activated T cell cDNA Gallus gallus cDNA clone pat.pk0074.e9.f 5' similar to H-ATPase B subunit, mRNA sequence.	Gallus gallus	37,785	15-Sep-99
		GB_OV:GGU20766	1645	U20766	Gallus gallus vacuolar H+-ATPase B subunit gene, complete cds.	Gallus gallus	38,244	07-DEC-1995
rxa01420	1065	GB_HTG2:AC005690	193424	AC005690	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	37,464	11-Apr-99
		GB_HTG2:AC005690	193424	AC005690	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	37,464	11-Apr-99
		GB_HTG2:AC006637	22092	AC006637	Caenorhabditis elegans clone F41B4, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces.	Caenorhabditis elegans	37,488	23-Feb-99
rxa01467	414	GB_HTG1:CEY102G3_	110000	AL020985	Caenorhabditis elegans chromosome V clone Y102G3, *** SEQUENCING IN	Caenorhabditis elegans	35,437	3-Dec-98
		GB_HTG1:CEY102G3_	110000	AL020985	Caenorhabditis elegans chromosome V clone Y102G3, *** SEQUENCING IN	Caenorhabditis elegans	35,437	3-Dec-98
		GB_HTG1:CEY113G7_	110000	AL031113	Caenorhabditis elegans chromosome V clone Y113G7, *** SEQUENCING IN	Caenorhabditis elegans	35,437	12-Jan-99
rxa01576	882	GB_BA2:AF030975	2511	AF030975	Aeromonas salmonicida chaperonin GroES and chaperonin GroEL genes, complete cds.	Aeromonas salmonicida	41,516	2-Apr-98
		GB_BA2:AF030975	2511	AF030975	Aeromonas salmonicida chaperonin GroES and chaperonin GroEL genes, complete cds.	Aeromonas salmonicida	38,171	2-Apr-98

Table 4 (continued)

		GB_EST22:AI068560	965	AI068560	mgae0003aC11f Magnaporthe grisea Appressorium Stage cDNA Library Pyricularia grisea cDNA clone mgae0003aC11f 5', mRNA sequence.	Pyricularia grisea	40,073	09-DEC-1999
rxa01580	840	GB_GSS14:AQ554460	681	AQ554460	RPCI-11-419F2.TV RPCI-11 Homo sapiens genomic clone RPCI-11-419F2, genomic survey sequence.	Homo sapiens	36,522	28-MAY-1999
		GB_IN2:AC005449	85518	AC005449	Drosophila melanogaster, chromosome 2R, region 44C4-44C5, P1 clone DS06765, complete sequence.	Drosophila melanogaster	36,609	23-DEC-1998
		GB_IN2:AC005449	85518	AC005449	Drosophila melanogaster, chromosome 2R, region 44C4-44C5, P1 clone DS06765, complete sequence.	Drosophila melanogaster	33,612	23-DEC-1998
rxa01584								
rxa01604	771	GB_HTG3:AC011352	160167	AC011352	Homo sapiens chromosome 5 clone CIT-HSPC_327F10, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Homo sapiens	33,688	06-OCT-1999
		GB_HTG3:AC011352	160167	AC011352	Homo sapiens chromosome 5 clone CIT-HSPC_327F10, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Homo sapiens	33,688	06-OCT-1999
		GB_HTG3:AC011402	168868	AC011402	Homo sapiens chromosome 5 clone CIT978SKB_38B5, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	33,688	06-OCT-1999
rxa01614	1146	GB_BA1:CGA224946	2408	AJ224946	Corynebacterium glutamicum DNA for L-Malate:quinone oxidoreductase.	Corynebacterium glutamicum	42,284	11-Aug-98
		GB_EST17:AA608825	439	AA608825	af03g07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030620 3' similar to TR:G976083 G976083 HISTONE H2A RELATED. ;, mRNA sequence.	Homo sapiens	40,092	02-MAR-1998
		GB_PR4:AC005377	102311	AC005377	Homo sapiens PAC clone DJ1136G02 from 7q32-q34, complete sequence.	Homo sapiens	37,811	28-Apr-99
rxa01629	1635	GB_BA1:CGPROPGEN	2936	Y12537	C.glutamicum proP gene.	Corynebacterium glutamicum	100,000	17-Nov-98
		GB_BA1:CGPROPGEN	2936	Y12537	C.glutamicum proP gene.	Corynebacterium glutamicum	100,000	17-Nov-98
		GB_PR4:AF191071	88481	AF191071	Homo sapiens chromosome 8 clone BAC 388D06, complete sequence.	Homo sapiens	35,612	11-OCT-1999
rxa01644	1401	GB_BA1:MSGB577COS	37770	L01263	M. leprae genomic dna sequence, cosmid b577.	Mycobacterium leprae	55,604	14-Jun-96
		GB_BA1:MLCB2407	35615	AL023596	Mycobacterium leprae cosmid B2407.	Mycobacterium leprae	36,416	27-Aug-99
		GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	55,844	24-Jun-99
rxa01667	1329	GB_BA1:CGU43536	3464	U43536	Corynebacterium glutamicum heat shock, ATP-binding protein (clpB) gene, complete cds.	Corynebacterium glutamicum	100,000	13-MAR-1997
		GB_HTG4:AC009841	164434	AC009841	Drosophila melanogaster chromosome 3L/77E1 clone RPCI98-13F11, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces.	Drosophila melanogaster	33,205	16-OCT-1999
		GB_HTG4:AC009841	164434	AC009841	Drosophila melanogaster chromosome 3L/77E1 clone RPCI98-13F11, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces.	Drosophila melanogaster	33,205	16-OCT-1999
rxa01722	1848	GB_GSS1:FR0022586	522	AL015452	F.rubripes GSS sequence, clone 077P23aB10, genomic survey sequence.	Fugu rubripes	40,192	10-DEC-1997
		GB_GSS1:FR0022584	485	AL015450	F.rubripes GSS sequence, clone 077P23aB11, genomic survey sequence.	Fugu rubripes	35,876	10-DEC-1997
		GB_IN1:CET26H2	37569	Z82055	Caenorhabditis elegans cosmid T26H2, complete sequence.	Caenorhabditis elegans	34,759	19-Nov-99

Table 4 (continued)

rxa01727	1401	GB_BA2:CORCSLYS	2821	M89931	Corynebacterium glutamicum beta C-S lyase (aecD) and branched-chain amino acid uptake carrier (brnQ) genes, complete cds, and hypothetical protein Yhbw (yhbw) gene, partial cds.	Corynebacterium glutamicum	99,929	4-Jun-98
		GB_HTG6:AC011037	167849	AC011037	Homo sapiens clone RP11-7F18, WORKING DRAFT SEQUENCE, 19 unordered pieces.	Homo sapiens	36,903	30-Nov-99
		GB_HTG6:AC011037	167849	AC011037	Homo sapiens clone RP11-7F18, WORKING DRAFT SEQUENCE, 19 unordered pieces.	Homo sapiens	35,642	30-Nov-99
rxa01737	1182	GB_BA1:SCGD3	33779	AL096822	Streptomyces coelicolor cosmid GD3.	Streptomyces coelicolor	38,054	8-Jul-99
		GB_HTG1:CNS01DSB	222193	AL121768	Homo sapiens chromosome 14 clone R-976B16, *** SEQUENCING IN PROGRESS ***, in ordered pieces.	Homo sapiens	35,147	05-OCT-1999
		GB_HTG1:CNS01DSB	222193	AL121768	Homo sapiens chromosome 14 clone R-976B16, *** SEQUENCING IN PROGRESS ***, in ordered pieces.	Homo sapiens	35,147	05-OCT-1999
rxa01762	1659	GB_BA1:MTCI28	36300	Z97050	Mycobacterium tuberculosis H37Rv complete genome; segment 10/162.	Mycobacterium tuberculosis	49,574	23-Jun-98
		GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	44,049	24-MAR-1999
		GB_BA1:SCE29	26477	AL035707	Streptomyces coelicolor cosmid E29.	Streptomyces coelicolor	40,246	12-MAR-1999
rxa01764	1056	GB_PL2:SPAC343	42947	AL109739	S.pombe chromosome I cosmid c343.	Schizosaccharomyces pombe	37,084	6-Sep-99
		GB_PL2:SPAC343	42947	AL109739	S.pombe chromosome I cosmid c343.	Schizosaccharomyces pombe	34,890	6-Sep-99
rxa01801	1140	GB_EST38:AW066306	334	AW066306	687009D03.y1 687 - Early embryo from Delaware Zea mays cDNA, mRNA sequence.	Zea mays	46,108	12-OCT-1999
		GB_GSS13:AQ484750	375	AQ484750	RPCI-11-248N4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-248N4, genomic survey sequence.	Homo sapiens	32,000	24-Apr-99
		GB_GSS13:AQ489971	252	AQ489971	RPCI-11-247N23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-247N23, genomic survey sequence.	Homo sapiens	36,111	24-Apr-99
rxa01823	900	GB_BA1:SCI51	40745	AL109848	Streptomyces coelicolor cosmid I51.	Streptomyces coelicolor A3(2)	35,779	16-Aug-99
		GB_BA1:ECU82598	136742	U82598	Escherichia coli genomic sequence of minutes 9 to 12.	Escherichia coli	39,211	15-Jan-97
		GB_BA1:BSUB0018	209510	Z99121	Bacillus subtilis complete genome (section 18 of 21): from 3399551 to 3609060.	Bacillus subtilis	36,999	26-Nov-97
rxa01853	675	GB_BA1:MTCY227	35946	Z77724	Mycobacterium tuberculosis H37Rv complete genome; segment 114/162.	Mycobacterium tuberculosis	37,612	17-Jun-98
		GB_HTG3:AC010189	265962	AC010189	Homo sapiens clone RPCI11-296K13, *** SEQUENCING IN PROGRESS ***, 80 unordered pieces.	Homo sapiens	39,006	16-Sep-99
		GB_HTG3:AC010189	265962	AC010189	Homo sapiens clone RPCI11-296K13, *** SEQUENCING IN PROGRESS ***, 80 unordered pieces.	Homo sapiens	39,006	16-Sep-99
rxa01881	558	GB_HTG4:AC011117	148447	AC011117	Homo sapiens chromosome 4 clone 173_C_09 map 4, *** SEQUENCING IN PROGRESS ***, 10 ordered pieces.	Homo sapiens	39,130	14-OCT-1999
		GB_HTG4:AC011117	148447	AC011117	Homo sapiens chromosome 4 clone 173_C_09 map 4, *** SEQUENCING IN PROGRESS ***, 10 ordered pieces.	Homo sapiens	39,130	14-OCT-1999
		GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	37,893	18-Jun-98

Table 4 (continued)

rxa01894	978	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	37,229	19-Jun-98
		GB_IN1:CELF46H5	38886	U41543	Caenorhabditis elegans cosmid F46H5.	Caenorhabditis elegans	38,525	29-Nov-96
		GB_HTG3:AC009204	115633	AC009204	Drosophila melanogaster chromosome 2 clone BACR03E19 (D1033) RPCI-98 03.E.19 map 36E-37C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 94 unordered pieces.	Drosophila melanogaster	31,579	18-Aug-99
rxa01897	666	GB_HTG1:CEY48B6	293827	AL021151	Caenorhabditis elegans chromosome II clone Y48B6, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	34,703	1-Apr-99
		GB_HTG1:CEY48B6	293827	AL021151	Caenorhabditis elegans chromosome II clone Y48B6, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	34,703	1-Apr-99
		GB_HTG1:CEY53F4_2	110000	Z92860	Caenorhabditis elegans chromosome II clone Y53F4, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	33,333	15-Oct-99
rxa01946	1298	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	65,560	17-Jun-98
		GB_BA1:SC5F2A	40105	AL049587	Streptomyces coelicolor cosmid 5F2A.	Streptomyces coelicolor	50,648	24-MAY-1999
		GB_BA1:SCARD1GN	2321	X84374	S.capreolus ard1 gene.	Streptomyces capreolus	44,973	23-Aug-95
rxa01980	756	GB_PL2:AC008262	99698	AC008262	Genomic sequence for Arabidopsis thaliana BAC F4N2 from chromosome I, complete sequence.	Arabidopsis thaliana	35,310	21-Aug-99
		GB_PL1:AB013388	73428	AB013388	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence.	Arabidopsis thaliana	35,505	20-Nov-99
		GB_PL1:AB013388	73428	AB013388	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence.	Arabidopsis thaliana	39,973	20-Nov-99
rxa01983	630	GB_HTG4:AC006467	175695	AC006467	Drosophila melanogaster chromosome 2 clone BACR03L08 (D532) RPCI-98 03.L.8 map 40A-40C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces.	Drosophila melanogaster	36,672	27-OCT-1999
		GB_HTG4:AC006467	175695	AC006467	Drosophila melanogaster chromosome 2 clone BACR03L08 (D532) RPCI-98 03.L.8 map 40A-40C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces.	Drosophila melanogaster	36,672	27-OCT-1999
		GB_HTG4:AC006467	175695	AC006467	Drosophila melanogaster chromosome 2 clone BACR03L08 (D532) RPCI-98 03.L.8 map 40A-40C strain y; cn bw sp, *** SEQUENCING IN PROGRESSo ***, 9 unordered pieces.	Drosophila melanogaster	32,367	27-OCT-1999
rxa02020	1111	GB_BA1:CGDNAAROP	2612	X85965	C.glutamicum ORF3 and aroP gene.	Corynebacterium glutamicum	100,000	30-Nov-97
		GB_PAT:A58887	1612	A58887	Sequence 1 from Patent WO9701637.	unidentified	100,000	06-MAR-1998
		GB_BA1:STYCARABA	4378	M95047	Salmonella typhimurium transport protein, complete cds, and transfer RNA-Arg.	Salmonella typhimurium	50,547	13-MAR-1996
rxa02029	1437	GB_HTG2:AC003023	104768	AC003023	Homo sapiens chromosome 11 clone pDJ363p2, *** SEQUENCING IN PROGRESS ***, 22 unordered pieces.	Homo sapiens	35,820	21-OCT-1997
		GB_HTG2:AC003023	104768	AC003023	Homo sapiens chromosome 11 clone pDJ363p2, *** SEQUENCING IN PROGRESS ***, 22 unordered pieces.	Homo sapiens	35,820	21-OCT-1997
		GB_HTG2:HS118B18	104729	AL034344	Homo sapiens chromosome 6 clone RP1-118B18 map p24.1-25.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	34,355	03-DEC-1999

Table 4 (continued)

rxa02030	1509	GB_PR4:AC007695	63247	AC007695	Homo sapiens 12q24 BAC RPCI11-124N23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	38,681	1-Sep-99
		GB_PR4:AC006464	99908	AC006464	Homo sapiens BAC clone NH0436C12 from 2, complete sequence.	Homo sapiens	35,445	22-OCT-1999
		GB_PR4:AC006464	99908	AC006464	Homo sapiens BAC clone NH0436C12 from 2, complete sequence.	Homo sapiens	35,968	22-OCT-1999
rxa02073	1653	GB_BA1:CGGDHA	2037	X72855	C.glutamicum GDHA gene.	Corynebacterium glutamicum	39,655	24-MAY-1993
		GB_BA1:CGGDH	2037	X59404	Corynebacterium glutamicum, gdh gen for glutamate dehydrogenase.	Corynebacterium glutamicum	44,444	30-Jul-99
		GB_BA2:SC2H4	25970	AL031514	Streptomyces coelicolor cosmid 2H4.	Streptomyces coelicolor A3(2)	38,452	19-OCT-1999
rxa02074								
rxa02095	1527	GB_EST18:AA703380	471	AA703380	zj12b06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:450035 3' similar to contains LTR5.t3 LTR5 repetitive element ;, mRNA sequence.	Homo sapiens	36,518	24-DEC-1997
		GB_HTG6:AC009769	122911	AC009769	Homo sapiens chromosome 8 clone RP11-202I12 map 8, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,473	07-DEC-1999
		GB_EST7:W70175	436	W70175	zd52c02.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:344258 5' similar to contains LTR5.b2 LTR5 repetitive element;, mRNA sequence.	Homo sapiens	34,174	16-OCT-1996
rxa02099	373	GB_BA1:CAJ10319	5368	AJ010319	Corynebacterium glutamicum amtP, glnB, glnD genes and partial ftsY and srp genes.	Corynebacterium glutamicum	100,000	14-MAY-1999
		GB_HTG3:AC011509	111353	AC011509	Homo sapiens chromosome 19 clone CITB-H1_2189E23, *** SEQUENCING IN PROGRESS ***, 35 unordered pieces.	Homo sapiens	33,423	07-OCT-1999
		GB_HTG3:AC011509	111353	AC011509	Homo sapiens chromosome 19 clone CITB-H1_2189E23, *** SEQUENCING IN PROGRESS ***, 35 unordered pieces.	Homo sapiens	33,423	07-OCT-1999
rxa02115	1197	GB_HTG5:AC010126	175986	AC010126	Homo sapiens clone GS502B02, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	36,717	13-Nov-99
		GB_HTG5:AC010126	175986	AC010126	Homo sapiens clone GS502B02, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	36,092	13-Nov-99
		GB_PR1:HUMHM145	2214	D10925	Human mRNA for HM145.	Homo sapiens	39,171	3-Feb-99
rxa02128	1818	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	38,682	17-Jun-98
		GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	35,746	17-Jun-98
		GB_GSS10:AQ161109	738	AQ161109	nbxb0006D03r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0006D03r, genomic survey sequence.	Oryza sativa	38,482	12-Sep-98
rxa02133	329	GB_BA2:MPAE000058	28530	AE000058	Mycoplasma pneumoniae section 58 of 63 of the complete genome.	Mycoplasma pneumoniae	32,317	18-Nov-96
		GB_HTG4:AC008308	151373	AC008308	Drosophila melanogaster chromosome 3 clone BACR10M16 (D743) RPCI-98 10.M.16 map 93C-93D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 186 unordered pieces.	Drosophila melanogaster	34,579	20-OCT-1999

Table 4 (continued)

		GB_HTG4:AC008308	151373	AC008308	Drosophila melanogaster chromosome 3 clone BACR10M16 (D743) RPCI-98 10.M.16 map 93C-93D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 186 unordered pieces.	Drosophila melanogaster	34,579	20-OCT-1999
rxa02150	924	GB_EST37:AW012260	358	AW012260	um06e09.y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2182312 5' similar to SW:AMPL_BOVIN P00727 CYTOSOL AMINOPEPTIDASE ;, mRNA sequence.	Mus musculus	39,385	10-Sep-99
		GB_GSS3:B87734	389	B87734	RPCI11-30D24.TP RPCI-11 Homo sapiens genomic clone RPCI-11-30D24, genomic survey sequence.	Homo sapiens	37,629	9-Apr-99
		GB_PR4:AC005042	192218	AC005042	Homo sapiens clone NH0552E01, complete sequence.	Homo sapiens	36,901	14-Jan-99
rxa02171	1776	GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome.	Rhodobacter capsulatus	53,714	12-MAY-1998
		GB_EST24:AI170522	367	AI170522	EST216450 Normalized rat lung, Bento Soares Rattus sp. cDNA clone RLUCO75 3' end, mRNA sequence.	Rattus sp.	44,186	20-Jan-99
		GB_PL1:PHVDLECA	1441	K03288	P.vulgaris phytohemagglutinin gene encoding erythroagglutinating phytohemagglutinin (PHA-E), complete cds.	Phaseolus vulgaris	39,103	27-Apr-93
rxa02173	1575	GB_BA1:CGGLTG	3013	X66112	C.glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	44,118	17-Feb-95
		GB_BA1:CGGLTG	3013	X66112	C.glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	36,189	17-Feb-95
		GB_BA2:AE000104	10146	AE000104	Rhizobium sp. NGR234 plasmid pNGR234a, section 41 of 46 of the complete plasmid sequence.	Rhizobium sp. NGR234	38,487	12-DEC-1997
rxa02224	1920	GB_BA2:CXU21300	8990	U21300	Corynebacterium striatum hypothetical protein YbhB gene, partial cds; ABC transporter TetB (tetB), ABC transporter TetA (tetA), transposase, 23S rRNA methyltransferase, and transposase genes, complete cds; and unknown genes.	Corynebacterium striatum	37,264	9-Apr-99
		GB_HTG3:AC009185	87184	AC009185	Homo sapiens chromosome 5 clone CIT-HSPC_248O19, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	36,459	07-OCT-1999
		GB_HTG3:AC009185	87184	AC009185	Homo sapiens chromosome 5 clone CIT-HSPC_248O19, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	36,459	07-OCT-1999
rxa02225	905	GB_BA2:MPAE000058	28530	AE000058	Mycoplasma pneumoniae section 58 of 63 of the complete genome.	Mycoplasma pneumoniae	35,498	18-Nov-96
		GB_EST26:AI337275	618	AI337275	tb96h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062245 3' similar to TR:Q15392 Q15392 ORF, COMPLETE CDS. ;, mRNA sequence.	Homo sapiens	35,589	18-MAR-1999
		GB_EST26:AI337275	618	AI337275	tb96h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062245 3' similar to TR:Q15392 Q15392 ORF, COMPLETE CDS. ;, mRNA sequence.	Homo sapiens	42,786	18-MAR-1999
rxa02233	1410	GB_BA1:ERWPNLB	1291	M65057	Erwinia carotovora pectin lyase (pnl) gene, complete cds.	Erwinia carotovora	37,780	26-Apr-93
		GB_EST30:AV021947	313	AV021947	AV021947 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA clone 1190024M23, mRNA sequence.	Mus musculus	39,423	28-Aug-99
		GB_EST33:AV087117	251	AV087117	AV087117 Mus musculus tongue C57BL/6J adult Mus musculus cDNA clone 2310028C15, mRNA sequence.	Mus musculus	47,410	25-Jun-99
rxa02253	1050	GB_EST11:AA250210	532	AA250210	mx79g10.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:692610 5' similar to TR:E236517 E236517 F44G4.1 ;, mRNA sequence.	Mus musculus	36,136	12-MAR-1997
		GB_EST11:AA250210	532	AA250210	mx79g10.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:692610 5' similar to TR:E236517 E236517 F44G4.1 ;, mRNA sequence.	Mus musculus	36,202	12-MAR-1997

Table 4 (continued)

rxa02261	1479	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_BA1:CGAMTGENE	2028	X93513	C.glutamicum amt gene.	Corynebacterium glutamicum	100,000	29-MAY-1996
		GB_BA1:CORPEPC	4885	M25819	C.glutamicum phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
rxa02268	1023	GB_PL2:AF087130	3478	AF087130	Neurospora crassa siderophore regulation protein (sre) gene, complete cds.	Neurospora crassa	39,268	22-OCT-1998
		GB_EST30:AI663709	408	AI663709	ud47a06.y1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone IMAGE:1449010 5' similar to TR:O75585 O75585 MITOGEN- AND STRESS-ACTIVATED PROTEIN KINASE-2 :, mRNA sequence.	Mus musculus	41,523	10-MAY-1999
		GB_RO:AF074714	3120	AF074714	Mus musculus mitogen- and stress-activated protein kinase-2 (mMSK2) mRNA, complete cds.	Mus musculus	38,347	24-OCT-1998
rxa02269	1095	GB_GSS4:AQ742825	847	AQ742825	HS_5482_B2_A04_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1058 Col=8 Row=B, genomic survey sequence.	Homo sapiens	37,703	16-Jul-99
		GB_HTG3:AC009293	162944	AC009293	Homo sapiens chromosome 18 clone 53_I_06 map 18, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Homo sapiens	37,006	13-Aug-99
		GB_HTG3:AC009293	162944	AC009293	Homo sapiens chromosome 18 clone 53_I_06 map 18, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Homo sapiens	37,006	13-Aug-99
rxa02309	1173	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	52,344	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	52,344	03-DEC-1996
		GB_HTG2:AC007163	186618	AC007163	Homo sapiens clone NH0091M05, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces.	Homo sapiens	37,263	23-Apr-99
rxa02310	1386	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	36,861	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	36,861	03-DEC-1996
		GB_PR3:HS279N11	169998	Z98255	Human DNA sequence from PAC 279N11 on chromosome Xq11.2-13.3.	Homo sapiens	34,516	23-Nov-99
rxa02321	1752	GB_BA1:AB018531	4961	AB018531	Corynebacterium glutamicum dtsR1 and dtsR2 genes, complete cds.	Corynebacterium glutamicum	99,030	19-OCT-1998
		GB_PAT:E17019	4961	E17019	Brevibacterium lactofermentum dtsR and dtsR2 genes.	Corynebacterium glutamicum	98,973	28-Jul-99
		GB_BA1:AB018530	2855	AB018530	Corynebacterium glutamicum dtsR gene, complete cds.	Corynebacterium glutamicum	99,030	19-OCT-1998
rxa02335	1896	GB_BA1:CGU35023	3195	U35023	Corynebacterium glutamicum thiosulfate sulfurtransferase (thtR) gene, partial cds, acyl CoA carboxylase (accBC) gene, complete cds.	Corynebacterium glutamicum	99,947	16-Jan-97
		GB_BA1:U00012	33312	U00012	Mycobacterium leprae cosmid B1308.	Mycobacterium leprae	40,247	30-Jan-96
		GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	67,568	10-Feb-99
rxa02364	750	GB_BA1:AP000006	319000	AP000006	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7).	Pyrococcus horikoshii	36,130	8-Feb-99
		GB_BA1:AP000006	319000	AP000006	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7).	Pyrococcus horikoshii	34,543	8-Feb-99

Table 4 (continued)

rxa02372	2010	GB_HTG3:AC011461	100974	AC011461	Homo sapiens chromosome 19 clone CIT-HSPC_429L19, *** SEQUENCING IN PROGRESS ***, 4 ordered pieces.	Homo sapiens	36,138	07-OCT-1999
		GB_HTG3:AC011461	100974	AC011461	Homo sapiens chromosome 19 clone CIT-HSPC_429L19, *** SEQUENCING IN PROGRESS ***, 4 ordered pieces.	Homo sapiens	36,138	07-OCT-1999
		GB_EST21:AA992021	279	AA992021	ot36c01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618848 3', mRNA sequence.	Homo sapiens	41,219	3-Jun-98
rxa02397	1119	GB_HTG4:AC009273	76175	AC009273	Arabidopsis thaliana chromosome 1 clone T1N6, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Arabidopsis thaliana	38,566	12-OCT-1999
		GB_HTG4:AC009273	76175	AC009273	Arabidopsis thaliana chromosome 1 clone T1N6, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Arabidopsis thaliana	38,566	12-OCT-1999
		GB_BA1:D90826	19493	D90826	E.coli genomic DNA, Kohara clone #335(40.9-41.3 min.).	Escherichia coli	39,600	21-MAR-1997
rxa02424	723	GB_EST13:AA334108	275	AA334108	EST38262 Embryo, 9 week Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	38,603	21-Apr-97
		GB_PR3:AC005224	166687	AC005224	Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.	Homo sapiens	36,111	14-Aug-98
		GB_PR3:AC005224	166687	AC005224	Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.	Homo sapiens	33,427	14-Aug-98
rxa02426	1656	GB_PAT:A06664	1350	A06664	B.stearothermophilus lct gene.	Bacillus stearothermophilus	39,936	29-Jul-93
		GB_PAT:A04115	1361	A04115	B.stearothermophilus recombinant lct gene.	synthetic construct	40,042	17-Feb-97
		GB_BA1:BACLDHL	1361	M14788	B.stearothermophilus lct gene encoding L-lactate dehydrogenase, complete cds.	Bacillus stearothermophilus	40,338	26-Apr-93
rxa02487	1827	GB_BA2:AF007101	32870	AF007101	Streptomyces hygroscopicus putative pteridine-dependent dioxygenase, PKS modules 1,2,3 and 4, and putative regulatory protein genes, complete cds and putative hydroxylase gene, partial cds.	Streptomyces hygroscopicus	43,298	13-Jan-98
		GB_BA1:MTCI364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162.	Mycobacterium tuberculosis	44,352	17-Jun-98
		GB_BA2:AF119621	15986	AF119621	Pseudomonas abietaniphila BKME-9 DitI (ditI), dioxygenase DitA oxygenase component small subunit (ditA2), dioxygenase DitA oxygenase component large subunit (ditA1), DitH (ditH), DitG (ditG), DitF (ditF), DitR (ditR), DitE (ditE), DitD (ditD), aromatic diterpenoid extradiol ring-cleavage dioygenase (ditC), DitB (ditB), and dioxygenase DitA ferredoxin component (ditA3) genes, complete cds; and unknown genes.	Pseudomonas abietaniphila	43,611	28-Apr-99
rxa02511	780	GB_PR4:AC002470	235395	AC002470	Homo sapiens Chromosome 22q11.2 BAC Clone b135h6 In BCRL2-GGT Region, complete sequence.	Homo sapiens	37,971	30-Nov-99
		GB_PR4:AC002472	147100	AC002472	Homo sapiens Chromosome 22q11.2 PAC Clone p_n5 In BCRL2-GGT Region, complete sequence.	Homo sapiens	38,239	13-Sep-99
		GB_EST34:AI806938	118	AI806938	wf24b07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356501 3' similar to SW:PLZF_HUMAN Q05516 ZINC FINGER PROTEIN PLZF ;, mRNA sequence.	Homo sapiens	38,983	7-Jul-99
rxa02512	1086	GB_BA1:MTCY1A10	25949	Z95387	Mycobacterium tuberculosis H37Rv complete genome; segment 117/162.	Mycobacterium tuberculosis	37,407	17-Jun-98
		GB_BA1:MLCL581	36225	Z96801	Mycobacterium leprae cosmid L581.	Mycobacterium leprae	43,193	24-Jun-97
		GB_OV:GGU43396	2738	U43396	Gallus gallus tropomyosin receptor kinase A (ctrkA) mRNA, complete cds.	Gallus gallus	38,789	18-Jan-96
rxa02527	1452	GB_BA2:AF008220	220060	AF008220	Bacillus subtilis rrnB-dnaB genomic region.	Bacillus subtilis	37,395	4-Feb-98

Table 4 (continued)

		GB_BA2:AF008220	220060	AF008220	Bacillus subtilis rrnB-dnaB genomic region.	Bacillus subtilis	36,218	4-Feb-98
		GB_HTG2:AC005861	112369	AC005861	Arabidopsis thaliana clone F23B24, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces.	Arabidopsis thaliana	38,407	29-Apr-99
rxa02547	2262	GB_PL1:AB006530	7344	AB006530	Citrullus lanatus Sat gene for serine acetyltransferase, complete cds and 5'-flanking region.	Citrullus lanatus	35,449	20-Aug-97
		GB_PL1:CNASA	5729	D85624	Citrullus vulgaris serine acetyltransferase (Sat) DNA, complete cds.	Citrullus lanatus	35,449	6-Feb-99
		GB_PL1:AB006530	7344	AB006530	Citrullus lanatus Sat gene for serine acetyltransferase, complete cds and 5'-flanking region.	Citrullus lanatus	34,646	20-Aug-97
rxa02566	1332	GB_EST32:AI727189	619	AI727189	BNLGHi7498 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AB020715) KIAA0908 protein [Homo sapiens], mRNA sequence.	Gossypium hirsutum	35,099	11-Jun-99
		GB_BA1:CGPUTP	3791	Y09163	C.glutamicum putP gene.	Corynebacterium glutamicum	38,562	8-Sep-97
		GB_PL2:SPAC13G6	33481	Z54308	S.pombe chromosome I cosmid c13G6.	Schizosaccharomyces pombe	35,774	18-OCT-1999
rxa02571	1152	GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	41,872	9-Apr-97
		GB_EST35:AI857385	488	AI857385	wl55e03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2428828 3', mRNA sequence.	Homo sapiens	39,139	26-Aug-99
		GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	38,552	9-Apr-97
rxa02578	1227	GB_PL1:AB016871	79109	AB016871	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16L22, complete sequence.	Arabidopsis thaliana	34,213	20-Nov-99
		GB_PL1:AB025602	55790	AB025602	Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:F14A1, complete sequence.	Arabidopsis thaliana	36,461	20-Nov-99
		GB_IN1:CELF36H9	35985	AF016668	Caenorhabditis elegans cosmid F36H9.	Caenorhabditis elegans	35,977	8-Aug-97
rxa02581	1983	GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	38,517	17-Jun-98
		GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	39,173	17-Jun-98
rxa02582	4953	GB_BA1:MTV026	23740	AL022076	Mycobacterium tuberculosis H37Rv complete genome; segment 157/162.	Mycobacterium tuberculosis	38,548	24-Jun-99
		GB_BA1:MTCY338	29372	Z74697	Mycobacterium tuberculosis H37Rv complete genome; segment 127/162.	Mycobacterium tuberculosis	46,263	17-Jun-98
		GB_BA1:SEERYABS	20444	X62569	S.erythraea eryA gene for 6-deoxyerythronolyde B synthase II & III.	Saccharopolyspora erythraea	45,053	28-Feb-92
rxa02583	1671	GB_BA2:AF113605	1593	AF113605	Streptomyces coelicolor propionyl-CoA carboxylase complex B subunit (pccB) gene, complete cds.	Streptomyces coelicolor	58,397	08-DEC-1999
		GB_BA1:SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2.	Streptomyces coelicolor	52,916	15-Jan-99
		GB_BA1:AB018531	4961	AB018531	Corynebacterium glutamicum dtsR1 and dtsR2 genes, complete cds.	Corynebacterium glutamicum	58,809	19-OCT-1998
rxa02599	600	GB_BA1:AEMML	2585	X99639	Ralstonia eutropha mmlH, mmlI & mmlJ genes.	Ralstonia eutropha	35,264	22-Jan-98

Table 4 (continued)

		GB_EST15:AA508926	422	AA508926	MBAFCW1C08T3 Brugia malayi adult female cDNA (SAW96MLW-BmAF) Brugia malayi cDNA clone AFCW1C08 5', mRNA sequence.	Brugia malayi	43,377	8-Jul-97
		GB_BA1:AEMML	2585	X99639	Ralstonia eutropha mmlH, mmlI & mmlJ genes.	Ralstonia eutropha	41,148	22-Jan-98
rxa02634	1734	GB_BA1:SYNPOO	1964	X17439	Synechocystis ndhC, psbG genes for NDH-C, PSII-G and ORF157.	Synechocystis PCC6803	38,145	10-Feb-99
		GB_GSS9:AQ101527	184	AQ101527	HS_2265_A1_E11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2265 Col=21 Row=I, genomic survey sequence.	Homo sapiens	38,798	27-Aug-98
		GB_IN1:MNE133341	399	AJ133341	Melarhaphe neritoides partial caM gene, exons 1-2.	Melarhaphe neritoides	39,098	2-Jun-99
rxa02638	999	GB_BA2:AE001756	10938	AE001756	Thermotoga maritima section 68 of 136 of the complete genome.	Thermotoga maritima	40,104	2-Jun-99
		GB_GSS12:AQ423878	689	AQ423878	CITBI-E1-2575E20.TF CITBI-E1 Homo sapiens genomic clone 2575E20, genomic survey sequence.	Homo sapiens	36,451	23-MAR-1999
		GB_HTG2:AC006765	274498	AC006765	Caenorhabditis elegans clone Y43H11, *** SEQUENCING IN PROGRESS***, 7 unordered pieces.	Caenorhabditis elegans	39,072	23-Feb-99
rxa02659	335	GB_EST36:AI900317	436	AI900317	sc04a02.y1 Gm-c1012 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:Gm-c1012-1155 5' similar to SW:PRS6_SOLTU P54778 26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG. ;, mRNA sequence.	Glycine max	41,566	06-DEC-1999
		GB_GSS12:AQ342831	683	AQ342831	RPCI11-122K17.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-122K17, genomic survey sequence.	Homo sapiens	34,762	07-MAY-1999
		GB_EST36:AI900856	779	AI900856	sb95c11.y1 Gm-c1012 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1012-429 5' similar to SW:PRS6_SOLTU P54778 26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG. ;, mRNA sequence.	Glycine max	39,063	06-DEC-1999
rxa02676	1512	GB_IN2:CELB0213	39134	AF039050	Caenorhabditis elegans cosmid B0213.	Caenorhabditis elegans	35,814	2-Jun-99
		GB_GSS1:CNS00PZB	364	AL085157	Arabidopsis thaliana genome survey sequence SP6 end of BAC F10D11 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Arabidopsis thaliana	38,462	28-Jun-99
		GB_RO:RNITPR2R	10708	X61677	Rat ITPR2 gene for type 2 inositol triphosphate receptor.	Rattus norvegicus	37,543	21-OCT-1991
rxa02677	882	GB_RO:D89728	5002	D89728	Mus musculus mRNA for LOK, complete cds.	Mus musculus	38,829	7-Feb-99
		GB_GSS8:AQ062004	362	AQ062004	CIT-HSP-2346O14.TR CIT-HSP Homo sapiens genomic clone 2346O14, genomic survey sequence.	Homo sapiens	36,565	31-Jul-98
		GB_GSS14:AQ555818	462	AQ555818	HS_5230_B1_G06_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=806 Col=11 Row=N, genomic survey sequence.	Homo sapiens	36,534	29-MAY-1999
rxa02691	930	GB_IN1:DME9736	7411	AJ009736	Drosophila melanogaster Idefix retroelement: gag, pol and env genes, partial.	Drosophila melanogaster	36,522	19-Jan-99
		GB_PR4:AC004801	193561	AC004801	Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.	Homo sapiens	39,341	2-Feb-99
		GB_PR4:AC004801	193561	AC004801	Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.	Homo sapiens	37,037	2-Feb-99
rxa02718	1170	GB_EST34:AV132028	258	AV132028	AV132028 Mus musculus C57BL/6J 11-day embryo Mus musculus cDNA clone 2700087F01, mRNA sequence.	Mus musculus	43,529	1-Jul-99
		GB_GSS10:AQ240654	452	AQ240654	CIT-HSP-2385D24.TFB.1 CIT-HSP Homo sapiens genomic clone 2385D24, genomic survey sequence.	Homo sapiens	40,044	30-Sep-98
		GB_GSS11:AQ309500	576	AQ309500	CIT-HSP-2384D24.TFD CIT-HSP Homo sapiens genomic clone 2384D24, genomic survey sequence.	Homo sapiens	38,869	22-DEC-1998

Table 4 (continued)

rxa02749	999	GB_BA2:AF086791	37867	AF086791	Zymomonas mobilis strain ZM4 clone 67E10 carbamoylphosphate synthetase small subunit (carA), carbamoylphosphate synthetase large subunit (carB), transcription elongation factor (greA), enolase (eno), pyruvate dehydrogenase alpha subunit (pdhA), pyruvate dehydrogenase beta subunit (pdhB), ribonuclease H (rnh), homoserine kinase homolog, alcohol dehydrogenase II (adhB), and excinuclease ABC subunit A (uvrA) genes, complete cds; and unknown genes.	Zymomonas mobilis	39,024	4-Nov-98
		GB_BA1:SYCSLRB	146271	D64000	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999.	Synechocystis sp.	34,573	13-Feb-99
		GB_BA2:AE001306	13316	AE001306	Chlamydia trachomatis section 33 of 87 of the complete genome.	Chlamydia trachomatis	38,940	2-Sep-98
rxa02767	906	GB_BA2:AF126953	1638	AF126953	Corynebacterium glutamicum cystathionine gamma-synthase (metB) gene, complete cds.	Corynebacterium glutamicum	100,000	10-Sep-99
		GB_BA1:SCI5	6661	AL079332	Streptomyces coelicolor cosmid I5.	Streptomyces coelicolor	37,486	16-Jun-99
		GB_PR3:HS90L6	190837	Z97353	Human DNA sequence from clone 90L6 on chromosome 22q11.21-11.23. Contains an RPL15 (60S Ribosomal Protein L15) pseudogene, ESTs, STSs and GSSs, complete sequence.	Homo sapiens	34,149	23-Nov-99
rxa02792	876	GB_BA2:AF099015	5000	AF099015	Streptomyces coelicolor strain A3(2) integrase (int), Fe-containing superoxide dismutase II (sodF2), Fe uptake system permease (ftrE), and Fe uptake system integral membrane protein (ftrD) genes, complete cds.	Streptomyces coelicolor	36,721	1-Jun-99
		GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	38,787	17-Apr-96
		GB_HTG3:AC011361	186148	AC011361	Homo sapiens chromosome 5 clone CIT-HSPC_482N19, *** SEQUENCING IN PROGRESS ***, 69 unordered pieces.	Homo sapiens	43,577	06-OCT-1999
rxa02794	1197	GB_PR4:AC005998	96556	AC005998	Homo sapiens clone DJ0622E21, complete sequence.	Homo sapiens	37,298	29-Jul-99
		GB_PR4:AC006008	57554	AC006008	Homo sapiens clone DJ0820A21, complete sequence.	Homo sapiens	36,638	17-Jun-99
		GB_PR3:HSDJ73H14	95556	AL080272	Human DNA sequence from clone 73H14 on chromosome Xq26.3-28, complete sequence.	Homo sapiens	39,726	23-Nov-99
rxa02809	375	GB_RO:MUSSPCTLT	3172	M22527	Mouse cytotoxic T lymphocyte-specific serine protease CCPII gene, complete	Mus musculus	47,518	19-Jan-96
		GB_RO:MUSGRC	894	M18459	Mouse granzyme C serine esterase mRNA, complete cds.	Mus musculus	44,939	12-Jun-93
		GB_RO:RNU57062	880	U57062	Rattus norvegicus natural killer cell protease 4 (RNKP-4) mRNA, complete cds.	Rattus norvegicus	41,554	31-Jul-96
rxa02811	484	GB_GSS6:AQ832862	476	AQ832862	HS_5261_A2_E10_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=837 Col=20 Row=I, genomic survey sequence.	Homo sapiens	35,610	27-Aug-99
		GB_GSS5:AQ784593	515	AQ784593	HS_3248_A2_F02_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3248 Col=4 Row=K, genomic survey sequence.	Homo sapiens	38,956	3-Aug-99
		GB_GSS13:AQ473140	397	AQ473140	CITBI-E1-2589G6.TF CITBI-E1 Homo sapiens genomic clone 2589G6, genomic survey sequence.	Homo sapiens	34,761	23-Apr-99
rxa02836	678	GB_EST18:AA696785	316	AA696785	GM08392.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM08392 5prime, mRNA sequence.	Drosophila melanogaster	40,604	28-Nov-98
		GB_EST18:AA696785	316	AA696785	GM08392.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM08392 5prime, mRNA sequence.	Drosophila melanogaster	38,281	28-Nov-98
rxs03212	1452	GB_BA1:CGBETPGEN	2339	X93514	C.glutamicum betP gene.	Corynebacterium glutamicum	99,931	8-Sep-97
		GB_BA1:SC5F2A	40105	AL049587	Streptomyces coelicolor cosmid 5F2A.	Streptomyces coelicolor A3(2)	57,557	24-MAY-1999

Table 4 (continued)

		GB_BA2:AF008220	220060	AF008220	Bacillus subtilis rrnB-dnaB genomic region.	Bacillus subtilis	40,000	4-Feb-98
rxs03220	725	GB_PL1:CKHUP2	2353	X66855	C.kessleri HUP2 mRNA.	Chlorella kessleri	45,328	17-Feb-97
		GB_EST38:AW048153	383	AW048153	UI-M-BH1-alq-h-05-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-alq-h-05-0-UI 3', mRNA sequence.	Mus musculus	41,758	18-Sep-99
		GB_PL1:CKHUP2	2353	X66855	C.kessleri HUP2 mRNA.	Chlorella kessleri	38,106	17-Feb-97

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose, 2.46 g/l $MgSO_4 \times 7H_2O$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(NH_4)_2SO_4$, 1 g/l NaCl, 2 g/l $MgSO_4 \times 7H_2O$, 0.2 g/l $CaCl_2$, 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $FeSO_4 \times H_2O$, 10 mg/l $ZnSO_4 \times 7\ H_2O$, 3 mg/l $MnCl_2 \times 4\ H_2O$, 30 mg/l H_3BO_3 20 mg/l $CoCl_2 \times 6\ H_2O$, 1 mg/l $NiCl_2 \times 6\ H_2O$, 3 mg/l $Na_2MoO_4 \times 2\ H_2O$, 500 mg/l complexing agent (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 μg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20 μg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30

min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.,* Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (see *e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g. Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain

the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*, Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli and C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer,

A *et al.* (1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other Corynebacterium or Brevibacterium species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) From Genes to Clones – Introduction to Gene Technology. VCH: Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene

product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for Corynebacteria are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Procaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex

compounds such as molasses or other by-products from sugar refinement. It can also be advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as NH_4Cl or $(NH_4)_2SO_4$, NH_4OH, nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers

such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It is also possible to maintain a constant culture pH through the addition of NaOH or NH_4OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes. For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD_{600} of O.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods,

applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) Enzymes. Longmans: London; Fersht, (1985) Enzyme Structure and Mechanism. Freeman: New York; Walsh, (1979) Enzymatic Reaction Mechanisms. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) Fundamentals of Enzymology. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) The Enzymes, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) Enzymkinetik, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) Methods of Enzymatic Analysis, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in Biomembranes, Molecular Structure and Function, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical

chromatography such as high performance liquid chromatography (see, for example, Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. Biochemical Engineering Fundamentals, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley and Sons; Fallon, A. *et al.* (1987) Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17.

Example 11: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci.* USA 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci.* USA

90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to MCT nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to MCT protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at http://www.gcg.com), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. John Wiley and Sons: New York). The gene sequences of the invention

were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label

may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as

described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18:

1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S-methionine, ^{35}S-cysteine, ^{14}C-labelled amino acids, ^{15}N-amino acids, $^{15}NO_3$ or $^{15}NH_4^+$ or ^{13}C-labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly, fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an MCT protein, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes an MCT protein involved in the production of a fine chemical.

3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.

9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.

10. A vector comprising the nucleic acid molecule of any one of claims 1-9.

11. The vector of claim 10, which is an expression vector.

12. A host cell transfected with the expression vector of claim 11.

13. The host cell of claim 12, wherein said cell is a microorganism.

14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium.*

15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.

16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated

fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.

18. An isolated MCT polypeptide from *Corynebacterium glutamicum*, or a portion thereof.

19. The polypeptide of claim 18, wherein said polypeptide is involved in the production of a fine chemical production.

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

22. The isolated polypeptide of any of claims 18-21, further comprising heterologous amino acid sequences.

23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.

24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.

26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.

27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.

28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium.*

29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum, Corynebacterium herculis, Corynebacterium, lilium, Corynebacterium acetoacidophilum, Corynebacterium acetoglutamicum, Corynebacterium acetophilum, Corynebacterium ammoniagenes, Corynebacterium fujiokense, Corynebacterium nitrilophilus, Brevibacterium ammoniagenes, Brevibacterium butanicum, Brevibacterium divaricatum, Brevibacterium flavum, Brevibacterium healii, Brevibacterium ketoglutamicum, Brevibacterium ketosoreductum, Brevibacterium lactofermentum, Brevibacterium linens, Brevibacterium paraffinolyticum,* and those strains set forth in Table 3.

30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.

31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

32. The method of claim 25, wherein said fine chemical is an amino acid.

33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.

34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.

35. A method for diagnosing the presence or activity of Corynebacterium diphtheriae in a subject, comprising detecting the presence of one or more of SEQ ID NOs 1 through 676 of the Sequence Listing in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of Corynebacterium diphtheriae in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the nucleic acid molecule is disrupted.

37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs in the Sequence Listing, wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth as odd-numbered SEQ ID NOs of the Sequence Listing s.

38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

SEQUENCE LISTING

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Ser Val Ile Met Ser Leu Pro Met Ala Phe Val Val Ala Thr Leu Ala
165 170 175

Val Arg Asp Ile Glu Gly Lys Ser Gly Glu Ile Ala Ser Pro Arg Ala
180 185 190

Val Leu Leu Gly Asn Ile Ser Phe Ala Phe Tyr Met Val Gln Phe Pro
195 200 205

Val Met Val Phe Val Gln Arg Tyr Phe Ile Ala Gly Lys Glu Tyr Gly
210 215 220

Phe Leu Gly Trp Ala Phe Tyr Ala Val Val Cys Phe Ile Val Ser Val
225 230 235 240

Ile Leu Ala Trp Val Leu Leu Pro Ser Leu Met Ile Leu
245 250

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<222> (101)..(1960)
<223> RXN02581

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Met Asp Leu Asp Lys
1 5

gcg att ggt tca ttc ttc gat gag aat gga gaa atc aac ctt cct cca 163
Ala Ile Gly Ser Phe Phe Asp Glu Asn Gly Glu Ile Asn Leu Pro Pro
10 15 20

ttc cta act ttg gca gcc atg ggt gag ttc atg tac cag gct gac atc 211
Phe Leu Thr Leu Ala Ala Met Gly Glu Phe Met Tyr Gln Ala Asp Ile
25 30 35

gct gaa ggc ggc ggg gat aaa cca cgc atg cat ttc tgg gac ttc tcc 259
Ala Glu Gly Gly Gly Asp Lys Pro Arg Met His Phe Trp Asp Phe Ser
40 45 50

gaa gac cgc gat ggc aag ctg att cag tac acc cga aac gag atc gat 307
Glu Asp Arg Asp Gly Lys Leu Ile Gln Tyr Thr Arg Asn Glu Ile Asp

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    55                  60                  65

act cgt atc aag gct gta gca ggc cgt ttg cag cag gtc gcc acc ctg     355
Thr Arg Ile Lys Ala Val Ala Gly Arg Leu Gln Gln Val Ala Thr Leu
 70                  75                  80                  85

ggt gat cgt gca gcg atc ctg gct aac aac agc cct gag tac att ttc     403
Gly Asp Arg Ala Ala Ile Leu Ala Asn Asn Ser Pro Glu Tyr Ile Phe
                 90                  95                 100

agc ttc ctc ggc gcg atc tac gct ggc atg gtc cct gtg ccg ctt tat     451
Ser Phe Leu Gly Ala Ile Tyr Ala Gly Met Val Pro Val Pro Leu Tyr
            105                 110                 115

gat cca aac gag cca gga cac gca gac cac ctc aac gct gtt ttc gca     499
Asp Pro Asn Glu Pro Gly His Ala Asp His Leu Asn Ala Val Phe Ala
        120                 125                 130

gac agc gag cca gtt gtc gtt ctg acc aac tcc aag tcc gca ggt gcc     547
Asp Ser Glu Pro Val Val Val Leu Thr Asn Ser Lys Ser Ala Gly Ala
    135                 140                 145

gtg cgc aag cac ttc tcc agc ctt cca gct gca gaa cgc cca cgc atc     595
Val Arg Lys His Phe Ser Ser Leu Pro Ala Ala Glu Arg Pro Arg Ile
150                 155                 160                 165

ctc tct gta gat tcc ttg cct gat tct ctc gcg gat tct tac gag aac     643
Leu Ser Val Asp Ser Leu Pro Asp Ser Leu Ala Asp Ser Tyr Glu Asn
                170                 175                 180

cca atg ctg acc gaa gcc ggc cgc cgc ctg gct gct ctg cgc cag tcc     691
Pro Met Leu Thr Glu Ala Gly Arg Arg Leu Ala Ala Leu Arg Gln Ser
            185                 190                 195

gcg ccc att gat ctg acc gca ttc ctg cag tac acc tcc ggc tcc acc     739
Ala Pro Ile Asp Leu Thr Ala Phe Leu Gln Tyr Thr Ser Gly Ser Thr
        200                 205                 210

cga acc cca gct ggc gtt gtt ctg acc aac cgc tcc atc ctg acc aac     787
Arg Thr Pro Ala Gly Val Val Leu Thr Asn Arg Ser Ile Leu Thr Asn
    215                 220                 225

gtc ttg cag atc ttc agc gcc gca cag ctg aaa acc cca ctg cgc ctg     835
Val Leu Gln Ile Phe Ser Ala Ala Gln Leu Lys Thr Pro Leu Arg Leu
230                 235                 240                 245

gtt tca tgg ctg cca ctg cac cac gac atg ggc att atc ctc gcg gcg     883
Val Ser Trp Leu Pro Leu His His Asp Met Gly Ile Ile Leu Ala Ala
                250                 255                 260

ttt gtc act atg ctt ggc ctg gac aac gag ttc atg aac cca cgc gat     931
Phe Val Thr Met Leu Gly Leu Asp Asn Glu Phe Met Asn Pro Arg Asp
            265                 270                 275

ttc gtg cag cag cct tcc cgc tgg att aag cag ctc aac cgt cgc gaa     979
Phe Val Gln Gln Pro Ser Arg Trp Ile Lys Gln Leu Asn Arg Arg Glu
        280                 285                 290

agc gac gtg gac gtt aac gtc tac acc gtg gtt cct aac ttc gcc ctc    1027
Ser Asp Val Asp Val Asn Val Tyr Thr Val Val Pro Asn Phe Ala Leu
    295                 300                 305
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gag ctt gca gca cgc tac gca aag cca gca gag gga gag acc ctg gat 1075
Glu Leu Ala Ala Arg Tyr Ala Lys Pro Ala Glu Gly Glu Thr Leu Asp
310 315 320 325

ctt tcc gca ttg gat gcc atc att atc ggt tcc gag cca gtc aca gaa 1123
Leu Ser Ala Leu Asp Ala Ile Ile Ile Gly Ser Glu Pro Val Thr Glu
330 335 340

aac gct ctg acc acc ttc cgt gaa gct ttc gag cct tac ggc ctg cct 1171
Asn Ala Leu Thr Thr Phe Arg Glu Ala Phe Glu Pro Tyr Gly Leu Pro
345 350 355

gtt cag acc ctg cgt cct tcc tac ggt ctt gca gaa gca tcc ctg ctg 1219
Val Gln Thr Leu Arg Pro Ser Tyr Gly Leu Ala Glu Ala Ser Leu Leu
360 365 370

gtc acc acc cca cag acc gaa aac cgc cca ctg atc tcc tac ttc gac 1267
Val Thr Thr Pro Gln Thr Glu Asn Arg Pro Leu Ile Ser Tyr Phe Asp
375 380 385

cgc gag gcc ttg gcc gaa aac cgc gtt gag ctt gta gaa aag ggc aat 1315
Arg Glu Ala Leu Ala Glu Asn Arg Val Glu Leu Val Glu Lys Gly Asn
390 395 400 405

aac aag gct gtt gct ttc gtc tcc aac ggc cag gtt gca gcc cca cag 1363
Asn Lys Ala Val Ala Phe Val Ser Asn Gly Gln Val Ala Ala Pro Gln
410 415 420

cag ctg gtc atc gtt gat tcc gaa acc gga acc gag ctg gca gac ggc 1411
Gln Leu Val Ile Val Asp Ser Glu Thr Gly Thr Glu Leu Ala Asp Gly
425 430 435

cag atc ggc gaa atc tgg acc cac ggc gaa aac act gct gca ggt tac 1459
Gln Ile Gly Glu Ile Trp Thr His Gly Glu Asn Thr Ala Ala Gly Tyr
440 445 450

ctc gac cgc gag gaa gac acc gca gaa acc ttc cgc aac cgt ctg acc 1507
Leu Asp Arg Glu Glu Asp Thr Ala Glu Thr Phe Arg Asn Arg Leu Thr
455 460 465

acc cgc ctg gaa gaa aac tcc cgc gca gaa ggt gct gcc gac gac aac 1555
Thr Arg Leu Glu Glu Asn Ser Arg Ala Glu Gly Ala Ala Asp Asp Asn
470 475 480 485

tac tgg atg gcc acc ggt gac ctc ggc gtc atc gta gac aac gag ctc 1603
Tyr Trp Met Ala Thr Gly Asp Leu Gly Val Ile Val Asp Asn Glu Leu
490 495 500

tac atc acc ggt cgt ctg aag gac ctc atc gtt gtc gca ggc cga aac 1651
Tyr Ile Thr Gly Arg Leu Lys Asp Leu Ile Val Val Ala Gly Arg Asn
505 510 515

cac tac cca cag gac atc gag tac acc gtc cag gct gct tcc gca cac 1699
His Tyr Pro Gln Asp Ile Glu Tyr Thr Val Gln Ala Ala Ser Ala His
520 525 530

atc cgt gca gat tcc gtc gca gca ttc gca gtc cca ggc gat gac att 1747
Ile Arg Ala Asp Ser Val Ala Ala Phe Ala Val Pro Gly Asp Asp Ile
535 540 545

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gaa aag ctc atc atc ctg gca gaa cgc gac acc act gca aac gaa gcc   1795
Glu Lys Leu Ile Ile Leu Ala Glu Arg Asp Thr Thr Ala Asn Glu Ala
550                 555                 560                 565

gac gat gca gct gct gaa gaa gca atc cgc tcc gcc gtt ggc act gca   1843
Asp Asp Ala Ala Ala Glu Glu Ala Ile Arg Ser Ala Val Gly Thr Ala
                570                 575                 580

cac ggt gtt gtt cca gaa gag atc cgt atc ctc gca cct gac gag atc   1891
His Gly Val Val Pro Glu Glu Ile Arg Ile Leu Ala Pro Asp Glu Ile
            585                 590                 595

gcg cgt tcc tcc tcc gga aag atc gca cgc cgc gtc aac cag cgc aac   1939
Ala Arg Ser Ser Ser Gly Lys Ile Ala Arg Arg Val Asn Gln Arg Asn
        600                 605                 610

tac att cag gaa caa gct aac tagttctttg cagacaccgc agg             1983
Tyr Ile Gln Glu Gln Ala Asn
    615                 620


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Met Asp Leu Asp Lys Ala Ile Gly Ser Phe Phe Asp Glu Asn Gly Glu
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             20                  25                  30

Tyr Gln Ala Asp Ile Ala Glu Gly Gly Gly Asp Lys Pro Arg Met His
         35                  40                  45

Phe Trp Asp Phe Ser Glu Asp Arg Asp Gly Lys Leu Ile Gln Tyr Thr
     50                  55                  60

Arg Asn Glu Ile Asp Thr Arg Ile Lys Ala Val Ala Gly Arg Leu Gln
 65                  70                  75                  80

Gln Val Ala Thr Leu Gly Asp Arg Ala Ala Ile Leu Ala Asn Asn Ser
                 85                  90                  95

Pro Glu Tyr Ile Phe Ser Phe Leu Gly Ala Ile Tyr Ala Gly Met Val
            100                 105                 110

Pro Val Pro Leu Tyr Asp Pro Asn Glu Pro Gly His Ala Asp His Leu
        115                 120                 125

Asn Ala Val Phe Ala Asp Ser Glu Pro Val Val Val Leu Thr Asn Ser
    130                 135                 140

Lys Ser Ala Gly Ala Val Arg Lys His Phe Ser Ser Leu Pro Ala Ala
145                 150                 155                 160

Glu Arg Pro Arg Ile Leu Ser Val Asp Ser Leu Pro Asp Ser Leu Ala
                165                 170                 175

Asp Ser Tyr Glu Asn Pro Met Leu Thr Glu Ala Gly Arg Arg Leu Ala
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180 185 190

Ala Leu Arg Gln Ser Ala Pro Ile Asp Leu Thr Ala Phe Leu Gln Tyr
195 200 205

Thr Ser Gly Ser Thr Arg Thr Pro Ala Gly Val Val Leu Thr Asn Arg
210 215 220

Ser Ile Leu Thr Asn Val Leu Gln Ile Phe Ser Ala Ala Gln Leu Lys
225 230 235 240

Thr Pro Leu Arg Leu Val Ser Trp Leu Pro Leu His His Asp Met Gly
245 250 255

Ile Ile Leu Ala Ala Phe Val Thr Met Leu Gly Leu Asp Asn Glu Phe
260 265 270

Met Asn Pro Arg Asp Phe Val Gln Gln Pro Ser Arg Trp Ile Lys Gln
275 280 285

Leu Asn Arg Arg Glu Ser Asp Val Asp Val Asn Val Tyr Thr Val Val
290 295 300

Pro Asn Phe Ala Leu Glu Leu Ala Ala Arg Tyr Ala Lys Pro Ala Glu
305 310 315 320

Gly Glu Thr Leu Asp Leu Ser Ala Leu Asp Ala Ile Ile Ile Gly Ser
325 330 335

Glu Pro Val Thr Glu Asn Ala Leu Thr Thr Phe Arg Glu Ala Phe Glu
340 345 350

Pro Tyr Gly Leu Pro Val Gln Thr Leu Arg Pro Ser Tyr Gly Leu Ala
355 360 365

Glu Ala Ser Leu Leu Val Thr Thr Pro Gln Thr Glu Asn Arg Pro Leu
370 375 380

Ile Ser Tyr Phe Asp Arg Glu Ala Leu Ala Glu Asn Arg Val Glu Leu
385 390 395 400

Val Glu Lys Gly Asn Asn Lys Ala Val Ala Phe Val Ser Asn Gly Gln
405 410 415

Val Ala Ala Pro Gln Gln Leu Val Ile Val Asp Ser Glu Thr Gly Thr
420 425 430

Glu Leu Ala Asp Gly Gln Ile Gly Glu Ile Trp Thr His Gly Glu Asn
435 440 445

Thr Ala Ala Gly Tyr Leu Asp Arg Glu Glu Asp Thr Ala Glu Thr Phe
450 455 460

Arg Asn Arg Leu Thr Thr Arg Leu Glu Glu Asn Ser Arg Ala Glu Gly
465 470 475 480

Ala Ala Asp Asp Asn Tyr Trp Met Ala Thr Gly Asp Leu Gly Val Ile
485 490 495

Val Asp Asn Glu Leu Tyr Ile Thr Gly Arg Leu Lys Asp Leu Ile Val
500 505 510

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Val Ala Gly Arg Asn His Tyr Pro Gln Asp Ile Glu Tyr Thr Val Gln
        515                 520                 525

Ala Ala Ser Ala His Ile Arg Ala Asp Ser Val Ala Ala Phe Ala Val
    530                 535                 540

Pro Gly Asp Asp Ile Glu Lys Leu Ile Ile Leu Ala Glu Arg Asp Thr
545                 550                 555                 560

Thr Ala Asn Glu Ala Asp Asp Ala Ala Ala Glu Glu Ala Ile Arg Ser
                565                 570                 575

Ala Val Gly Thr Ala His Gly Val Val Pro Glu Glu Ile Arg Ile Leu
            580                 585                 590

Ala Pro Asp Glu Ile Ala Arg Ser Ser Ser Gly Lys Ile Ala Arg Arg
        595                 600                 605

Val Asn Gln Arg Asn Tyr Ile Gln Glu Gln Ala Asn
    610                 615                 620


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&lt;211&gt; 1550
&lt;212&gt; DNA
&lt;213&gt; Corynebacterium glutamicum

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&lt;221&gt; CDS
&lt;222&gt; (1)..(1527)
&lt;223&gt; FRXA02581

&lt;400&gt; 11
gtc cct gtg ccg ctt tat gat cca aac gag cca gga cac gca gac cac      48
Val Pro Val Pro Leu Tyr Asp Pro Asn Glu Pro Gly His Ala Asp His
  1               5                  10                  15

ctc aac gct gtt ttc gca gac agc gag cca gtt gtc gtt ctg acc aac      96
Leu Asn Ala Val Phe Ala Asp Ser Glu Pro Val Val Val Leu Thr Asn
             20                  25                  30

tcc aag tcc gca ggt gcc gtg cgc aag cac ttc tcc agc ctt cca gct     144
Ser Lys Ser Ala Gly Ala Val Arg Lys His Phe Ser Ser Leu Pro Ala
         35                  40                  45

gca gaa cgc cca cgc atc ctc tct gta gat tcc ttg cct gat tct ctc     192
Ala Glu Arg Pro Arg Ile Leu Ser Val Asp Ser Leu Pro Asp Ser Leu
     50                  55                  60

gcg gat tct tac gag aac cca atg ctg acc gaa gcc ggc cgc cgc ctg     240
Ala Asp Ser Tyr Glu Asn Pro Met Leu Thr Glu Ala Gly Arg Arg Leu
 65                  70                  75                  80

gct gct ctg cgc cag tcc gcg ccc att gat ctg acc gca ttc ctg cag     288
Ala Ala Leu Arg Gln Ser Ala Pro Ile Asp Leu Thr Ala Phe Leu Gln
                 85                  90                  95

tac acc tcc ggc tcc acc cga acc cca gct ggc gtt gtt ctg acc aac     336
Tyr Thr Ser Gly Ser Thr Arg Thr Pro Ala Gly Val Val Leu Thr Asn
            100                 105                 110
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cgc tcc atc ctg acc aac gtc ttg cag atc ttc agc gcc gca cag ctg 384
Arg Ser Ile Leu Thr Asn Val Leu Gln Ile Phe Ser Ala Ala Gln Leu
115 120 125

aaa acc cca ctg cgc ctg gtt tca tgg ctg cca ctg cac cac gac atg 432
Lys Thr Pro Leu Arg Leu Val Ser Trp Leu Pro Leu His His Asp Met
130 135 140

ggc att atc ctc gcg gcg ttt gtc act atg ctt ggc ctg gac aac gag 480
Gly Ile Ile Leu Ala Ala Phe Val Thr Met Leu Gly Leu Asp Asn Glu
145 150 155 160

ttc atg aac cca cgc gat ttc gtg cag cag cct tcc cgc tgg att aag 528
Phe Met Asn Pro Arg Asp Phe Val Gln Gln Pro Ser Arg Trp Ile Lys
165 170 175

cag ctc aac cgt cgc gaa agc gac gtg gac gtt aac gtc tac acc gtg 576
Gln Leu Asn Arg Arg Glu Ser Asp Val Asp Val Asn Val Tyr Thr Val
180 185 190

gtt cct aac ttc gcc ctc gag ctt gca gca cgc tac gca aag cca gca 624
Val Pro Asn Phe Ala Leu Glu Leu Ala Ala Arg Tyr Ala Lys Pro Ala
195 200 205

gag gga gag acc ctg gat ctt tcc gca ttg gat gcc atc att atc ggt 672
Glu Gly Glu Thr Leu Asp Leu Ser Ala Leu Asp Ala Ile Ile Ile Gly
210 215 220

tcc gag cca gtc aca gaa aac gct ctg acc acc ttc cgt gaa gct ttc 720
Ser Glu Pro Val Thr Glu Asn Ala Leu Thr Thr Phe Arg Glu Ala Phe
225 230 235 240

gag cct tac ggc ctg cct gtt cag acc ctg cgt cct tcc tac ggt ctt 768
Glu Pro Tyr Gly Leu Pro Val Gln Thr Leu Arg Pro Ser Tyr Gly Leu
245 250 255

gca gaa gca tcc ctg ctg gtc acc acc cca cag acc gaa aac cgc cca 816
Ala Glu Ala Ser Leu Leu Val Thr Thr Pro Gln Thr Glu Asn Arg Pro
260 265 270

ctg atc tcc tac ttc gac cgc gag gcc ttg gcc gaa aac cgc gtt gag 864
Leu Ile Ser Tyr Phe Asp Arg Glu Ala Leu Ala Glu Asn Arg Val Glu
275 280 285

ctt gta gaa aag ggc aat aac aag gct gtt gct ttc gtc tcc aac ggc 912
Leu Val Glu Lys Gly Asn Asn Lys Ala Val Ala Phe Val Ser Asn Gly
290 295 300

cag gtt gca gcc cca cag cag ctg gtc atc gtt gat tcc gaa acc gga 960
Gln Val Ala Ala Pro Gln Gln Leu Val Ile Val Asp Ser Glu Thr Gly
305 310 315 320

acc gag ctg gca gac ggc cag atc ggc gaa atc tgg acc cac ggc gaa 1008
Thr Glu Leu Ala Asp Gly Gln Ile Gly Glu Ile Trp Thr His Gly Glu
325 330 335

aac act gct gca ggt tac ctc gac cgc gag gaa gac acc gca gaa acc 1056
Asn Thr Ala Ala Gly Tyr Leu Asp Arg Glu Glu Asp Thr Ala Glu Thr
340 345 350

ttc cgc aac cgt ctg acc acc cgc ctg gaa gaa aac tcc cgc gca gaa 1104
Phe Arg Asn Arg Leu Thr Thr Arg Leu Glu Glu Asn Ser Arg Ala Glu
355 360 365

ggt gct gcc gac gac aac tac tgg atg gcc acc ggt gac ctc ggc gtc 1152
Gly Ala Ala Asp Asp Asn Tyr Trp Met Ala Thr Gly Asp Leu Gly Val
370 375 380

atc gta gac aac gag ctc tac atc acc ggt cgt ctg aag gac ctc atc 1200
Ile Val Asp Asn Glu Leu Tyr Ile Thr Gly Arg Leu Lys Asp Leu Ile
385 390 395 400

gtt gtc gca ggc cga aac cac tac cca cag gac atc gag tac acc gtc 1248
Val Val Ala Gly Arg Asn His Tyr Pro Gln Asp Ile Glu Tyr Thr Val
405 410 415

cag gct gct tcc gca cac atc cgt gca gat tcc gtc gca gca ttc gca 1296
Gln Ala Ala Ser Ala His Ile Arg Ala Asp Ser Val Ala Ala Phe Ala
420 425 430

gtc cca ggc gat gac att gaa aag ctc atc atc ctg gca gaa cgc gac 1344
Val Pro Gly Asp Asp Ile Glu Lys Leu Ile Ile Leu Ala Glu Arg Asp
435 440 445

acc act gca aac gaa gcc gac gat gca gct gct gaa gaa gca atc cgc 1392
Thr Thr Ala Asn Glu Ala Asp Asp Ala Ala Ala Glu Glu Ala Ile Arg
450 455 460

tcc gcc gtt ggc act gca cac ggt gtt gtt cca gaa gag atc cgt atc 1440
Ser Ala Val Gly Thr Ala His Gly Val Val Pro Glu Glu Ile Arg Ile
465 470 475 480

ctc gca cct gac gag atc gcg cgt tcc tcc tcc gga aag atc gca cgc 1488
Leu Ala Pro Asp Glu Ile Ala Arg Ser Ser Ser Gly Lys Ile Ala Arg
485 490 495

cgc gtc aac cag cgc aac tac att cag gaa caa gct aac tagttctttg 1537
Arg Val Asn Gln Arg Asn Tyr Ile Gln Glu Gln Ala Asn
500 505

cagacaccgc agg 1550

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20 25 30

Ser Lys Ser Ala Gly Ala Val Arg Lys His Phe Ser Ser Leu Pro Ala
35 40 45

Ala Glu Arg Pro Arg Ile Leu Ser Val Asp Ser Leu Pro Asp Ser Leu
50 55 60

Ala Asp Ser Tyr Glu Asn Pro Met Leu Thr Glu Ala Gly Arg Arg Leu
65 70 75 80

Ala Ala Leu Arg Gln Ser Ala Pro Ile Asp Leu Thr Ala Phe Leu Gln
85 90 95

Tyr Thr Ser Gly Ser Thr Arg Thr Pro Ala Gly Val Val Leu Thr Asn
100 105 110

Arg Ser Ile Leu Thr Asn Val Leu Gln Ile Phe Ser Ala Ala Gln Leu
115 120 125

Lys Thr Pro Leu Arg Leu Val Ser Trp Leu Pro Leu His His Asp Met
130 135 140

Gly Ile Ile Leu Ala Ala Phe Val Thr Met Leu Gly Leu Asp Asn Glu
145 150 155 160

Phe Met Asn Pro Arg Asp Phe Val Gln Gln Pro Ser Arg Trp Ile Lys
165 170 175

Gln Leu Asn Arg Arg Glu Ser Asp Val Asp Val Asn Val Tyr Thr Val
180 185 190

Val Pro Asn Phe Ala Leu Glu Leu Ala Ala Arg Tyr Ala Lys Pro Ala
195 200 205

Glu Gly Glu Thr Leu Asp Leu Ser Ala Leu Asp Ala Ile Ile Ile Gly
210 215 220

Ser Glu Pro Val Thr Glu Asn Ala Leu Thr Thr Phe Arg Glu Ala Phe
225 230 235 240

Glu Pro Tyr Gly Leu Pro Val Gln Thr Leu Arg Pro Ser Tyr Gly Leu
245 250 255

Ala Glu Ala Ser Leu Leu Val Thr Thr Pro Gln Thr Glu Asn Arg Pro
260 265 270

Leu Ile Ser Tyr Phe Asp Arg Glu Ala Leu Ala Glu Asn Arg Val Glu
275 280 285

Leu Val Glu Lys Gly Asn Asn Lys Ala Val Ala Phe Val Ser Asn Gly
290 295 300

Gln Val Ala Ala Pro Gln Gln Leu Val Ile Val Asp Ser Glu Thr Gly
305 310 315 320

Thr Glu Leu Ala Asp Gly Gln Ile Gly Glu Ile Trp Thr His Gly Glu
325 330 335

Asn Thr Ala Ala Gly Tyr Leu Asp Arg Glu Glu Asp Thr Ala Glu Thr
340 345 350

Phe Arg Asn Arg Leu Thr Thr Arg Leu Glu Glu Asn Ser Arg Ala Glu
355 360 365

Gly Ala Ala Asp Asp Asn Tyr Trp Met Ala Thr Gly Asp Leu Gly Val
370 375 380

Ile Val Asp Asn Glu Leu Tyr Ile Thr Gly Arg Leu Lys Asp Leu Ile

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385                 390                 395                 400

Val Val Ala Gly Arg Asn His Tyr Pro Gln Asp Ile Glu Tyr Thr Val
                405                 410                 415

Gln Ala Ala Ser Ala His Ile Arg Ala Asp Ser Val Ala Ala Phe Ala
            420                 425                 430

Val Pro Gly Asp Asp Ile Glu Lys Leu Ile Ile Leu Ala Glu Arg Asp
        435                 440                 445

Thr Thr Ala Asn Glu Ala Asp Asp Ala Ala Ala Glu Glu Ala Ile Arg
    450                 455                 460

Ser Ala Val Gly Thr Ala His Gly Val Val Pro Glu Glu Ile Arg Ile
465                 470                 475                 480

Leu Ala Pro Asp Glu Ile Ala Arg Ser Ser Ser Gly Lys Ile Ala Arg
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Arg Val Asn Gln Arg Asn Tyr Ile Gln Glu Gln Ala Asn
            500                 505


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<222> (101)..(4930)
<223> RXA02582

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                                           Met Glu Gln Ser Gln
                                           1               5

tcg tcg gat cag aag atg acc gtt gaa cag gtt cgc acc tgg ctc cgt   163
Ser Ser Asp Gln Lys Met Thr Val Glu Gln Val Arg Thr Trp Leu Arg
                10                  15                  20

gat tgg gtt gtc cgc acc acg ggt att ccg gtg gag gaa gtt acg gat   211
Asp Trp Val Val Arg Thr Thr Gly Ile Pro Val Glu Glu Val Thr Asp
            25                  30                  35

gac aag gca atg gag acc ttt ggc ctt tcc tct cgc gat gtt gtt gtg   259
Asp Lys Ala Met Glu Thr Phe Gly Leu Ser Ser Arg Asp Val Val Val
        40                  45                  50

ttg tct ggt gag ctg gaa aac ctg ctg gac acc tcc ttg gat gcc acc   307
Leu Ser Gly Glu Leu Glu Asn Leu Leu Asp Thr Ser Leu Asp Ala Thr
    55                  60                  65

atc gct tat gag tac cca acg atc cgt agt ttg gcg cag cgc ctt gtt   355
Ile Ala Tyr Glu Tyr Pro Thr Ile Arg Ser Leu Ala Gln Arg Leu Val
70                  75                  80                  85
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gag ggc gag cct cgt cgt gca cat acc cag cgt gaa ttg aat ttc tcc 403
Glu Gly Glu Pro Arg Arg Ala His Thr Gln Arg Glu Leu Asn Phe Ser
90 95 100

gcg gtg agc gat tcc cca ggt tcc cac gat att gcg gtt gtc ggt atg 451
Ala Val Ser Asp Ser Pro Gly Ser His Asp Ile Ala Val Val Gly Met
105 110 115

gct gcg cgt tac cca ggc gct gag agc ctg gag gat atg tgg aag cta 499
Ala Ala Arg Tyr Pro Gly Ala Glu Ser Leu Glu Asp Met Trp Lys Leu
120 125 130

ctc gtc gag ggc cgt gac ggt atc tcg gat cta ccg att ggc cgt tgg 547
Leu Val Glu Gly Arg Asp Gly Ile Ser Asp Leu Pro Ile Gly Arg Trp
135 140 145

tct gag tat gca ggc gat gag gtt atg tct cgg aag atg gaa gag ttt 595
Ser Glu Tyr Ala Gly Asp Glu Val Met Ser Arg Lys Met Glu Glu Phe
150 155 160 165

tct acc atc ggt ggc tac ctg tca gat atc tct agc ttt gat gcg gag 643
Ser Thr Ile Gly Gly Tyr Leu Ser Asp Ile Ser Ser Phe Asp Ala Glu
170 175 180

ttc ttt ggt ctg tct ccg ctc gag gcc gcc aac atg gat cct cag cag 691
Phe Phe Gly Leu Ser Pro Leu Glu Ala Ala Asn Met Asp Pro Gln Gln
185 190 195

cgt att ttg ctg gag cta acg tgg gag gct ttg gag tac gct cgc atc 739
Arg Ile Leu Leu Glu Leu Thr Trp Glu Ala Leu Glu Tyr Ala Arg Ile
200 205 210

gca cca aac act ttg cgt ggc gaa gcc gtg ggc gtg ttc ata ggt tcc 787
Ala Pro Asn Thr Leu Arg Gly Glu Ala Val Gly Val Phe Ile Gly Ser
215 220 225

tcc aac aac gat tac ggc atg atg atc gct gcc gat cca gca gaa gca 835
Ser Asn Asn Asp Tyr Gly Met Met Ile Ala Ala Asp Pro Ala Glu Ala
230 235 240 245

cat cct tat gcg ctg act ggt act tct agt gcg att gtc gct aac cgc 883
His Pro Tyr Ala Leu Thr Gly Thr Ser Ser Ala Ile Val Ala Asn Arg
250 255 260

att aac tac gct ttc gat ttc cgc ggt cct tcc gtc aac gtg gat acc 931
Ile Asn Tyr Ala Phe Asp Phe Arg Gly Pro Ser Val Asn Val Asp Thr
265 270 275

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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(517)
<223> RXA01138

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gctgcgagac actgtcggat cgttcccttc aggtgtcacg gtg gtc acc act acc 115
Val Val Thr Thr Thr
1 5

gat ggg gaa gtg gac cac ggg ttg act gtg agt gcg ttc gtg tcc ttg 163
Asp Gly Glu Val Asp His Gly Leu Thr Val Ser Ala Phe Val Ser Leu
10 15 20

tcg ttg gag cct gcc atg gtg ttg gtg agt atc gat aag aaa tca agc 211
Ser Leu Glu Pro Ala Met Val Leu Val Ser Ile Asp Lys Lys Ser Ser
25 30 35

gtt gtg ccg ttt ttg gag cag ggt tca cca gtt gct gtg tct gtg tta 259
Val Val Pro Phe Leu Glu Gln Gly Ser Pro Val Ala Val Ser Val Leu
40 45 50

tcg gaa gag cag agc gat ttg gcc atc aca ttt ggc cgt cat ctg gaa 307
Ser Glu Glu Gln Ser Asp Leu Ala Ile Thr Phe Gly Arg His Leu Glu
55 60 65

aac aaa ttc gac ggc gtt tcc att aag cgt tca aca aac agg gca gcg 355
Asn Lys Phe Asp Gly Val Ser Ile Lys Arg Ser Thr Asn Arg Ala Ala
70 75 80 85

gtc ttg gaa ggt gcg tca gca tgg ttg agt ggc gct gtg gtg gat aaa 403
Val Leu Glu Gly Ala Ser Ala Trp Leu Ser Gly Ala Val Val Asp Lys
90 95 100

tac cca ggt gga gat cac ttt att atc acc att gcc gtg gaa gag tgt 451
Tyr Pro Gly Gly Asp His Phe Ile Ile Thr Ile Ala Val Glu Glu Cys
105 110 115

gct cac gac gag gag caa aag cca ctt ctt tac cac cgt ggc agg ctt 499
Ala His Asp Glu Glu Gln Lys Pro Leu Leu Tyr His Arg Gly Arg Leu
120 125 130

ttt cag tgg caa gaa gat taattctcca ccccttcatt ttc 540
Phe Gln Trp Gln Glu Asp
135

<210> 16
<211> 139
<212> PRT
<213> Corynebacterium glutamicum

<400> 16
Val Val Thr Thr Thr Asp Gly Glu Val Asp His Gly Leu Thr Val Ser
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Ala Phe Val Ser Leu Ser Leu Glu Pro Ala Met Val Leu Val Ser Ile
20 25 30

Asp Lys Lys Ser Ser Val Val Pro Phe Leu Glu Gln Gly Ser Pro Val
35 40 45

Ala Val Ser Val Leu Ser Glu Glu Gln Ser Asp Leu Ala Ile Thr Phe
50 55 60

Gly Arg His Leu Glu Asn Lys Phe Asp Gly Val Ser Ile Lys Arg Ser
65 70 75 80

Thr Asn Arg Ala Ala Val Leu Glu Gly Ala Ser Ala Trp Leu Ser Gly
85 90 95

Ala Val Val Asp Lys Tyr Pro Gly Gly Asp His Phe Ile Ile Thr Ile
100 105 110

Ala Val Glu Glu Cys Ala His Asp Glu Glu Gln Lys Pro Leu Leu Tyr
115 120 125

His Arg Gly Arg Leu Phe Gln Trp Gln Glu Asp
130 135

<210> 17
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)
<223> RXA01980

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gccgccctag aattcactaa gtttccgata tctttaaccc atg cag atc att gat   115
                                            Met Gln Ile Ile Asp
                                             1               5

ctc tct cat gcg ttc gcg ccc gga caa ccc cac tac cct ggg gat cca   163
Leu Ser His Ala Phe Ala Pro Gly Gln Pro His Tyr Pro Gly Asp Pro
                10                  15                  20

gat caa gaa att aag acg gtc tcc acg att gaa aac gat ggc ttt tta   211
Asp Gln Glu Ile Lys Thr Val Ser Thr Ile Glu Asn Asp Gly Phe Leu
            25                  30                  35

atg cat caa tac aga ctt gtt ggt ccc tgg gga acg cat gta gat gca   259
Met His Gln Tyr Arg Leu Val Gly Pro Trp Gly Thr His Val Asp Ala
        40                  45                  50

cct gca cat ttc gat cca caa ggt cgg acg ctt gat cag atc cct gtg   307
Pro Ala His Phe Asp Pro Gln Gly Arg Thr Leu Asp Gln Ile Pro Val
    55                  60                  65

gag gaa acg cat tta ccc ctt tat tgc ctg agg ttt tct cgc ccc gat   355
Glu Glu Thr His Leu Pro Leu Tyr Cys Leu Arg Phe Ser Arg Pro Asp
70                  75                  80                  85

cta tgt act gct gct gat ata gaa gcg ttt gaa cat aca cac ggg aaa   403
Leu Cys Thr Ala Ala Asp Ile Glu Ala Phe Glu His Thr His Gly Lys
                90                  95                  100

atc gaa cca gga tcc ttc gtc gca ctc cac act gga tgg gaa tgg ggt   451
Ile Glu Pro Gly Ser Phe Val Ala Leu His Thr Gly Trp Glu Trp Gly
            105                 110                 115

aaa caa ggg atc gca ccc ggc tgg tct atc gag gct tta gaa atc ctc   499
Lys Gln Gly Ile Ala Pro Gly Trp Ser Ile Glu Ala Leu Glu Ile Leu
        120                 125                 130

cat gcc cgt gga gtc att gcc att ggc cac gat ctt ccc gat aca gat   547
His Ala Arg Gly Val Ile Ala Ile Gly His Asp Leu Pro Asp Thr Asp
    135                 140                 145

cct tca ctg gag gca cag cgc tgg tgg ctg tgc cgt gac cat tgg cag   595
Pro Ser Leu Glu Ala Gln Arg Trp Trp Leu Cys Arg Asp His Trp Gln
150                 155                 160                 165

att gaa aac ctc acc aat ttg gac aag gtt cct gca acg ggt gcg atg   643
Ile Glu Asn Leu Thr Asn Leu Asp Lys Val Pro Ala Thr Gly Ala Met
                170                 175                 180

att gct tgt cct tgg cca gtt cca aaa gat ggt gct agt ttc cca gtg   691
Ile Ala Cys Pro Trp Pro Val Pro Lys Asp Gly Ala Ser Phe Pro Val
            185                 190                 195

cgt cca att gct ctc gtc cca gag cac cta tcc cct act cgc           733
Arg Pro Ile Ala Leu Val Pro Glu His Leu Ser Pro Thr Arg
        200                 205                 210

taaagcgaac ggcagcacct tct                                         756
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<210> 18
<211> 211
<212> PRT
<213> Corynebacterium glutamicum

<400> 18
Met Gln Ile Ile Asp Leu Ser His Ala Phe Ala Pro Gly Gln Pro His
1 5 10 15

Tyr Pro Gly Asp Pro Asp Gln Glu Ile Lys Thr Val Ser Thr Ile Glu
20 25 30

Asn Asp Gly Phe Leu Met His Gln Tyr Arg Leu Val Gly Pro Trp Gly
35 40 45

Thr His Val Asp Ala Pro Ala His Phe Asp Pro Gln Gly Arg Thr Leu
50 55 60

Asp Gln Ile Pro Val Glu Glu Thr His Leu Pro Leu Tyr Cys Leu Arg
65 70 75 80

Phe Ser Arg Pro Asp Leu Cys Thr Ala Ala Asp Ile Glu Ala Phe Glu
85 90 95

His Thr His Gly Lys Ile Glu Pro Gly Ser Phe Val Ala Leu His Thr
100 105 110

Gly Trp Glu Trp Gly Lys Gln Gly Ile Ala Pro Gly Trp Ser Ile Glu
115 120 125

Ala Leu Glu Ile Leu His Ala Arg Gly Val Ile Ala Ile Gly His Asp
130 135 140

Leu Pro Asp Thr Asp Pro Ser Leu Glu Ala Gln Arg Trp Trp Leu Cys
145 150 155 160

Arg Asp His Trp Gln Ile Glu Asn Leu Thr Asn Leu Asp Lys Val Pro
165 170 175

Ala Thr Gly Ala Met Ile Ala Cys Pro Trp Pro Val Pro Lys Asp Gly
180 185 190

Ala Ser Phe Pro Val Arg Pro Ile Ala Leu Val Pro Glu His Leu Ser
195 200 205

Pro Thr Arg
210

<210> 19
<211> 1830
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1807)
<223> RXN01007

<400> 19

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tctgaaccaa tataccgatc agtctaaaag tgtgttaagt tctggaacat aaattagctg 60

acacgtaaag taacttaaag attcactgga ggtaagccta gtg ttt aaa aag cac   115
                                           Val Phe Lys Lys His
                                            1               5

aga cac ggt ctc ggc tcc ccc gaa acc aaa cca cgc tca ata acc cgc   163
Arg His Gly Leu Gly Ser Pro Glu Thr Lys Pro Arg Ser Ile Thr Arg
                10                  15                  20

cgg ttt ttc acc gcg gcc gcc gct acg ctg gca gga ttg gca gtc ctg   211
Arg Phe Phe Thr Ala Ala Ala Ala Thr Leu Ala Gly Leu Ala Val Leu
            25                  30                  35

tcc ggc tgc aca gca caa ccc tca caa gca gaa gac aac acg ctc act   259
Ser Gly Cys Thr Ala Gln Pro Ser Gln Ala Glu Asp Asn Thr Leu Thr
        40                  45                  50

tac tta gag cca cag ttc ttc cgc acc ctg tac cca cca tca gcg ggc   307
Tyr Leu Glu Pro Gln Phe Phe Arg Thr Leu Tyr Pro Pro Ser Ala Gly
    55                  60                  65

ttt tac ccc aac ggc agt gtg gtg aac aac att gca gac cgc ttg ctc   355
Phe Tyr Pro Asn Gly Ser Val Val Asn Asn Ile Ala Asp Arg Leu Leu
 70                  75                  80                  85

tac cag gat cct gaa acc ttg gaa ctc aag ccg tgg atc gcc acc gaa   403
Tyr Gln Asp Pro Glu Thr Leu Glu Leu Lys Pro Trp Ile Ala Thr Glu
                90                  95                  100

ctc cca gaa gta aac gaa gac gcc acg gaa ttt acc ttc aac atc cgc   451
Leu Pro Glu Val Asn Glu Asp Ala Thr Glu Phe Thr Phe Asn Ile Arg
            105                 110                 115

acc gat gtc acc tac tcc gat ggc acc ccg ctg acg gct gaa aac gtg   499
Thr Asp Val Thr Tyr Ser Asp Gly Thr Pro Leu Thr Ala Glu Asn Val
        120                 125                 130

gtg aaa aac ttc gat ctc tat ggc ctc ggc gat caa gat cga cgc ctc   547
Val Lys Asn Phe Asp Leu Tyr Gly Leu Gly Asp Gln Asp Arg Arg Leu
    135                 140                 145

acc atc tct gag cag atc acc aac tac gac cac ggc gaa gta gta gat   595
Thr Ile Ser Glu Gln Ile Thr Asn Tyr Asp His Gly Glu Val Val Asp
150                 155                 160                 165

gag gac acc gtc cga ttc cac ttc tct gag cct gca cct ggt ttt gct   643
Glu Asp Thr Val Arg Phe His Phe Ser Glu Pro Ala Pro Gly Phe Ala
                170                 175                 180

cag gcc acc agc tcc ttc aac gct ggc ctt tat gcc gat tcc acc ttg   691
Gln Ala Thr Ser Ser Phe Asn Ala Gly Leu Tyr Ala Asp Ser Thr Leu
            185                 190                 195

gag ttc gcc aat gag gat ttc gcg cca ggc aac gcc caa aac gtc atc   739
Glu Phe Ala Asn Glu Asp Phe Ala Pro Gly Asn Ala Gln Asn Val Ile
        200                 205                 210

ggc tcc ggt cct ttc gtg atc acc gat gaa acc cta ggc acc aac ctc   787
Gly Ser Gly Pro Phe Val Ile Thr Asp Glu Thr Leu Gly Thr Asn Leu
    215                 220                 225
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acc ttg act gcg cgt gag gat tac gat tgg gca cca cca tca cgc gaa     835
Thr Leu Thr Ala Arg Glu Asp Tyr Asp Trp Ala Pro Pro Ser Arg Glu
230                 235                 240                 245

cat caa ggt cgc gcg aag ctt gac gcc gtc aat tat gtc ctc gcg ggt     883
His Gln Gly Arg Ala Lys Leu Asp Ala Val Asn Tyr Val Leu Ala Gly
                250                 255                 260

gaa gaa tcc gtc cgc atc gga gcc atc gtt gct ggc caa ggt gat atc     931
Glu Glu Ser Val Arg Ile Gly Ala Ile Val Ala Gly Gln Gly Asp Ile
            265                 270                 275

gcc cgc cag atc gaa gcg cca gtg gag gca cac ctg aag gat gca ggc     979
Ala Arg Gln Ile Glu Ala Pro Val Glu Ala His Leu Lys Asp Ala Gly
        280                 285                 290

atc ccg atc atc tcc gca gcc acc aac ggt gtg aac aac agc ttc aac    1027
Ile Pro Ile Ile Ser Ala Ala Thr Asn Gly Val Asn Asn Ser Phe Asn
    295                 300                 305

ttc cgc ttc aaa aac gag ctg ctc tca gac atc cgt gtt cgc caa gct    1075
Phe Arg Phe Lys Asn Glu Leu Leu Ser Asp Ile Arg Val Arg Gln Ala
310                 315                 320                 325

ctg atc cac gcg atc gac cgc gaa aag atc atg cgt gtg ctg ttt agt    1123
Leu Ile His Ala Ile Asp Arg Glu Lys Ile Met Arg Val Leu Phe Ser
                330                 335                 340

gat tcc tat ccg ctg gca act tct gtg ctt gcg caa aat gca ctg ggc    1171
Asp Ser Tyr Pro Leu Ala Thr Ser Val Leu Ala Gln Asn Ala Leu Gly
            345                 350                 355

tac aaa gaa caa gta gat gcc tat gtc tac gac cta gac aaa gca aca    1219
Tyr Lys Glu Gln Val Asp Ala Tyr Val Tyr Asp Leu Asp Lys Ala Thr
        360                 365                 370

gct ctg ctt gac gaa gcc ggc tgg acc ctt gat agc gac ggc atg cgt    1267
Ala Leu Leu Asp Glu Ala Gly Trp Thr Leu Asp Ser Asp Gly Met Arg
    375                 380                 385

cgc aag gac ggt gaa ctt cta gag ctc acc ttc aac gaa gcc ctc cca    1315
Arg Lys Asp Gly Glu Leu Leu Glu Leu Thr Phe Asn Glu Ala Leu Pro
390                 395                 400                 405

cag cct cgt tca cgc gaa gtt gtc acc atg gtc caa gaa cag ctc ggt    1363
Gln Pro Arg Ser Arg Glu Val Val Thr Met Val Gln Glu Gln Leu Gly
                410                 415                 420

gat ctg ggc atc aag gtc aac ctc aac cca ggt gac caa gca gcc cag    1411
Asp Leu Gly Ile Lys Val Asn Leu Asn Pro Gly Asp Gln Ala Ala Gln
            425                 430                 435

gac gct gac tcc aag gat ctc aac aag atc cag gtt cgc cac acc atg    1459
Asp Ala Asp Ser Lys Asp Leu Asn Lys Ile Gln Val Arg His Thr Met
        440                 445                 450

gtg ggt cgc gca gac tat gac gtg ctg aaa tcc cag ctg tac tcc acc    1507
Val Gly Arg Ala Asp Tyr Asp Val Leu Lys Ser Gln Leu Tyr Ser Thr
    455                 460                 465
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aac cgc aac gag ctg ttg aac atg acc gtg gaa ggg gag acc gcc gat 1555
Asn Arg Asn Glu Leu Leu Asn Met Thr Val Glu Gly Glu Thr Ala Asp
470 475 480 485

att ggc gat cct cat ttg gag gaa ctc ctc atg gct att gca tcc agc 1603
Ile Gly Asp Pro His Leu Glu Glu Leu Leu Met Ala Ile Ala Ser Ser
490 495 500

cca cgc gaa gag gac cgt gca gca gca tct gcc gca gca cag gat tac 1651
Pro Arg Glu Glu Asp Arg Ala Ala Ala Ser Ala Ala Ala Gln Asp Tyr
505 510 515

atc acc gag cag gca tat gtt ctt cca ctg ttt gaa gag cca gtt gtc 1699
Ile Thr Glu Gln Ala Tyr Val Leu Pro Leu Phe Glu Glu Pro Val Val
520 525 530

tac ggc gtg cag cct tac gtg aag ggc ttt agc ccc gaa gtg atc ggc 1747
Tyr Gly Val Gln Pro Tyr Val Lys Gly Phe Ser Pro Glu Val Ile Gly
535 540 545

cgc ccc agc ttc tat gag acc tac att gac cat tcc agc gac cat tcc 1795
Arg Pro Ser Phe Tyr Glu Thr Tyr Ile Asp His Ser Ser Asp His Ser
550 555 560 565

agt gag gag gac taaatgacta cctcgcagat tct 1830
Ser Glu Glu Asp

<210> 20
<211> 569
<212> PRT
<213> Corynebacterium glutamicum

<400> 20
Val Phe Lys Lys His Arg His Gly Leu Gly Ser Pro Glu Thr Lys Pro
1 5 10 15

Arg Ser Ile Thr Arg Arg Phe Phe Thr Ala Ala Ala Ala Thr Leu Ala
20 25 30

Gly Leu Ala Val Leu Ser Gly Cys Thr Ala Gln Pro Ser Gln Ala Glu
35 40 45

Asp Asn Thr Leu Thr Tyr Leu Glu Pro Gln Phe Phe Arg Thr Leu Tyr
50 55 60

Pro Pro Ser Ala Gly Phe Tyr Pro Asn Gly Ser Val Val Asn Asn Ile
65 70 75 80

Ala Asp Arg Leu Leu Tyr Gln Asp Pro Glu Thr Leu Glu Leu Lys Pro
85 90 95

Trp Ile Ala Thr Glu Leu Pro Glu Val Asn Glu Asp Ala Thr Glu Phe
100 105 110

Thr Phe Asn Ile Arg Thr Asp Val Thr Tyr Ser Asp Gly Thr Pro Leu
115 120 125

Thr Ala Glu Asn Val Val Lys Asn Phe Asp Leu Tyr Gly Leu Gly Asp
130 135 140

Gln Asp Arg Arg Leu Thr Ile Ser Glu Gln Ile Thr Asn Tyr Asp His
145 150 155 160

Gly Glu Val Val Asp Glu Asp Thr Val Arg Phe His Phe Ser Glu Pro
165 170 175

Ala Pro Gly Phe Ala Gln Ala Thr Ser Ser Phe Asn Ala Gly Leu Tyr
180 185 190

Ala Asp Ser Thr Leu Glu Phe Ala Asn Glu Asp Phe Ala Pro Gly Asn
195 200 205

Ala Gln Asn Val Ile Gly Ser Gly Pro Phe Val Ile Thr Asp Glu Thr
210 215 220

Leu Gly Thr Asn Leu Thr Leu Thr Ala Arg Glu Asp Tyr Asp Trp Ala
225 230 235 240

Pro Pro Ser Arg Glu His Gln Gly Arg Ala Lys Leu Asp Ala Val Asn
245 250 255

Tyr Val Leu Ala Gly Glu Glu Ser Val Arg Ile Gly Ala Ile Val Ala
260 265 270

Gly Gln Gly Asp Ile Ala Arg Gln Ile Glu Ala Pro Val Glu Ala His
275 280 285

Leu Lys Asp Ala Gly Ile Pro Ile Ile Ser Ala Ala Thr Asn Gly Val
290 295 300

Asn Asn Ser Phe Asn Phe Arg Phe Lys Asn Glu Leu Leu Ser Asp Ile
305 310 315 320

Arg Val Arg Gln Ala Leu Ile His Ala Ile Asp Arg Glu Lys Ile Met
325 330 335

Arg Val Leu Phe Ser Asp Ser Tyr Pro Leu Ala Thr Ser Val Leu Ala
340 345 350

Gln Asn Ala Leu Gly Tyr Lys Glu Gln Val Asp Ala Tyr Val Tyr Asp
355 360 365

Leu Asp Lys Ala Thr Ala Leu Leu Asp Glu Ala Gly Trp Thr Leu Asp
370 375 380

Ser Asp Gly Met Arg Arg Lys Asp Gly Glu Leu Leu Glu Leu Thr Phe
385 390 395 400

Asn Glu Ala Leu Pro Gln Pro Arg Ser Arg Glu Val Val Thr Met Val
405 410 415

Gln Glu Gln Leu Gly Asp Leu Gly Ile Lys Val Asn Leu Asn Pro Gly
420 425 430

Asp Gln Ala Ala Gln Asp Ala Asp Ser Lys Asp Leu Asn Lys Ile Gln
435 440 445

Val Arg His Thr Met Val Gly Arg Ala Asp Tyr Asp Val Leu Lys Ser
450 455 460

Gln Leu Tyr Ser Thr Asn Arg Asn Glu Leu Leu Asn Met Thr Val Glu
465 470 475 480

Gly Glu Thr Ala Asp Ile Gly Asp Pro His Leu Glu Glu Leu Leu Met
485 490 495

Ala Ile Ala Ser Ser Pro Arg Glu Glu Asp Arg Ala Ala Ala Ser Ala
500 505 510

Ala Ala Gln Asp Tyr Ile Thr Glu Gln Ala Tyr Val Leu Pro Leu Phe
515 520 525

Glu Glu Pro Val Val Tyr Gly Val Gln Pro Tyr Val Lys Gly Phe Ser
530 535 540

Pro Glu Val Ile Gly Arg Pro Ser Phe Tyr Glu Thr Tyr Ile Asp His
545 550 555 560

Ser Ser Asp His Ser Ser Glu Glu Asp
565

<210> 21
<211> 858
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(835)
<223> RXN00784

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atctattcca actacgcgta aaacgaggac gtttaaagct atg tct att gaa ttc 115
Met Ser Ile Glu Phe
1 5

tcc gca cca gca aaa atg aaa atc gaa gtg tgg agc gac atc atg tgc 163
Ser Ala Pro Ala Lys Met Lys Ile Glu Val Trp Ser Asp Ile Met Cys
10 15 20

ccc ttc tgc tac atc ggc aaa aag cgc ctc gac gac gcc cta agt acc 211
Pro Phe Cys Tyr Ile Gly Lys Lys Arg Leu Asp Asp Ala Leu Ser Thr
25 30 35

ttt gac cag gcc gga cgc atc gaa gtg gaa tac aag agc ttc gaa ctc 259
Phe Asp Gln Ala Gly Arg Ile Glu Val Glu Tyr Lys Ser Phe Glu Leu
40 45 50

atg cca ggc cta gaa acc cac cca ctg cgt tcc gac gtt gaa tac ctc 307
Met Pro Gly Leu Glu Thr His Pro Leu Arg Ser Asp Val Glu Tyr Leu
55 60 65

gcc gac gcc aag ggc atg agc ctc gag cag gcc cgc caa atg aac ggc 355
Ala Asp Ala Lys Gly Met Ser Leu Glu Gln Ala Arg Gln Met Asn Gly
70 75 80 85

caa gtc caa gca atg gca caa gcc acc gga ctt gaa atg aat cct gac 403
Gln Val Gln Ala Met Ala Gln Ala Thr Gly Leu Glu Met Asn Pro Asp

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                    90                  95                  100

gaa acc atc gcg gcc aac acc atc aac gcg cac cgc ctt acc cac ttc    451
Glu Thr Ile Ala Ala Asn Thr Ile Asn Ala His Arg Leu Thr His Phe
            105                 110                 115

gcg aaa gcc cac ggc aag caa caa gaa gtg gcg cag gaa ctc ttc aag    499
Ala Lys Ala His Gly Lys Gln Gln Glu Val Ala Gln Glu Leu Phe Lys
        120                 125                 130

gct cac ttc gta gac ggc aag aac gtt gat gac ctc gat gtg ctg gtc    547
Ala His Phe Val Asp Gly Lys Asn Val Asp Asp Leu Asp Val Leu Val
    135                 140                 145

tcc att gct gca gag gtt ggt ctc gat gcc agt gca gcc cgc gaa gct    595
Ser Ile Ala Ala Glu Val Gly Leu Asp Ala Ser Ala Ala Arg Glu Ala
150                 155                 160                 165

ctc gaa tcc gac gtg tac acc aac gaa gtc caa caa gac gtc cac gaa    643
Leu Glu Ser Asp Val Tyr Thr Asn Glu Val Gln Gln Asp Val His Glu
                170                 175                 180

gcc cgc caa ctc ggc gtc caa ggt gtg ccc ttc ttt gta ttc gac cgc    691
Ala Arg Gln Leu Gly Val Gln Gly Val Pro Phe Phe Val Phe Asp Arg
            185                 190                 195

aaa tac gcc atc aac ggc gcc caa caa gaa gaa gta ttc acc ggc acc    739
Lys Tyr Ala Ile Asn Gly Ala Gln Gln Glu Glu Val Phe Thr Gly Thr
        200                 205                 210

gta gaa aaa gcc ttc gaa gag tgg gca gcc gaa aac cca gtc agc cca    787
Val Glu Lys Ala Phe Glu Glu Trp Ala Ala Glu Asn Pro Val Ser Pro
    215                 220                 225

ttt gag gtc att gac ggc caa agc tgc tcc gtc gac ggc acc tgc aac    835
Phe Glu Val Ile Asp Gly Gln Ser Cys Ser Val Asp Gly Thr Cys Asn
230                 235                 240                 245

taacttttgg gacctatgtg cgt                                          858


<210> 22
<211> 245
<212> PRT
<213> Corynebacterium glutamicum

<400> 22
Met Ser Ile Glu Phe Ser Ala Pro Ala Lys Met Lys Ile Glu Val Trp
  1               5                  10                  15

Ser Asp Ile Met Cys Pro Phe Cys Tyr Ile Gly Lys Lys Arg Leu Asp
            20                  25                  30

Asp Ala Leu Ser Thr Phe Asp Gln Ala Gly Arg Ile Glu Val Glu Tyr
        35                  40                  45

Lys Ser Phe Glu Leu Met Pro Gly Leu Glu Thr His Pro Leu Arg Ser
    50                  55                  60

Asp Val Glu Tyr Leu Ala Asp Ala Lys Gly Met Ser Leu Glu Gln Ala
65                  70                  75                  80
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Arg Gln Met Asn Gly Gln Val Gln Ala Met Ala Gln Ala Thr Gly Leu
                85                  90                  95

Glu Met Asn Pro Asp Glu Thr Ile Ala Ala Asn Thr Ile Asn Ala His
            100                 105                 110

Arg Leu Thr His Phe Ala Lys Ala His Gly Lys Gln Gln Glu Val Ala
        115                 120                 125

Gln Glu Leu Phe Lys Ala His Phe Val Asp Gly Lys Asn Val Asp Asp
    130                 135                 140

Leu Asp Val Leu Val Ser Ile Ala Ala Glu Val Gly Leu Asp Ala Ser
145                 150                 155                 160

Ala Ala Arg Glu Ala Leu Glu Ser Asp Val Tyr Thr Asn Glu Val Gln
                165                 170                 175

Gln Asp Val His Glu Ala Arg Gln Leu Gly Val Gln Gly Val Pro Phe
            180                 185                 190

Phe Val Phe Asp Arg Lys Tyr Ala Ile Asn Gly Ala Gln Gln Glu Glu
        195                 200                 205

Val Phe Thr Gly Thr Val Glu Lys Ala Phe Glu Glu Trp Ala Ala Glu
    210                 215                 220

Asn Pro Val Ser Pro Phe Glu Val Ile Asp Gly Gln Ser Cys Ser Val
225                 230                 235                 240

Asp Gly Thr Cys Asn
                245


<210> 23
<211> 1896
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1873)
<223> RXA02335

<400> 23
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gtctacccac tgagtcatca atttaaatca ggagttatta gtg tca gtc gag act     115
                                          Val Ser Val Glu Thr
                                          1               5

agg aag atc acc aag gtt ctt gtc gct aac cgt ggt gag att gca atc     163
Arg Lys Ile Thr Lys Val Leu Val Ala Asn Arg Gly Glu Ile Ala Ile
                10                  15                  20

cgc gtg ttc cgt gca gct cga gat gaa ggc atg gga tct gtc gcc gtc     211
Arg Val Phe Arg Ala Ala Arg Asp Glu Gly Met Gly Ser Val Ala Val
            25                  30                  35

tac gca gag cca gat gca gat gca cca ttc gtg tca tat gca gac gag     259
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```
Tyr Ala Glu Pro Asp Ala Asp Ala Pro Phe Val Ser Tyr Ala Asp Glu
        40                  45                  50

gct ttt gcc ctc ggt ggc caa aca tcc gct gag tcc tac ctt gtc att    307
Ala Phe Ala Leu Gly Gly Gln Thr Ser Ala Glu Ser Tyr Leu Val Ile
    55                  60                  65

gac aag atc atc gat gcg gcc cgc aag tcc ggc gcc gac gcc atc cac    355
Asp Lys Ile Ile Asp Ala Ala Arg Lys Ser Gly Ala Asp Ala Ile His
 70                  75                  80                  85

ccc ggc tac ggc ttc ctc gca gaa aac gct gac ttc gca gaa gca gtc    403
Pro Gly Tyr Gly Phe Leu Ala Glu Asn Ala Asp Phe Ala Glu Ala Val
                90                  95                 100

atc aac gaa ggc ctg atc tgg att gga cct tca cct gag tcc atc cgc    451
Ile Asn Glu Gly Leu Ile Trp Ile Gly Pro Ser Pro Glu Ser Ile Arg
            105                 110                 115

tcc ctc ggc gac aag gtc acc gct cgc cac atc gca gat acc gcc aag    499
Ser Leu Gly Asp Lys Val Thr Ala Arg His Ile Ala Asp Thr Ala Lys
        120                 125                 130

gct cca atg gct cct ggc acc aag gaa cca gta aaa gac gca gca gaa    547
Ala Pro Met Ala Pro Gly Thr Lys Glu Pro Val Lys Asp Ala Ala Glu
    135                 140                 145

gtt gtg gct ttc gct gaa gaa ttc ggt ctc cca atc gcc atc aag gca    595
Val Val Ala Phe Ala Glu Glu Phe Gly Leu Pro Ile Ala Ile Lys Ala
150                 155                 160                 165

gct ttc ggt ggc ggc gga cgt ggc atg aag gtt gcc tac aag atg gaa    643
Ala Phe Gly Gly Gly Gly Arg Gly Met Lys Val Ala Tyr Lys Met Glu
                170                 175                 180

gaa gtc gct gac ctc ttc gag tcc gca acc cgt gaa gca acc gca gcg    691
Glu Val Ala Asp Leu Phe Glu Ser Ala Thr Arg Glu Ala Thr Ala Ala
            185                 190                 195

ttc ggc cgc ggc gag tgc ttc gtg gag cgc tac ctg gac aag gca cgc    739
Phe Gly Arg Gly Glu Cys Phe Val Glu Arg Tyr Leu Asp Lys Ala Arg
        200                 205                 210

cac gtt gag gct cag gtc atc gcc gat aag cac ggc aac gtt gtt gtc    787
His Val Glu Ala Gln Val Ile Ala Asp Lys His Gly Asn Val Val Val
    215                 220                 225

gcc gga acc cgt gac tgc tcc ctg cag cgc cgt ttc cag aag ctc gtc    835
Ala Gly Thr Arg Asp Cys Ser Leu Gln Arg Arg Phe Gln Lys Leu Val
230                 235                 240                 245

gaa gaa gca cca gca cca ttc ctc acc gat gac cag cgc gag cgt ctc    883
Glu Glu Ala Pro Ala Pro Phe Leu Thr Asp Asp Gln Arg Glu Arg Leu
                250                 255                 260

cac tcc tcc gcg aag gct atc tgt aag gaa gct ggc tac tac ggt gca    931
His Ser Ser Ala Lys Ala Ile Cys Lys Glu Ala Gly Tyr Tyr Gly Ala
            265                 270                 275

ggc acc gtt gag tac ctc gtt ggc tcc gac ggc ctg atc tcc ttc ctc    979
Gly Thr Val Glu Tyr Leu Val Gly Ser Asp Gly Leu Ile Ser Phe Leu
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280 285 290

gag gtc aac acc cgc ctc cag gtg gaa cac cca gtc acc gaa gag acc 1027
Glu Val Asn Thr Arg Leu Gln Val Glu His Pro Val Thr Glu Glu Thr
295 300 305

acc ggc atc gac ctg gtc cgc gaa atg ttc cgc atc gca gaa ggc cac 1075
Thr Gly Ile Asp Leu Val Arg Glu Met Phe Arg Ile Ala Glu Gly His
310 315 320 325

gag ctc tcc atc aag gaa gat cca gct cca cgc ggc cac gca ttc gag 1123
Glu Leu Ser Ile Lys Glu Asp Pro Ala Pro Arg Gly His Ala Phe Glu
330 335 340

ttc cgc atc aac ggc gaa gac gct ggc tcc aac ttc atg cct gca cca 1171
Phe Arg Ile Asn Gly Glu Asp Ala Gly Ser Asn Phe Met Pro Ala Pro
345 350 355

ggc aag atc acc agc tac cgc gag cca cag ggc cca ggc gtc cgc atg 1219
Gly Lys Ile Thr Ser Tyr Arg Glu Pro Gln Gly Pro Gly Val Arg Met
360 365 370

gac tcc ggt gtc gtt gaa ggt tcc gaa atc tcc gga cag ttc gac tcc 1267
Asp Ser Gly Val Val Glu Gly Ser Glu Ile Ser Gly Gln Phe Asp Ser
375 380 385

atg ctg gca aag ctg atc gtt tgg ggc gac acc cgc gag cag gct ctc 1315
Met Leu Ala Lys Leu Ile Val Trp Gly Asp Thr Arg Glu Gln Ala Leu
390 395 400 405

cag cgc tcc cgc cgt gca ctt gca gag tac gtt gtc gag ggc atg cca 1363
Gln Arg Ser Arg Arg Ala Leu Ala Glu Tyr Val Val Glu Gly Met Pro
410 415 420

acc gtt atc cca ttc cac cag cac atc gtg gaa aac cca gca ttc gtg 1411
Thr Val Ile Pro Phe His Gln His Ile Val Glu Asn Pro Ala Phe Val
425 430 435

ggc aac gac gaa ggc ttc gag atc tac acc aag tgg atc gaa gag gtt 1459
Gly Asn Asp Glu Gly Phe Glu Ile Tyr Thr Lys Trp Ile Glu Glu Val
440 445 450

tgg gat aac cca atc gca cct tac gtt gac gct tcc gag ctc gac gaa 1507
Trp Asp Asn Pro Ile Ala Pro Tyr Val Asp Ala Ser Glu Leu Asp Glu
455 460 465

gat gag gac aag acc cca gca cag aag gtt gtt gtg gag atc aac ggc 1555
Asp Glu Asp Lys Thr Pro Ala Gln Lys Val Val Val Glu Ile Asn Gly
470 475 480 485

cgt cgc gtt gag gtt gca ctc cca ggc gat ctg gca ctc ggt ggc acc 1603
Arg Arg Val Glu Val Ala Leu Pro Gly Asp Leu Ala Leu Gly Gly Thr
490 495 500

gct ggt cct aag aag aag gcc aag aag cgt cgc gca ggt ggt gca aag 1651
Ala Gly Pro Lys Lys Lys Ala Lys Lys Arg Arg Ala Gly Gly Ala Lys
505 510 515

gct ggc gta tcc ggc gat gca gtg gca gct cca atg cag ggc act gtc 1699
Ala Gly Val Ser Gly Asp Ala Val Ala Ala Pro Met Gln Gly Thr Val
520 525 530

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atc aag gtc aac gtc gaa gaa ggc gct gaa gtc aac gaa ggc gac acc    1747
Ile Lys Val Asn Val Glu Glu Gly Ala Glu Val Asn Glu Gly Asp Thr
    535                 540                 545

gtt gtt gtc ctc gag gct atg aag atg gaa aac cct gtg aag gct cat    1795
Val Val Val Leu Glu Ala Met Lys Met Glu Asn Pro Val Lys Ala His
550                 555                 560                 565

aag tcc gga acc gta acc ggc ctt act gtc gct gca ggc gag ggt gtc    1843
Lys Ser Gly Thr Val Thr Gly Leu Thr Val Ala Ala Gly Glu Gly Val
                570                 575                 580

aac aag ggc gtt gtt ctc ctc gag atc aag taagttcttg gattcctgtt      1893
Asn Lys Gly Val Val Leu Leu Glu Ile Lys
            585                 590

agt                                                                1896
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<210> 24
<211> 591
<212> PRT
<213> Corynebacterium glutamicum

<400> 24

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Val Ser Val Glu Thr Arg Lys Ile Thr Lys Val Leu Val Ala Asn Arg
  1               5                  10                  15

Gly Glu Ile Ala Ile Arg Val Phe Arg Ala Ala Arg Asp Glu Gly Met
             20                  25                  30

Gly Ser Val Ala Val Tyr Ala Glu Pro Asp Ala Asp Ala Pro Phe Val
         35                  40                  45

Ser Tyr Ala Asp Glu Ala Phe Ala Leu Gly Gly Gln Thr Ser Ala Glu
     50                  55                  60

Ser Tyr Leu Val Ile Asp Lys Ile Ile Asp Ala Ala Arg Lys Ser Gly
 65                  70                  75                  80

Ala Asp Ala Ile His Pro Gly Tyr Gly Phe Leu Ala Glu Asn Ala Asp
                 85                  90                  95

Phe Ala Glu Ala Val Ile Asn Glu Gly Leu Ile Trp Ile Gly Pro Ser
            100                 105                 110

Pro Glu Ser Ile Arg Ser Leu Gly Asp Lys Val Thr Ala Arg His Ile
        115                 120                 125

Ala Asp Thr Ala Lys Ala Pro Met Ala Pro Gly Thr Lys Glu Pro Val
    130                 135                 140

Lys Asp Ala Ala Glu Val Val Ala Phe Ala Glu Glu Phe Gly Leu Pro
145                 150                 155                 160

Ile Ala Ile Lys Ala Ala Phe Gly Gly Gly Gly Arg Gly Met Lys Val
                165                 170                 175

Ala Tyr Lys Met Glu Glu Val Ala Asp Leu Phe Glu Ser Ala Thr Arg
            180                 185                 190
```

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Glu Ala Thr Ala Ala Phe Gly Arg Gly Glu Cys Phe Val Glu Arg Tyr
        195                 200                 205

Leu Asp Lys Ala Arg His Val Glu Ala Gln Val Ile Ala Asp Lys His
    210                 215                 220

Gly Asn Val Val Val Ala Gly Thr Arg Asp Cys Ser Leu Gln Arg Arg
225                 230                 235                 240

Phe Gln Lys Leu Val Glu Glu Ala Pro Ala Pro Phe Leu Thr Asp Asp
                245                 250                 255

Gln Arg Glu Arg Leu His Ser Ser Ala Lys Ala Ile Cys Lys Glu Ala
            260                 265                 270

Gly Tyr Tyr Gly Ala Gly Thr Val Glu Tyr Leu Val Gly Ser Asp Gly
        275                 280                 285

Leu Ile Ser Phe Leu Glu Val Asn Thr Arg Leu Gln Val Glu His Pro
    290                 295                 300

Val Thr Glu Glu Thr Thr Gly Ile Asp Leu Val Arg Glu Met Phe Arg
305                 310                 315                 320

Ile Ala Glu Gly His Glu Leu Ser Ile Lys Glu Asp Pro Ala Pro Arg
                325                 330                 335

Gly His Ala Phe Glu Phe Arg Ile Asn Gly Glu Asp Ala Gly Ser Asn
            340                 345                 350

Phe Met Pro Ala Pro Gly Lys Ile Thr Ser Tyr Arg Glu Pro Gln Gly
        355                 360                 365

Pro Gly Val Arg Met Asp Ser Gly Val Val Glu Gly Ser Glu Ile Ser
    370                 375                 380

Gly Gln Phe Asp Ser Met Leu Ala Lys Leu Ile Val Trp Gly Asp Thr
385                 390                 395                 400

Arg Glu Gln Ala Leu Gln Arg Ser Arg Arg Ala Leu Ala Glu Tyr Val
                405                 410                 415

Val Glu Gly Met Pro Thr Val Ile Pro Phe His Gln His Ile Val Glu
            420                 425                 430

Asn Pro Ala Phe Val Gly Asn Asp Glu Gly Phe Glu Ile Tyr Thr Lys
        435                 440                 445

Trp Ile Glu Glu Val Trp Asp Asn Pro Ile Ala Pro Tyr Val Asp Ala
    450                 455                 460

Ser Glu Leu Asp Glu Asp Glu Asp Lys Thr Pro Ala Gln Lys Val Val
465                 470                 475                 480

Val Glu Ile Asn Gly Arg Arg Val Glu Val Ala Leu Pro Gly Asp Leu
                485                 490                 495

Ala Leu Gly Gly Thr Ala Gly Pro Lys Lys Lys Ala Lys Lys Arg Arg
            500                 505                 510
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Ala Gly Gly Ala Lys Ala Gly Val Ser Gly Asp Ala Val Ala Ala Pro
        515                 520                 525

Met Gln Gly Thr Val Ile Lys Val Asn Val Glu Glu Gly Ala Glu Val
    530                 535                 540

Asn Glu Gly Asp Thr Val Val Val Leu Glu Ala Met Lys Met Glu Asn
545                 550                 555                 560

Pro Val Lys Ala His Lys Ser Gly Thr Val Thr Gly Leu Thr Val Ala
                565                 570                 575

Ala Gly Glu Gly Val Asn Lys Gly Val Val Leu Leu Glu Ile Lys
            580                 585                 590


&lt;210&gt; 25
&lt;211&gt; 1575
&lt;212&gt; DNA
&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (101)..(1552)
&lt;223&gt; RXA02173

&lt;400&gt; 25
ctaaattggg cttagatctt ccgcctctaa ataggtatgc agagacattc gaattaatta 60

acaaagccat ttttcggccg tggagaagcg ttttccgact atg gtg tgg ggc atg    115
                                           Met Val Trp Gly Met
                                            1               5

gaa cac act tca gca ttg acg ctc ata gac tcg gtt ttg gac cct gac    163
Glu His Thr Ser Ala Leu Thr Leu Ile Asp Ser Val Leu Asp Pro Asp
                10                  15                  20

agc ttc att tct tgg aat gaa act ccc caa tat gac aac ctc aat caa    211
Ser Phe Ile Ser Trp Asn Glu Thr Pro Gln Tyr Asp Asn Leu Asn Gln
            25                  30                  35

ggc tat gca gag acc ttg gag cgg gct cga agc aag gcc aaa tgc gat    259
Gly Tyr Ala Glu Thr Leu Glu Arg Ala Arg Ser Lys Ala Lys Cys Asp
        40                  45                  50

gaa tcg gta att act gga gaa ggc acc gtg gag ggc att ccg gta gcc    307
Glu Ser Val Ile Thr Gly Glu Gly Thr Val Glu Gly Ile Pro Val Ala
    55                  60                  65

gtt att ttg tcc gat ttt tcc ttc ctc ggc ggt tct ttg ggc acg gtc    355
Val Ile Leu Ser Asp Phe Ser Phe Leu Gly Gly Ser Leu Gly Thr Val
70                  75                  80                  85

gcg tcg gtg cgc atc atg aag gcg att cac cgc gcc aca gag ctg aaa    403
Ala Ser Val Arg Ile Met Lys Ala Ile His Arg Ala Thr Glu Leu Lys
                90                  95                  100

ctc cca ctg ctg gtc tcc cct gct tcc ggt ggt gcg cgc atg cag gaa    451
Leu Pro Leu Leu Val Ser Pro Ala Ser Gly Gly Ala Arg Met Gln Glu
            105                 110                 115
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gac aat cga gct ttt gtc atg atg gtg tcc ata acc gcg gct gtg cag 499
Asp Asn Arg Ala Phe Val Met Met Val Ser Ile Thr Ala Ala Val Gln
120 125 130

cgt cac cgc gag gcg cat ttg ccg ttc ctg gtg tat ttg cgc aat ccc 547
Arg His Arg Glu Ala His Leu Pro Phe Leu Val Tyr Leu Arg Asn Pro
135 140 145

acg atg ggt ggc gcc atg gcc tcg tgg ggt tca tct ggg cat ctc act 595
Thr Met Gly Gly Ala Met Ala Ser Trp Gly Ser Ser Gly His Leu Thr
150 155 160 165

ttt gcg gaa ccc ggc gcg cag ata ggt ttc ctg ggt cct cgc gtg gtg 643
Phe Ala Glu Pro Gly Ala Gln Ile Gly Phe Leu Gly Pro Arg Val Val
170 175 180

gag tta acc act ggg cat gcg ctt cca gac ggt gtg cag cag gcg gag 691
Glu Leu Thr Thr Gly His Ala Leu Pro Asp Gly Val Gln Gln Ala Glu
185 190 195

aat ttg gtg aaa act ggt gtg att gat gga att gtg tcg cca ctc caa 739
Asn Leu Val Lys Thr Gly Val Ile Asp Gly Ile Val Ser Pro Leu Gln
200 205 210

ttg cgt gca gcg gtg gca aaa acc ctc aag gtt att cag ccg gta gag 787
Leu Arg Ala Ala Val Ala Lys Thr Leu Lys Val Ile Gln Pro Val Glu
215 220 225

gca acg gat cgt ttt tct cca aca act cct ggc gtg gca ctt ccg gtg 835
Ala Thr Asp Arg Phe Ser Pro Thr Thr Pro Gly Val Ala Leu Pro Val
230 235 240 245

atg gag gcg att gcg cgt tct cgt gac ccg cag agg cct gga atc ggg 883
Met Glu Ala Ile Ala Arg Ser Arg Asp Pro Gln Arg Pro Gly Ile Gly
250 255 260

gag att atg gaa acg ttg ggg gca gac gtc gtc aag ctt tct ggt gcg 931
Glu Ile Met Glu Thr Leu Gly Ala Asp Val Val Lys Leu Ser Gly Ala
265 270 275

cgt gct ggc gca ttg agc ccg gct gtg cgc gtt gcc ctg gcg cgc atc 979
Arg Ala Gly Ala Leu Ser Pro Ala Val Arg Val Ala Leu Ala Arg Ile
280 285 290

ggg ggc cgg ccc gtg gtg ctg att ggg cag gat cgc cgc ttc acg ctt 1027
Gly Gly Arg Pro Val Val Leu Ile Gly Gln Asp Arg Arg Phe Thr Leu
295 300 305

ggg ccg cag gag ctg cgt ttt gcg cgt cgt ggc att tcg ctg gcg cgc 1075
Gly Pro Gln Glu Leu Arg Phe Ala Arg Arg Gly Ile Ser Leu Ala Arg
310 315 320 325

gag cta aac ctg ccg atc gtg tcc atc atc gac acc tcc ggc gcc gaa 1123
Glu Leu Asn Leu Pro Ile Val Ser Ile Ile Asp Thr Ser Gly Ala Glu
330 335 340

ttg tcg cag gcg gct gag gag ctc ggc atc gca agc tcg att gcg cgc 1171
Leu Ser Gln Ala Ala Glu Glu Leu Gly Ile Ala Ser Ser Ile Ala Arg
345 350 355

acc ttg tcc aag ctt atc gac gct ccc ctc ccc acc gtt tcg gtc att 1219

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Thr Leu Ser Lys Leu Ile Asp Ala Pro Leu Pro Thr Val Ser Val Ile
        360                 365                 370

att ggt cag ggc gtt ggc ggt ggc gcg ctg gcc atg ctg ccc gcc gat    1267
Ile Gly Gln Gly Val Gly Gly Gly Ala Leu Ala Met Leu Pro Ala Asp
    375                 380                 385

ctg gtc tac gcg gcc gaa aac gcg tgg ctg tcc gca ttg cca cca gag    1315
Leu Val Tyr Ala Ala Glu Asn Ala Trp Leu Ser Ala Leu Pro Pro Glu
390                 395                 400                 405

ggc gcc tcg gcc atc ctc ttc cgc gac acc aac cac gcc gcg gaa atc    1363
Gly Ala Ser Ala Ile Leu Phe Arg Asp Thr Asn His Ala Ala Glu Ile
                410                 415                 420

ata gag cga caa ggc gtg cag gcg cac gca ctt tta agc caa ggg ctt    1411
Ile Glu Arg Gln Gly Val Gln Ala His Ala Leu Leu Ser Gln Gly Leu
            425                 430                 435

atc gac ggg atc gtc gcc gaa acc gag cac ttt gtt gaa gaa att ctc    1459
Ile Asp Gly Ile Val Ala Glu Thr Glu His Phe Val Glu Glu Ile Leu
        440                 445                 450

ggc aca atc agc aac gcc ctc tcc gaa ttg gat aac aat ccg gag agg    1507
Gly Thr Ile Ser Asn Ala Leu Ser Glu Leu Asp Asn Asn Pro Glu Arg
    455                 460                 465

gcg gga cgc gac agt cgc ttc aca cga ttt gag cgt tta gcg cag        1552
Ala Gly Arg Asp Ser Arg Phe Thr Arg Phe Glu Arg Leu Ala Gln
470                 475                 480

taaagaaaat tatgcgctga tca                                          1575


<210> 26
<211> 484
<212> PRT
<213> Corynebacterium glutamicum

<400> 26
Met Val Trp Gly Met Glu His Thr Ser Ala Leu Thr Leu Ile Asp Ser
  1               5                  10                  15

Val Leu Asp Pro Asp Ser Phe Ile Ser Trp Asn Glu Thr Pro Gln Tyr
             20                  25                  30

Asp Asn Leu Asn Gln Gly Tyr Ala Glu Thr Leu Glu Arg Ala Arg Ser
        35                  40                  45

Lys Ala Lys Cys Asp Glu Ser Val Ile Thr Gly Glu Gly Thr Val Glu
    50                  55                  60

Gly Ile Pro Val Ala Val Ile Leu Ser Asp Phe Ser Phe Leu Gly Gly
 65                  70                  75                  80

Ser Leu Gly Thr Val Ala Ser Val Arg Ile Met Lys Ala Ile His Arg
                 85                  90                  95

Ala Thr Glu Leu Lys Leu Pro Leu Leu Val Ser Pro Ala Ser Gly Gly
            100                 105                 110
```

Ala Arg Met Gln Glu Asp Asn Arg Ala Phe Val Met Met Val Ser Ile
115 120 125

Thr Ala Ala Val Gln Arg His Arg Glu Ala His Leu Pro Phe Leu Val
130 135 140

Tyr Leu Arg Asn Pro Thr Met Gly Gly Ala Met Ala Ser Trp Gly Ser
145 150 155 160

Ser Gly His Leu Thr Phe Ala Glu Pro Gly Ala Gln Ile Gly Phe Leu
165 170 175

Gly Pro Arg Val Val Glu Leu Thr Thr Gly His Ala Leu Pro Asp Gly
180 185 190

Val Gln Gln Ala Glu Asn Leu Val Lys Thr Gly Val Ile Asp Gly Ile
195 200 205

Val Ser Pro Leu Gln Leu Arg Ala Ala Val Ala Lys Thr Leu Lys Val
210 215 220

Ile Gln Pro Val Glu Ala Thr Asp Arg Phe Ser Pro Thr Thr Pro Gly
225 230 235 240

Val Ala Leu Pro Val Met Glu Ala Ile Ala Arg Ser Arg Asp Pro Gln
245 250 255

Arg Pro Gly Ile Gly Glu Ile Met Glu Thr Leu Gly Ala Asp Val Val
260 265 270

Lys Leu Ser Gly Ala Arg Ala Gly Ala Leu Ser Pro Ala Val Arg Val
275 280 285

Ala Leu Ala Arg Ile Gly Gly Arg Pro Val Val Leu Ile Gly Gln Asp
290 295 300

Arg Arg Phe Thr Leu Gly Pro Gln Glu Leu Arg Phe Ala Arg Arg Gly
305 310 315 320

Ile Ser Leu Ala Arg Glu Leu Asn Leu Pro Ile Val Ser Ile Ile Asp
325 330 335

Thr Ser Gly Ala Glu Leu Ser Gln Ala Ala Glu Glu Leu Gly Ile Ala
340 345 350

Ser Ser Ile Ala Arg Thr Leu Ser Lys Leu Ile Asp Ala Pro Leu Pro
355 360 365

Thr Val Ser Val Ile Ile Gly Gln Gly Val Gly Gly Gly Ala Leu Ala
370 375 380

Met Leu Pro Ala Asp Leu Val Tyr Ala Ala Glu Asn Ala Trp Leu Ser
385 390 395 400

Ala Leu Pro Pro Glu Gly Ala Ser Ala Ile Leu Phe Arg Asp Thr Asn
405 410 415

His Ala Ala Glu Ile Ile Glu Arg Gln Gly Val Gln Ala His Ala Leu
420 425 430

Leu Ser Gln Gly Leu Ile Asp Gly Ile Val Ala Glu Thr Glu His Phe

435 440 445

Val Glu Glu Ile Leu Gly Thr Ile Ser Asn Ala Leu Ser Glu Leu Asp
450 455 460

Asn Asn Pro Glu Arg Ala Gly Arg Asp Ser Arg Phe Thr Arg Phe Glu
465 470 475 480

Arg Leu Ala Gln

<210> 27
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1033)
<223> RXA01764

<400> 27
ttttcaaaat taatagttga cattttcaac gttatgagtt ttcattggta tcacgccccg 60

acgaagtgtc tgggatcaca aaccttcaaa ggagtttgaa atg tct ctc aat gga 115
Met Ser Leu Asn Gly
1 5

aaa gtc gcc atc gtt acc gga tct ggt gca gga ctt ggt cgt tcc ttc 163
Lys Val Ala Ile Val Thr Gly Ser Gly Ala Gly Leu Gly Arg Ser Phe
10 15 20

gct cag gag ctt gcc cgt cag ggt gca tct gtc atc gtc aat gac gta 211
Ala Gln Glu Leu Ala Arg Gln Gly Ala Ser Val Ile Val Asn Asp Val
25 30 35

aac cag gca gcc gca gat gag act gtc gca gca atc acc gaa gcc ggc 259
Asn Gln Ala Ala Ala Asp Glu Thr Val Ala Ala Ile Thr Glu Ala Gly
40 45 50

ggc aaa gcc gcc gcc gtt atc gcc ccc gtt gga ccc tct gaa agc gcc 307
Gly Lys Ala Ala Ala Val Ile Ala Pro Val Gly Pro Ser Glu Ser Ala
55 60 65

gca ttg ctg gtg cgg gag gcc gtc gac aag ttc ggt tct ttg gac att 355
Ala Leu Leu Val Arg Glu Ala Val Asp Lys Phe Gly Ser Leu Asp Ile
70 75 80 85

ctt gtc aca aac gcg ggc atc ctt cgt gat agg tcc ctg ctg aag atg 403
Leu Val Thr Asn Ala Gly Ile Leu Arg Asp Arg Ser Leu Leu Lys Met
90 95 100

acg gac gat gat ttc gat gca gtc att aac gtg cac ctc aag ggc act 451
Thr Asp Asp Asp Phe Asp Ala Val Ile Asn Val His Leu Lys Gly Thr
105 110 115

ttc acc tgt gtt cgc gag gca ttt gga tac ttc aag gag aat gga atc 499
Phe Thr Cys Val Arg Glu Ala Phe Gly Tyr Phe Lys Glu Asn Gly Ile
120 125 130

gcg ggg cgc atc gtc acg att ggt tct ccc acc ggg cag cgc ggc aac 547
Ala Gly Arg Ile Val Thr Ile Gly Ser Pro Thr Gly Gln Arg Gly Asn
135 140 145

ttc gga cag agc aat tac gct gca gct aag gcg ggc att gtg ggt atg 595
Phe Gly Gln Ser Asn Tyr Ala Ala Ala Lys Ala Gly Ile Val Gly Met
150 155 160 165

gtt cgc acg tgg gcg ctg gag atg aag cgc gca ggt gtc acc att aac 643
Val Arg Thr Trp Ala Leu Glu Met Lys Arg Ala Gly Val Thr Ile Asn
170 175 180

gcg atc att ccg gaa gca gcc acc gat atg acc aag acg gtg cca tat 691
Ala Ile Ile Pro Glu Ala Ala Thr Asp Met Thr Lys Thr Val Pro Tyr
185 190 195

ttc cag aag gct gta gag gcc gat gag cgt ggc gag gcc atg cca gca 739
Phe Gln Lys Ala Val Glu Ala Asp Glu Arg Gly Glu Ala Met Pro Ala
200 205 210

ttc ttc cgc gag acc cta ggt ttt ggc act cct cag gat gtt gcg gga 787
Phe Phe Arg Glu Thr Leu Gly Phe Gly Thr Pro Gln Asp Val Ala Gly
215 220 225

ctt gtg gcc ttc ctt tcc tct gat gag gca gcg aat att tct gga cag 835
Leu Val Ala Phe Leu Ser Ser Asp Glu Ala Ala Asn Ile Ser Gly Gln
230 235 240 245

gcc atc ggt gca ggc ggc gac cgc atg cag gtg tgg aag cac cca gag 883
Ala Ile Gly Ala Gly Gly Asp Arg Met Gln Val Trp Lys His Pro Glu
250 255 260

cca gca gtt act gaa ttt aac cca ggt ggc tgg acc tat gaa gca ctg 931
Pro Ala Val Thr Glu Phe Asn Pro Gly Gly Trp Thr Tyr Glu Ala Leu
265 270 275

cag gaa cgt ggc aag aac att att gag ggc aac ctg cag tcc gtc ggt 979
Gln Glu Arg Gly Lys Asn Ile Ile Glu Gly Asn Leu Gln Ser Val Gly
280 285 290

gtc gtt ttc cct gaa ctg ccg gca gag ctt cag cca caa atc cca gtc 1027
Val Val Phe Pro Glu Leu Pro Ala Glu Leu Gln Pro Gln Ile Pro Val
295 300 305

aag gca taacaccgca caccaagaat ttt 1056
Lys Ala
310

<210> 28
<211> 311
<212> PRT
<213> Corynebacterium glutamicum

<400> 28
Met Ser Leu Asn Gly Lys Val Ala Ile Val Thr Gly Ser Gly Ala Gly
1 5 10 15

Leu Gly Arg Ser Phe Ala Gln Glu Leu Ala Arg Gln Gly Ala Ser Val
20 25 30

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Ile Val Asn Asp Val Asn Gln Ala Ala Ala Asp Glu Thr Val Ala Ala
        35                  40                  45

Ile Thr Glu Ala Gly Gly Lys Ala Ala Ala Val Ile Ala Pro Val Gly
    50                  55                  60

Pro Ser Glu Ser Ala Ala Leu Leu Val Arg Glu Ala Val Asp Lys Phe
65                  70                  75                  80

Gly Ser Leu Asp Ile Leu Val Thr Asn Ala Gly Ile Leu Arg Asp Arg
                85                  90                  95

Ser Leu Leu Lys Met Thr Asp Asp Asp Phe Asp Ala Val Ile Asn Val
            100                 105                 110

His Leu Lys Gly Thr Phe Thr Cys Val Arg Glu Ala Phe Gly Tyr Phe
        115                 120                 125

Lys Glu Asn Gly Ile Ala Gly Arg Ile Val Thr Ile Gly Ser Pro Thr
    130                 135                 140

Gly Gln Arg Gly Asn Phe Gly Gln Ser Asn Tyr Ala Ala Ala Lys Ala
145                 150                 155                 160

Gly Ile Val Gly Met Val Arg Thr Trp Ala Leu Glu Met Lys Arg Ala
                165                 170                 175

Gly Val Thr Ile Asn Ala Ile Ile Pro Glu Ala Ala Thr Asp Met Thr
            180                 185                 190

Lys Thr Val Pro Tyr Phe Gln Lys Ala Val Glu Ala Asp Glu Arg Gly
        195                 200                 205

Glu Ala Met Pro Ala Phe Phe Arg Glu Thr Leu Gly Phe Gly Thr Pro
    210                 215                 220

Gln Asp Val Ala Gly Leu Val Ala Phe Leu Ser Ser Asp Glu Ala Ala
225                 230                 235                 240

Asn Ile Ser Gly Gln Ala Ile Gly Ala Gly Gly Asp Arg Met Gln Val
                245                 250                 255

Trp Lys His Pro Glu Pro Ala Val Thr Glu Phe Asn Pro Gly Gly Trp
            260                 265                 270

Thr Tyr Glu Ala Leu Gln Glu Arg Gly Lys Asn Ile Ile Glu Gly Asn
        275                 280                 285

Leu Gln Ser Val Gly Val Val Phe Pro Glu Leu Pro Ala Glu Leu Gln
    290                 295                 300

Pro Gln Ile Pro Val Lys Ala
305                 310
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<210> 29
<211> 1827
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(1804)
<223> RXN02487

<400> 29
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atactaaagg gcactaaagc aacgcagttg aagggacacc atg tca gca tac gaa 115
Met Ser Ala Tyr Glu
1 5

acc aaa gaa tgg ctc cag cac tac cca gag tgg acg cca cac tcg ctg 163
Thr Lys Glu Trp Leu Gln His Tyr Pro Glu Trp Thr Pro His Ser Leu
10 15 20

gaa tat ggc gac acc acc ctg ctg gac gtt tac gac aac aac ctg gcc 211
Glu Tyr Gly Asp Thr Thr Leu Leu Asp Val Tyr Asp Asn Asn Leu Ala
25 30 35

att aac gca gac aag cca gcc acc tac ttt ttc ggt cgt tca caa acc 259
Ile Asn Ala Asp Lys Pro Ala Thr Tyr Phe Phe Gly Arg Ser Gln Thr
40 45 50

tac ggt gaa ctg gac aaa gaa gtc cgc aaa act gcc gct ggc ctg cgc 307
Tyr Gly Glu Leu Asp Lys Glu Val Arg Lys Thr Ala Ala Gly Leu Arg
55 60 65

gca cta ggt gtc cgc ccc ggc gat cac gta gcg att atc ctc ccc aac 355
Ala Leu Gly Val Arg Pro Gly Asp His Val Ala Ile Ile Leu Pro Asn
70 75 80 85

tgc cca cag cac atc gca gct ttc tac gca gtg ctg aaa ctc ggc gca 403
Cys Pro Gln His Ile Ala Ala Phe Tyr Ala Val Leu Lys Leu Gly Ala
90 95 100

gta gtc att gag cac aac ccg ctc tac acc gcc cac gaa ctg ctc gaa 451
Val Val Ile Glu His Asn Pro Leu Tyr Thr Ala His Glu Leu Leu Glu
105 110 115

ccc ttc aaa gac cac ggt gcc cgc gtt gcc atc gtc tgg gac aaa gcc 499
Pro Phe Lys Asp His Gly Ala Arg Val Ala Ile Val Trp Asp Lys Ala
120 125 130

tcc ccc acc gtc gaa cag cta cgt gga cag acc cag ttg gaa acc atc 547
Ser Pro Thr Val Glu Gln Leu Arg Gly Gln Thr Gln Leu Glu Thr Ile
135 140 145

gtg tcg gtc aac atg atc aac gcg atg cca cca ctc cag cgc cta gca 595
Val Ser Val Asn Met Ile Asn Ala Met Pro Pro Leu Gln Arg Leu Ala
150 155 160 165

ctt cgg ctc cca atc cct gca ctg cgc aag agc cgc gaa tcc ctc tcc 643
Leu Arg Leu Pro Ile Pro Ala Leu Arg Lys Ser Arg Glu Ser Leu Ser
170 175 180

ggc gca gcc ccc aac acc gtt cct ttt gaa acc ctg acc agc gca gca 691
Gly Ala Ala Pro Asn Thr Val Pro Phe Glu Thr Leu Thr Ser Ala Ala
185 190 195

atg ggc ggc gac ggc gac gac gta gtt tca gaa ccc acc gtg acc aaa 739
Met Gly Gly Asp Gly Asp Asp Val Val Ser Glu Pro Thr Val Thr Lys

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        200                 205                 210

gaa tcc gtc gcg ctg atc ctc tac acc tcc ggc acc acc gga cgc ccc    787
Glu Ser Val Ala Leu Ile Leu Tyr Thr Ser Gly Thr Thr Gly Arg Pro
    215                 220                 225

aag ggt gcc cag ctc acc cac gga aac ctg ttc ttc aat ctt ctt caa    835
Lys Gly Ala Gln Leu Thr His Gly Asn Leu Phe Phe Asn Leu Leu Gln
230                 235                 240                 245

gga aag cac tgg gtt cca ggt ctc gga gac aaa cca gaa cgc atg ctt    883
Gly Lys His Trp Val Pro Gly Leu Gly Asp Lys Pro Glu Arg Met Leu
                250                 255                 260

gca gcc cta cca atg ttc cac gca tac ggt ctg acc atg gtc ggc aca    931
Ala Ala Leu Pro Met Phe His Ala Tyr Gly Leu Thr Met Val Gly Thr
            265                 270                 275

ctg tcc gtg ttc atc ggt ggc gaa atg gtg cta ctt ccc acc cca cgc    979
Leu Ser Val Phe Ile Gly Gly Glu Met Val Leu Leu Pro Thr Pro Arg
        280                 285                 290

atc gac ctg atc atg aac gta atg aaa aag cac acc cca acc tgg cta    1027
Ile Asp Leu Ile Met Asn Val Met Lys Lys His Thr Pro Thr Trp Leu
    295                 300                 305

cca ggc gtg ccc acc ctt tac gaa aaa atc gtc gac gcc tcc gaa aaa    1075
Pro Gly Val Pro Thr Leu Tyr Glu Lys Ile Val Asp Ala Ser Glu Lys
310                 315                 320                 325

gaa gga atc ccc atc aag gga gtc cgc aac gcc ttc tcc ggt gca tcc    1123
Glu Gly Ile Pro Ile Lys Gly Val Arg Asn Ala Phe Ser Gly Ala Ser
                330                 335                 340

aca ctc tcc cag cgc acc gtt gaa cgc tgg gaa aag cac acc ggc gga    1171
Thr Leu Ser Gln Arg Thr Val Glu Arg Trp Glu Lys His Thr Gly Gly
            345                 350                 355

cgc ctc gtc gaa ggc tac ggc ctc acc gaa acc tcc ccc atc atc gtg    1219
Arg Leu Val Glu Gly Tyr Gly Leu Thr Glu Thr Ser Pro Ile Ile Val
        360                 365                 370

ggt aac ccc atg agc gat cac cga cgc caa ggc tac gta gga atc ccc    1267
Gly Asn Pro Met Ser Asp His Arg Arg Gln Gly Tyr Val Gly Ile Pro
    375                 380                 385

ttc ccc gac acc atc gtg cgc atc gca aac cca gaa aac ctc gac gaa    1315
Phe Pro Asp Thr Ile Val Arg Ile Ala Asn Pro Glu Asn Leu Asp Glu
390                 395                 400                 405

acc atg ccc gac ggc agc gaa ggc gaa gtc cta gtc aag ggc cca cag    1363
Thr Met Pro Asp Gly Ser Glu Gly Glu Val Leu Val Lys Gly Pro Gln
                410                 415                 420

gtg ttc aag ggt tac ctc aac cag gaa gaa gcc acc aag aac agc ttc    1411
Val Phe Lys Gly Tyr Leu Asn Gln Glu Glu Ala Thr Lys Asn Ser Phe
            425                 430                 435

cac ggc gag tgg tac cgc acc ggc gac gtc gga gtg atg gaa gaa gac    1459
His Gly Glu Trp Tyr Arg Thr Gly Asp Val Gly Val Met Glu Glu Asp
        440                 445                 450
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ggg ttc atc cgc cta gtt gct cgc atc aag gaa gtc atc atc act ggc 1507
Gly Phe Ile Arg Leu Val Ala Arg Ile Lys Glu Val Ile Ile Thr Gly
455 460 465

ggt ttc aac gtg tac cca gct gag gtt gaa gaa gtc ctc gca gag cac 1555
Gly Phe Asn Val Tyr Pro Ala Glu Val Glu Glu Val Leu Ala Glu His
470 475 480 485

cca gac att gaa gat tcc gca gtc gtt ggt atc ccg cgt gaa gac ggc 1603
Pro Asp Ile Glu Asp Ser Ala Val Val Gly Ile Pro Arg Glu Asp Gly
490 495 500

tcc gaa aac gtc gtt gct gcc atc act ttg gtg gaa ggt gca gcg ctg 1651
Ser Glu Asn Val Val Ala Ala Ile Thr Leu Val Glu Gly Ala Ala Leu
505 510 515

gat ccg gat ggc ctg aag gaa ttc gcc cgc aag aac ctc acc cgc tac 1699
Asp Pro Asp Gly Leu Lys Glu Phe Ala Arg Lys Asn Leu Thr Arg Tyr
520 525 530

aag gtt ccg cgc act ttc tac cac ttt gag gag atg ccg cgg gat cag 1747
Lys Val Pro Arg Thr Phe Tyr His Phe Glu Glu Met Pro Arg Asp Gln
535 540 545

atg ggc aag att agg cgt cgt gaa gtg cag gcg gag ttg ttg aag aag 1795
Met Gly Lys Ile Arg Arg Arg Glu Val Gln Ala Glu Leu Leu Lys Lys
550 555 560 565

ctc ggc aag tagacgccga tttaagaggt cga 1827
Leu Gly Lys

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<212> PRT
<213> Corynebacterium glutamicum

<400> 30
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1 5 10 15

Thr Pro His Ser Leu Glu Tyr Gly Asp Thr Thr Leu Leu Asp Val Tyr
20 25 30

Asp Asn Asn Leu Ala Ile Asn Ala Asp Lys Pro Ala Thr Tyr Phe Phe
35 40 45

Gly Arg Ser Gln Thr Tyr Gly Glu Leu Asp Lys Glu Val Arg Lys Thr
50 55 60

Ala Ala Gly Leu Arg Ala Leu Gly Val Arg Pro Gly Asp His Val Ala
65 70 75 80

Ile Ile Leu Pro Asn Cys Pro Gln His Ile Ala Ala Phe Tyr Ala Val
85 90 95

Leu Lys Leu Gly Ala Val Val Ile Glu His Asn Pro Leu Tyr Thr Ala
100 105 110

His Glu Leu Leu Glu Pro Phe Lys Asp His Gly Ala Arg Val Ala Ile
115 120 125

Val Trp Asp Lys Ala Ser Pro Thr Val Glu Gln Leu Arg Gly Gln Thr
130 135 140

Gln Leu Glu Thr Ile Val Ser Val Asn Met Ile Asn Ala Met Pro Pro
145 150 155 160

Leu Gln Arg Leu Ala Leu Arg Leu Pro Ile Pro Ala Leu Arg Lys Ser
165 170 175

Arg Glu Ser Leu Ser Gly Ala Ala Pro Asn Thr Val Pro Phe Glu Thr
180 185 190

Leu Thr Ser Ala Ala Met Gly Gly Asp Gly Asp Asp Val Val Ser Glu
195 200 205

Pro Thr Val Thr Lys Glu Ser Val Ala Leu Ile Leu Tyr Thr Ser Gly
210 215 220

Thr Thr Gly Arg Pro Lys Gly Ala Gln Leu Thr His Gly Asn Leu Phe
225 230 235 240

Phe Asn Leu Leu Gln Gly Lys His Trp Val Pro Gly Leu Gly Asp Lys
245 250 255

Pro Glu Arg Met Leu Ala Ala Leu Pro Met Phe His Ala Tyr Gly Leu
260 265 270

Thr Met Val Gly Thr Leu Ser Val Phe Ile Gly Gly Glu Met Val Leu
275 280 285

Leu Pro Thr Pro Arg Ile Asp Leu Ile Met Asn Val Met Lys Lys His
290 295 300

Thr Pro Thr Trp Leu Pro Gly Val Pro Thr Leu Tyr Glu Lys Ile Val
305 310 315 320

Asp Ala Ser Glu Lys Glu Gly Ile Pro Ile Lys Gly Val Arg Asn Ala
325 330 335

Phe Ser Gly Ala Ser Thr Leu Ser Gln Arg Thr Val Glu Arg Trp Glu
340 345 350

Lys His Thr Gly Gly Arg Leu Val Glu Gly Tyr Gly Leu Thr Glu Thr
355 360 365

Ser Pro Ile Ile Val Gly Asn Pro Met Ser Asp His Arg Arg Gln Gly
370 375 380

Tyr Val Gly Ile Pro Phe Pro Asp Thr Ile Val Arg Ile Ala Asn Pro
385 390 395 400

Glu Asn Leu Asp Glu Thr Met Pro Asp Gly Ser Glu Gly Glu Val Leu
405 410 415

Val Lys Gly Pro Gln Val Phe Lys Gly Tyr Leu Asn Gln Glu Glu Ala
420 425 430

Thr Lys Asn Ser Phe His Gly Glu Trp Tyr Arg Thr Gly Asp Val Gly

435 440 445

Val Met Glu Glu Asp Gly Phe Ile Arg Leu Val Ala Arg Ile Lys Glu
450 455 460

Val Ile Ile Thr Gly Gly Phe Asn Val Tyr Pro Ala Glu Val Glu Glu
465 470 475 480

Val Leu Ala Glu His Pro Asp Ile Glu Asp Ser Ala Val Val Gly Ile
485 490 495

Pro Arg Glu Asp Gly Ser Glu Asn Val Val Ala Ala Ile Thr Leu Val
500 505 510

Glu Gly Ala Ala Leu Asp Pro Asp Gly Leu Lys Glu Phe Ala Arg Lys
515 520 525

Asn Leu Thr Arg Tyr Lys Val Pro Arg Thr Phe Tyr His Phe Glu Glu
530 535 540

Met Pro Arg Asp Gln Met Gly Lys Ile Arg Arg Arg Glu Val Gln Ala
545 550 555 560

Glu Leu Leu Lys Lys Leu Gly Lys
565

<210> 31
<211> 411
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(388)
<223> FRXA02487

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tgctcgcatc aagaaagtca tcatcactgg cggtttcaac gtg tac cca gct gag 115
Val Tyr Pro Ala Glu
1 5

gtt gaa gaa gtc ctc gca gag cac cca gac att gaa gat tcc gca gtc 163
Val Glu Glu Val Leu Ala Glu His Pro Asp Ile Glu Asp Ser Ala Val
10 15 20

gtt ggt atc ccg cgt gaa gac ggc tcc gaa aac gtc gtt gct gcc atc 211
Val Gly Ile Pro Arg Glu Asp Gly Ser Glu Asn Val Val Ala Ala Ile
25 30 35

act ttg gtg gaa ggt gca gcg ctg gat ccg gat ggc ctg aag gaa ttc 259
Thr Leu Val Glu Gly Ala Ala Leu Asp Pro Asp Gly Leu Lys Glu Phe
40 45 50

gcc cgc aag aac ctc acc cgc tac aag gtt ccg cgc act ttc tac cac 307
Ala Arg Lys Asn Leu Thr Arg Tyr Lys Val Pro Arg Thr Phe Tyr His
55 60 65

ttt gag gag atg ccg cgg gat cag atg ggc aag att agg cgt cgt gaa 355

Phe Glu Glu Met Pro Arg Asp Gln Met Gly Lys Ile Arg Arg Arg Glu
70 75 80 85

gtg cag gcg gag ttg ttg aag aag ctc ggc aag tagacgccga tttaagaggt 408
Val Gln Ala Glu Leu Leu Lys Lys Leu Gly Lys
90 95

cga 411

<210> 32
<211> 96
<212> PRT
<213> Corynebacterium glutamicum

<400> 32
Val Tyr Pro Ala Glu Val Glu Glu Val Leu Ala Glu His Pro Asp Ile
1 5 10 15

Glu Asp Ser Ala Val Val Gly Ile Pro Arg Glu Asp Gly Ser Glu Asn
20 25 30

Val Val Ala Ala Ile Thr Leu Val Glu Gly Ala Ala Leu Asp Pro Asp
35 40 45

Gly Leu Lys Glu Phe Ala Arg Lys Asn Leu Thr Arg Tyr Lys Val Pro
50 55 60

Arg Thr Phe Tyr His Phe Glu Glu Met Pro Arg Asp Gln Met Gly Lys
65 70 75 80

Ile Arg Arg Arg Glu Val Gln Ala Glu Leu Leu Lys Lys Leu Gly Lys
85 90 95

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<223> FRXA02490

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atactaaagg gcactaaagc aacgcagttg aagggacacc atg tca gca tac gaa 115
Met Ser Ala Tyr Glu
1 5

acc aaa gaa tgg ctc cag cac tac cca gag tgg acg cca cac tcg ctg 163
Thr Lys Glu Trp Leu Gln His Tyr Pro Glu Trp Thr Pro His Ser Leu
10 15 20

gaa tat ggc gac acc acc ctg ctg gac gtt tac gac aac aac ctg gcc 211
Glu Tyr Gly Asp Thr Thr Leu Leu Asp Val Tyr Asp Asn Asn Leu Ala

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                25                      30                      35

att aac gca gac aag cca gcc acc tac ttt ttc ggt cgt tca caa acc    259
Ile Asn Ala Asp Lys Pro Ala Thr Tyr Phe Phe Gly Arg Ser Gln Thr
        40                      45                      50

tac ggt gaa ctg gac aaa gaa gtc cgc aaa act gcc gct ggc ctg cgc    307
Tyr Gly Glu Leu Asp Lys Glu Val Arg Lys Thr Ala Ala Gly Leu Arg
    55                      60                      65

gca cta ggt gtc cgc ccc ggc gat cac gta gcg att atc ctc ccc aac    355
Ala Leu Gly Val Arg Pro Gly Asp His Val Ala Ile Ile Leu Pro Asn
70                      75                      80                  85

tgc cca cag cac atc gca gct ttc tac gca gtg ctg aaa ctc ggc gca    403
Cys Pro Gln His Ile Ala Ala Phe Tyr Ala Val Leu Lys Leu Gly Ala
                90                      95                      100

gta gtc att gag cac aac ccg ctc tac acc gcc cac gaa ctg ctc gaa    451
Val Val Ile Glu His Asn Pro Leu Tyr Thr Ala His Glu Leu Leu Glu
            105                     110                     115

ccc ttc aaa gac cac ggt gcc cgc gtt gcc atc gtc tgg gac aaa gcc    499
Pro Phe Lys Asp His Gly Ala Arg Val Ala Ile Val Trp Asp Lys Ala
        120                     125                     130

tcc ccc acc gtc gaa cag cta cgt gga cag acc cag ttg gaa acc atc    547
Ser Pro Thr Val Glu Gln Leu Arg Gly Gln Thr Gln Leu Glu Thr Ile
    135                     140                     145

gtg tcg gtc aac atg atc aac gcg atg cca cca ctc cag cgc cta gca    595
Val Ser Val Asn Met Ile Asn Ala Met Pro Pro Leu Gln Arg Leu Ala
150                     155                     160                 165

ctt cgg ctc cca atc cct gca ctg cgc aag agc cgc gaa tcc ctc tcc    643
Leu Arg Leu Pro Ile Pro Ala Leu Arg Lys Ser Arg Glu Ser Leu Ser
                170                     175                     180

ggc gca gcc ccc aac acc gtt cct ttt gaa acc ctg acc agc gca gca    691
Gly Ala Ala Pro Asn Thr Val Pro Phe Glu Thr Leu Thr Ser Ala Ala
            185                     190                     195

atg ggc ggc gac ggc gac gac gta gtt tca gaa ccc acc gtg acc aaa    739
Met Gly Gly Asp Gly Asp Asp Val Val Ser Glu Pro Thr Val Thr Lys
        200                     205                     210

gaa tcc gtc gcg ctg atc ctc tac acc tcc ggc acc acc gga cgc ccc    787
Glu Ser Val Ala Leu Ile Leu Tyr Thr Ser Gly Thr Thr Gly Arg Pro
    215                     220                     225

aag ggt gcc cag ctc acc cac gga aac ctg ttc tcc aat ctc ctc caa    835
Lys Gly Ala Gln Leu Thr His Gly Asn Leu Phe Ser Asn Leu Leu Gln
230                     235                     240                 245

gga aag cac tgg gtt cca ggt ctc gga gac aaa cca gaa cgc atg ctt    883
Gly Lys His Trp Val Pro Gly Leu Gly Asp Lys Pro Glu Arg Met Leu
                250                     255                     260

gca gcc cta cca atg ttc cac gca tac ggt                            913
Ala Ala Leu Pro Met Phe His Ala Tyr Gly
            265                     270
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<210> 34
<211> 271
<212> PRT
<213> Corynebacterium glutamicum

<400> 34
Met Ser Ala Tyr Glu Thr Lys Glu Trp Leu Gln His Tyr Pro Glu Trp
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Thr Pro His Ser Leu Glu Tyr Gly Asp Thr Thr Leu Leu Asp Val Tyr
            20   25   30

Asp Asn Asn Leu Ala Ile Asn Ala Asp Lys Pro Ala Thr Tyr Phe Phe
        35   40   45

Gly Arg Ser Gln Thr Tyr Gly Glu Leu Asp Lys Glu Val Arg Lys Thr
    50   55   60

Ala Ala Gly Leu Arg Ala Leu Gly Val Arg Pro Gly Asp His Val Ala
65   70   75   80

Ile Ile Leu Pro Asn Cys Pro Gln His Ile Ala Ala Phe Tyr Ala Val
                85   90   95

Leu Lys Leu Gly Ala Val Val Ile Glu His Asn Pro Leu Tyr Thr Ala
            100   105   110

His Glu Leu Leu Glu Pro Phe Lys Asp His Gly Ala Arg Val Ala Ile
        115   120   125

Val Trp Asp Lys Ala Ser Pro Thr Val Glu Gln Leu Arg Gly Gln Thr
    130   135   140

Gln Leu Glu Thr Ile Val Ser Val Asn Met Ile Asn Ala Met Pro Pro
145   150   155   160

Leu Gln Arg Leu Ala Leu Arg Leu Pro Ile Pro Ala Leu Arg Lys Ser
                165   170   175

Arg Glu Ser Leu Ser Gly Ala Ala Pro Asn Thr Val Pro Phe Glu Thr
            180   185   190

Leu Thr Ser Ala Ala Met Gly Gly Asp Gly Asp Asp Val Val Ser Glu
        195   200   205

Pro Thr Val Thr Lys Glu Ser Val Ala Leu Ile Leu Tyr Thr Ser Gly
    210   215   220

Thr Thr Gly Arg Pro Lys Gly Ala Gln Leu Thr His Gly Asn Leu Phe
225   230   235   240

Ser Asn Leu Leu Gln Gly Lys His Trp Val Pro Gly Leu Gly Asp Lys
                245   250   255

Pro Glu Arg Met Leu Ala Ala Leu Pro Met Phe His Ala Tyr Gly
            260   265   270

<210> 35

<211> 414
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(391)
<223> RXA01467

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taagtcttag cctacaagcg ctttgaggta gtttgggatc atg gat ttc aac gac 115
Met Asp Phe Asn Asp
1 5

aaa gcc gct tca gaa aac gct gta aag act ggc gca gaa ggc ccc aac 163
Lys Ala Ala Ser Glu Asn Ala Val Lys Thr Gly Ala Glu Gly Pro Asn
10 15 20

gtt ttc gcg agc gtg gcc aag att ttg cag gat gtt ggc gga att tca 211
Val Phe Ala Ser Val Ala Lys Ile Leu Gln Asp Val Gly Gly Ile Ser
25 30 35

gcc gaa gac gtc act ccg gaa tct cgt ttt act gag gat ttg gca gtg 259
Ala Glu Asp Val Thr Pro Glu Ser Arg Phe Thr Glu Asp Leu Ala Val
40 45 50

agc tca ctc aat tac atc gag ttg att gtc aat gcg gag gac gca ttt 307
Ser Ser Leu Asn Tyr Ile Glu Leu Ile Val Asn Ala Glu Asp Ala Phe
55 60 65

ggt gtt cgc att gag gac gcc gat gcc aag gat ttg acc acc gtg cag 355
Gly Val Arg Ile Glu Asp Ala Asp Ala Lys Asp Leu Thr Thr Val Gln
70 75 80 85

gat ttg att gac ttt att aac acc aat aag gct gat tagcgggaaa 401
Asp Leu Ile Asp Phe Ile Asn Thr Asn Lys Ala Asp
90 95

atttcgccca aaa 414

<210> 36
<211> 97
<212> PRT
<213> Corynebacterium glutamicum

<400> 36
Met Asp Phe Asn Asp Lys Ala Ala Ser Glu Asn Ala Val Lys Thr Gly
1 5 10 15

Ala Glu Gly Pro Asn Val Phe Ala Ser Val Ala Lys Ile Leu Gln Asp
20 25 30

Val Gly Gly Ile Ser Ala Glu Asp Val Thr Pro Glu Ser Arg Phe Thr
35 40 45

Glu Asp Leu Ala Val Ser Ser Leu Asn Tyr Ile Glu Leu Ile Val Asn
50 55 60

Ala Glu Asp Ala Phe Gly Val Arg Ile Glu Asp Ala Asp Ala Lys Asp
65 70 75 80

Leu Thr Thr Val Gln Asp Leu Ile Asp Phe Ile Asn Thr Asn Lys Ala
85 90 95

Asp

<210> 37
<211> 298
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(298)
<223> RXA00796

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gttgatacat caacttaatt aacttttaga ggagtacacc atg agc aag atc gcc 115
Met Ser Lys Ile Ala
1 5

atc atc acc ggt tcc acc cgt cca ggc cgc gtc aac att gac gta gcc 163
Ile Ile Thr Gly Ser Thr Arg Pro Gly Arg Val Asn Ile Asp Val Ala
10 15 20

aac tgg gtt ctc gag cgc gca caa gag cgc aac gat gca cag tac gag 211
Asn Trp Val Leu Glu Arg Ala Gln Glu Arg Asn Asp Ala Gln Tyr Glu
25 30 35

ctc gtt gat atc gcc gat ttc aac ttc ccc gtc ctc gac gaa gca atg 259
Leu Val Asp Ile Ala Asp Phe Asn Phe Pro Val Leu Asp Glu Ala Met
40 45 50

cca gcc ggc tac ggc cag tat gca aac gag cac acc aag 298
Pro Ala Gly Tyr Gly Gln Tyr Ala Asn Glu His Thr Lys
55 60 65

<210> 38
<211> 66
<212> PRT
<213> Corynebacterium glutamicum

<400> 38
Met Ser Lys Ile Ala Ile Ile Thr Gly Ser Thr Arg Pro Gly Arg Val
1 5 10 15

Asn Ile Asp Val Ala Asn Trp Val Leu Glu Arg Ala Gln Glu Arg Asn
20 25 30

Asp Ala Gln Tyr Glu Leu Val Asp Ile Ala Asp Phe Asn Phe Pro Val
35 40 45

Leu Asp Glu Ala Met Pro Ala Gly Tyr Gly Gln Tyr Ala Asn Glu His
50 55 60

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Thr Lys
 65


<210> 39
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<212> DNA
<213> Corynebacterium glutamicum

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<223> RXA01897

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tcactaggct ggcctttatt gtttccggaa aggggttgct atg aaa att ggt gtc   115
                                           Met Lys Ile Gly Val
                                            1               5

atc ctg ggc agt atc cgc gaa ggc cgc ttc ggc caa ggc gtt gcc gat   163
Ile Leu Gly Ser Ile Arg Glu Gly Arg Phe Gly Gln Gly Val Ala Asp
                10                  15                  20

tgg gtc atg gaa caa atc ggg gct tat gac gca ccc gat gtg gaa ttt   211
Trp Val Met Glu Gln Ile Gly Ala Tyr Asp Ala Pro Asp Val Glu Phe
            25                  30                  35

gaa ctc atc gac ctc aaa gct ttc aac gtg ccc ctg ttg gaa tcc gcg   259
Glu Leu Ile Asp Leu Lys Ala Phe Asn Val Pro Leu Leu Glu Ser Ala
        40                  45                  50

aca gtt cca ggt tcc gcg gat aaa cag tac gac gac ccg cgc gta act   307
Thr Val Pro Gly Ser Ala Asp Lys Gln Tyr Asp Asp Pro Arg Val Thr
    55                  60                  65

gcc tgg tca cag gcc att gat gcc tgc gat gcc ttc ctt ttc atc acc   355
Ala Trp Ser Gln Ala Ile Asp Ala Cys Asp Ala Phe Leu Phe Ile Thr
70                  75                  80                  85

ccg gaa tac aac cac ggt gtg ccc ggc gcg ttc aaa aat gcg tat gac   403
Pro Glu Tyr Asn His Gly Val Pro Gly Ala Phe Lys Asn Ala Tyr Asp
                90                  95                  100

atc ctg ggc aat gaa tgg ctg aac aaa acc gtc ggt ttc att tcc tac   451
Ile Leu Gly Asn Glu Trp Leu Asn Lys Thr Val Gly Phe Ile Ser Tyr
            105                 110                 115

ggt gca gtc gaa ggg atc cgt gtt gtc gaa cag tgg cgt cag atc gtc   499
Gly Ala Val Glu Gly Ile Arg Val Val Glu Gln Trp Arg Gln Ile Val
        120                 125                 130

gcc acc ttc aac atg tac gat atc cgc agc cag cta tcc ttt tcc acc   547
Ala Thr Phe Asn Met Tyr Asp Ile Arg Ser Gln Leu Ser Phe Ser Thr
    135                 140                 145

ttc acc gag aac aac aac ggc act ttt gcg ccc aat gat cga cgc ccc   595
Phe Thr Glu Asn Asn Asn Gly Thr Phe Ala Pro Asn Asp Arg Arg Pro
150                 155                 160                 165
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ggt gaa cta atc cgc ctc ctt gat agc ctc cta acg gct gtc cgc gat    643
Gly Glu Leu Ile Arg Leu Leu Asp Ser Leu Leu Thr Ala Val Arg Asp
                170                 175                 180

taaggctctg aaatactaat gag                                          666


<210> 40
<211> 181
<212> PRT
<213> Corynebacterium glutamicum

<400> 40
Met Lys Ile Gly Val Ile Leu Gly Ser Ile Arg Glu Gly Arg Phe Gly
1               5                   10                  15

Gln Gly Val Ala Asp Trp Val Met Glu Gln Ile Gly Ala Tyr Asp Ala
            20                  25                  30

Pro Asp Val Glu Phe Glu Leu Ile Asp Leu Lys Ala Phe Asn Val Pro
        35                  40                  45

Leu Leu Glu Ser Ala Thr Val Pro Gly Ser Ala Asp Lys Gln Tyr Asp
    50                  55                  60

Asp Pro Arg Val Thr Ala Trp Ser Gln Ala Ile Asp Ala Cys Asp Ala
65                  70                  75                  80

Phe Leu Phe Ile Thr Pro Glu Tyr Asn His Gly Val Pro Gly Ala Phe
                85                  90                  95

Lys Asn Ala Tyr Asp Ile Leu Gly Asn Glu Trp Leu Asn Lys Thr Val
            100                 105                 110

Gly Phe Ile Ser Tyr Gly Ala Val Glu Gly Ile Arg Val Val Glu Gln
        115                 120                 125

Trp Arg Gln Ile Val Ala Thr Phe Asn Met Tyr Asp Ile Arg Ser Gln
    130                 135                 140

Leu Ser Phe Ser Thr Phe Thr Glu Asn Asn Asn Gly Thr Phe Ala Pro
145                 150                 155                 160

Asn Asp Arg Arg Pro Gly Glu Leu Ile Arg Leu Leu Asp Ser Leu Leu
                165                 170                 175

Thr Ala Val Arg Asp
            180


<210> 41
<211> 375
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (1)..(375)
<223> RXN02809
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<400> 41
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Asn Leu Ser Val Pro Ala Ala Leu Thr Asn Ala Leu Ser Tyr Leu Ser
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gca gag tgg aac aac aag gct gca ggc atc gtc tcc tac ggc tcc gca 96
Ala Glu Trp Asn Asn Lys Ala Ala Gly Ile Val Ser Tyr Gly Ser Ala
20 25 30

atg ggc gtt cgc gca gct gag cac ctc cgc ggc atc ctt tcc gag ctt 144
Met Gly Val Arg Ala Ala Glu His Leu Arg Gly Ile Leu Ser Glu Leu
35 40 45

cag atc gca cac gtt caa aag acc ggc ctg ctg agc atc ttc acc gac 192
Gln Ile Ala His Val Gln Lys Thr Gly Leu Leu Ser Ile Phe Thr Asp
50 55 60

ttc gaa tac cct aac ttc aag cct tcc gag cag ggc atc tcc tct gtg 240
Phe Glu Tyr Pro Asn Phe Lys Pro Ser Glu Gln Gly Ile Ser Ser Val
65 70 75 80

gac gct atg ctt gag cag ctt gtt gtc tgg acc aag gca atg tcc acc 288
Asp Ala Met Leu Glu Gln Leu Val Val Trp Thr Lys Ala Met Ser Thr
85 90 95

att cgc gag tct gcg aac gtc tat cac tta aga acc cct cac aaa agt 336
Ile Arg Glu Ser Ala Asn Val Tyr His Leu Arg Thr Pro His Lys Ser
100 105 110

ggc gag ctc ccc gac tgg gac tcg cct ctt ttc gta ttc 375
Gly Glu Leu Pro Asp Trp Asp Ser Pro Leu Phe Val Phe
115 120 125

<210> 42
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<212> PRT
<213> Corynebacterium glutamicum

<400> 42
Asn Leu Ser Val Pro Ala Ala Leu Thr Asn Ala Leu Ser Tyr Leu Ser
1 5 10 15

Ala Glu Trp Asn Asn Lys Ala Ala Gly Ile Val Ser Tyr Gly Ser Ala
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Met Gly Val Arg Ala Ala Glu His Leu Arg Gly Ile Leu Ser Glu Leu
35 40 45

Gln Ile Ala His Val Gln Lys Thr Gly Leu Leu Ser Ile Phe Thr Asp
50 55 60

Phe Glu Tyr Pro Asn Phe Lys Pro Ser Glu Gln Gly Ile Ser Ser Val
65 70 75 80

Asp Ala Met Leu Glu Gln Leu Val Val Trp Thr Lys Ala Met Ser Thr
85 90 95

Ile Arg Glu Ser Ala Asn Val Tyr His Leu Arg Thr Pro His Lys Ser
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Gly Glu Leu Pro Asp Trp Asp Ser Pro Leu Phe Val Phe
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<222> (1)..(273)
<223> FRXA02809

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Ala Ala Leu Thr Asn Ala Leu Ser Tyr Leu Ser Ala Glu Trp Asn Asn
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aag gct gca ggc atc gtc tcc tac ggc tcc gca atg ggc gtt cgc gca      96
Lys Ala Ala Gly Ile Val Ser Tyr Gly Ser Ala Met Gly Val Arg Ala
             20                  25                  30

gct gag cac ctc cgc ggc atc ctt tcc gag ctt cag atc gca cac gtt      144
Ala Glu His Leu Arg Gly Ile Leu Ser Glu Leu Gln Ile Ala His Val
         35                  40                  45

caa aag acc ggc ctg ctg agc atc ttc acc gac ttc gaa tac cct aac      192
Gln Lys Thr Gly Leu Leu Ser Ile Phe Thr Asp Phe Glu Tyr Pro Asn
     50                  55                  60

ttc aag cct tcc gag cag ggc atc tcc tct gtg gac gct atg ctt gag      240
Phe Lys Pro Ser Glu Gln Gly Ile Ser Ser Val Asp Ala Met Leu Glu
 65                  70                  75                  80

cag ctt gtt gtc tgg acc aag gca atg tcc acc                          273
Gln Leu Val Val Trp Thr Lys Ala Met Ser Thr
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<210> 44
<211> 91
<212> PRT
<213> Corynebacterium glutamicum

<400> 44
Ala Ala Leu Thr Asn Ala Leu Ser Tyr Leu Ser Ala Glu Trp Asn Asn
  1               5                  10                  15

Lys Ala Ala Gly Ile Val Ser Tyr Gly Ser Ala Met Gly Val Arg Ala
             20                  25                  30

Ala Glu His Leu Arg Gly Ile Leu Ser Glu Leu Gln Ile Ala His Val
         35                  40                  45

Gln Lys Thr Gly Leu Leu Ser Ile Phe Thr Asp Phe Glu Tyr Pro Asn
     50                  55                  60

Phe Lys Pro Ser Glu Gln Gly Ile Ser Ser Val Asp Ala Met Leu Glu
 65                  70                  75                  80
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Gln Leu Val Val Trp Thr Lys Ala Met Ser Thr
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<210> 45
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<212> DNA
<213> Corynebacterium glutamicum

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cgactccatc gaagagtccg catccggccg tatcgttacc gtg cgc atc gtg ctc    115
                                            Val Arg Ile Val Leu
                                            1               5

acc acc gaa ggc gaa gta gca gcc aag ctg gtt acc cgc ttc gca att    163
Thr Thr Glu Gly Glu Val Ala Ala Lys Leu Val Thr Arg Phe Ala Ile
                10                  15                  20

cgt gga cgc atc acc acc aac gaa atg gct gca cca gca gat tcc tac    211
Arg Gly Arg Ile Thr Thr Asn Glu Met Ala Ala Pro Ala Asp Ser Tyr
            25                  30                  35

ggc gca cgc gac gaa gtt gtc gag gca acc cct cgt tcc ttc atc cgc    259
Gly Ala Arg Asp Glu Val Val Glu Ala Thr Pro Arg Ser Phe Ile Arg
        40                  45                  50

cag gca act gtt tct gca cct gca gac atg acc cca ttc gcc atg gtt    307
Gln Ala Thr Val Ser Ala Pro Ala Asp Met Thr Pro Phe Ala Met Val
    55                  60                  65

tct ggt gac tac aac cca att cac acc tct gac aac gct gca aag ctt    355
Ser Gly Asp Tyr Asn Pro Ile His Thr Ser Asp Asn Ala Ala Lys Leu
70                  75                  80                  85

gtt ggc ctg gac gca gct ctt gtc cac ggc atg tgg ctg tcc gct acc    403
Val Gly Leu Asp Ala Ala Leu Val His Gly Met Trp Leu Ser Ala Thr
                90                  95                  100

gca cag cac ctc gct ggt ctt ggc tct gag gtc att ggt tgg acc tac    451
Ala Gln His Leu Ala Gly Leu Gly Ser Glu Val Ile Gly Trp Thr Tyr
            105                 110                 115

tcc atg tac ggc atg gtt caa ctc aac gac gtt gtt gac atc acc gtc    499
Ser Met Tyr Gly Met Val Gln Leu Asn Asp Val Val Asp Ile Thr Val
        120                 125                 130

gag cgt gtt ggc cgc gca ggt ctg aag cct gca tac gag gtc acc tgc    547
Glu Arg Val Gly Arg Ala Gly Leu Lys Pro Ala Tyr Glu Val Thr Cys
    135                 140                 145

cgc att gat ggc aac gtt gtc tcc cgc gga cag gca ctg ctc aag gct    595
Arg Ile Asp Gly Asn Val Val Ser Arg Gly Gln Ala Leu Leu Lys Ala
150                 155                 160                 165
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cct tcc acc gct tat gtt tac cca agc cag ggc atc cag gct aag ggc    643
Pro Ser Thr Ala Tyr Val Tyr Pro Ser Gln Gly Ile Gln Ala Lys Gly
                170                 175                 180

atg ggc caa ggc gat cgc acc gca agc gca gag gct cgc gct gtg tgg    691
Met Gly Gln Gly Asp Arg Thr Ala Ser Ala Glu Ala Arg Ala Val Trp
            185                 190                 195

gag cgt gca gat gca cac acc cgc gca aac ctg ggc ttc tcc atc cag    739
Glu Arg Ala Asp Ala His Thr Arg Ala Asn Leu Gly Phe Ser Ile Gln
        200                 205                 210

cag gtc att gat gaa aac cca act gag ctg aag gtc ggg gac acc acc    787
Gln Val Ile Asp Glu Asn Pro Thr Glu Leu Lys Val Gly Asp Thr Thr
    215                 220                 225

ttc gtg cac cca gct ggg gtt ttg aac ctc acc cag ttc acg cag gtc    835
Phe Val His Pro Ala Gly Val Leu Asn Leu Thr Gln Phe Thr Gln Val
230                 235                 240                 245

gcg ctc gcc gtg gtt gcc tac gct cag acc gag cgc ctc aag gct gca    883
Ala Leu Ala Val Val Ala Tyr Ala Gln Thr Glu Arg Leu Lys Ala Ala
                250                 255                 260

aac gca att gtc gac ggc tcc ctc tac gca ggc cac tcc ctc ggc gag    931
Asn Ala Ile Val Asp Gly Ser Leu Tyr Ala Gly His Ser Leu Gly Glu
            265                 270                 275

tac acc gca ctg gca tcc ttg ggc aac atc ttc gaa ctc gaa ggc gtc    979
Tyr Thr Ala Leu Ala Ser Leu Gly Asn Ile Phe Glu Leu Glu Gly Val
        280                 285                 290

atc gac gtt gtg ttc tcc cgc ggt tcc gca atg cac tcc ctg gtt cca    1027
Ile Asp Val Val Phe Ser Arg Gly Ser Ala Met His Ser Leu Val Pro
    295                 300                 305

cgt gat gag aag ggc cgt tcc aac tac ggt ctt gcc gca ttc cgt ccg    1075
Arg Asp Glu Lys Gly Arg Ser Asn Tyr Gly Leu Ala Ala Phe Arg Pro
310                 315                 320                 325

aac atg atc aac gtt gca gcc acc gag gtg gag aac tgg gtt gac cgt    1123
Asn Met Ile Asn Val Ala Ala Thr Glu Val Glu Asn Trp Val Asp Arg
                330                 335                 340

gtc gct gaa gaa tcc ggc gaa ttc ctg cag atc gtt aac tac aac gtt    1171
Val Ala Glu Glu Ser Gly Glu Phe Leu Gln Ile Val Asn Tyr Asn Val
            345                 350                 355

gat ggc cag cag tac gca gtc gca ggt acc ttg gct ggc ctg aag gcc    1219
Asp Gly Gln Gln Tyr Ala Val Ala Gly Thr Leu Ala Gly Leu Lys Ala
        360                 365                 370

ctc aag gct tct gca tct gca aac cca cgt gct tac gtg aac att cca    1267
Leu Lys Ala Ser Ala Ser Ala Asn Pro Arg Ala Tyr Val Asn Ile Pro
    375                 380                 385

ggc att gac gtg cca ttc cac tcc agc gtc ctg cgc cca ggc gtt cct    1315
Gly Ile Asp Val Pro Phe His Ser Ser Val Leu Arg Pro Gly Val Pro
390                 395                 400                 405

gct ttc gca gag aag ctg gac gag ctg ctg cca gag acc atc gac att    1363
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Ala Phe Ala Glu Lys Leu Asp Glu Leu Leu Pro Glu Thr Ile Asp Ile
                410                 415                 420

gat gct ctt cgc ggc cgc tac atc ccg aac ctg gtt gct cgt cct ttc    1411
Asp Ala Leu Arg Gly Arg Tyr Ile Pro Asn Leu Val Ala Arg Pro Phe
            425                 430                 435

gag ctc acc cag agc ttc gtg gat gcc atc ctt gct gtt gtt cca tcc    1459
Glu Leu Thr Gln Ser Phe Val Asp Ala Ile Leu Ala Val Val Pro Ser
        440                 445                 450

gag cgc ctc aag ggc atc aag gtg gag gac acc gac gag aac acc ctg    1507
Glu Arg Leu Lys Gly Ile Lys Val Glu Asp Thr Asp Glu Asn Thr Leu
    455                 460                 465

gca cgt ctg ctc ctc atc gag ctg ctg tct tgg cag ttc gca tcc cct    1555
Ala Arg Leu Leu Leu Ile Glu Leu Leu Ser Trp Gln Phe Ala Ser Pro
470                 475                 480                 485

gtg cgt tgg atc gaa acc cag gct ctg atc atc gat acc gtc gat cag    1603
Val Arg Trp Ile Glu Thr Gln Ala Leu Ile Ile Asp Thr Val Asp Gln
                490                 495                 500

atc atc gag gtc ggc ttg gca gca tcg cca acc ctg acc aac ctg gca    1651
Ile Ile Glu Val Gly Leu Ala Ala Ser Pro Thr Leu Thr Asn Leu Ala
            505                 510                 515

ctg cgc acc atg gat gtc att ggc aag tcc cgc cca gta ttc aac gtg    1699
Leu Arg Thr Met Asp Val Ile Gly Lys Ser Arg Pro Val Phe Asn Val
        520                 525                 530

gag cgc gac cag gac acc gtt atg ctc aac gat gtt cgc cag gca cct    1747
Glu Arg Asp Gln Asp Thr Val Met Leu Asn Asp Val Arg Gln Ala Pro
    535                 540                 545

gtt gct gag gtt gaa gaa gaa gca gtt gag gaa gca cct gca gca gcc    1795
Val Ala Glu Val Glu Glu Glu Ala Val Glu Glu Ala Pro Ala Ala Ala
550                 555                 560                 565

gca gct cca gca gct gag gca cca gtt gct gca gct cca gta gcc gca    1843
Ala Ala Pro Ala Ala Glu Ala Pro Val Ala Ala Ala Pro Val Ala Ala
                570                 575                 580

gcc gca cct gca cct gtt gga aac gca cct gaa ctg aag ttc aac gct    1891
Ala Ala Pro Ala Pro Val Gly Asn Ala Pro Glu Leu Lys Phe Asn Ala
            585                 590                 595

gcc aat gcc atc atg gtt ctc ttc gct gtc cag aac aag atc aac att    1939
Ala Asn Ala Ile Met Val Leu Phe Ala Val Gln Asn Lys Ile Asn Ile
        600                 605                 610

gat cag atc acc gca gcg gat acc tct gag acc ctg acc aac ggt gtg    1987
Asp Gln Ile Thr Ala Ala Asp Thr Ser Glu Thr Leu Thr Asn Gly Val
    615                 620                 625

tcc tca cgc cgt aac cag atg ctc atg gac atg tcc acc gag ctg tcc    2035
Ser Ser Arg Arg Asn Gln Met Leu Met Asp Met Ser Thr Glu Leu Ser
630                 635                 640                 645

gtc cca acc atc gac ggc gca gct gac gct gac gta gct acc ctg cag    2083
Val Pro Thr Ile Asp Gly Ala Ala Asp Ala Asp Val Ala Thr Leu Gln
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                650                 655                 660

gga cgt gtt gtc acc gca gct cct ggc tac aag cct ttc gga cca gtt    2131
Gly Arg Val Val Thr Ala Ala Pro Gly Tyr Lys Pro Phe Gly Pro Val
            665                 670                 675

ctt tcc gag acc gtt cgt gca cgt ctt cgc gca ctg acc ggt gca gca    2179
Leu Ser Glu Thr Val Arg Ala Arg Leu Arg Ala Leu Thr Gly Ala Ala
        680                 685                 690

ggt ctg aag acc tcc tac atc ggc gat cgc gtg acc ggc acc tgg gga    2227
Gly Leu Lys Thr Ser Tyr Ile Gly Asp Arg Val Thr Gly Thr Trp Gly
    695                 700                 705

ctt cca gaa agc tgg acc gca cac gtt gag gtt gaa ttg ctg ctg ggc    2275
Leu Pro Glu Ser Trp Thr Ala His Val Glu Val Glu Leu Leu Leu Gly
710                 715                 720                 725

acc cgc gaa ggc gag tcc gtc cgc ggc ggc aac ctg ggt agc ctg cct    2323
Thr Arg Glu Gly Glu Ser Val Arg Gly Gly Asn Leu Gly Ser Leu Pro
                730                 735                 740

gct aac gca tcc agc aag ggc gac gtc gat gcg ctt atc gac gca gcc    2371
Ala Asn Ala Ser Ser Lys Gly Asp Val Asp Ala Leu Ile Asp Ala Ala
            745                 750                 755

gtg cag aat gtt gct gca gcc aac ggc acc agc gtc tcc atg tcc tcc    2419
Val Gln Asn Val Ala Ala Ala Asn Gly Thr Ser Val Ser Met Ser Ser
        760                 765                 770

ggc ggt gca gct tca ggt ggc gga gtt gtt gat tcc gca gca ctt gat    2467
Gly Gly Ala Ala Ser Gly Gly Gly Val Val Asp Ser Ala Ala Leu Asp
    775                 780                 785

gcc tac gca tcc acc gtc act ggt gaa gaa ggc gtc ctg gca aac gtt    2515
Ala Tyr Ala Ser Thr Val Thr Gly Glu Glu Gly Val Leu Ala Asn Val
790                 795                 800                 805

gct cgc ggc atc ctg tct cag ctt ggt ctc gac acc aag gac gag gtt    2563
Ala Arg Gly Ile Leu Ser Gln Leu Gly Leu Asp Thr Lys Asp Glu Val
                810                 815                 820

gaa ggc gca gag atc gac acc gaa ctc tac gac gct gtc gaa gca gaa    2611
Glu Gly Ala Glu Ile Asp Thr Glu Leu Tyr Asp Ala Val Glu Ala Glu
            825                 830                 835

ctg ggc acc ggc tgg ctg aag ctt gtc acc cca gtg ttc tcc gct gat    2659
Leu Gly Thr Gly Trp Leu Lys Leu Val Thr Pro Val Phe Ser Ala Asp
        840                 845                 850

cgt gcg atc ttg ttc gac gac cgt tgg gca tct gca cgt gaa gat ctg    2707
Arg Ala Ile Leu Phe Asp Asp Arg Trp Ala Ser Ala Arg Glu Asp Leu
    855                 860                 865

gca cgc ctt gcc aac ggc gag gat att gcc gtc gag cgc ttt gct gga    2755
Ala Arg Leu Ala Asn Gly Glu Asp Ile Ala Val Glu Arg Phe Ala Gly
870                 875                 880                 885

acg ggg gag acc gtc gtc aag caa gct gca tgg tgg gct gag cac gtt    2803
Thr Gly Glu Thr Val Val Lys Gln Ala Ala Trp Trp Ala Glu His Val
                890                 895                 900
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gaa gac acc gct ctc gct gca acc ctg aag cag gtt tcc gag gtg gct 2851
Glu Asp Thr Ala Leu Ala Ala Thr Leu Lys Gln Val Ser Glu Val Ala
905 910 915

gcg aag cca gcc aac gag cca cac atc gac gat gtt gcg ctg gtt acc 2899
Ala Lys Pro Ala Asn Glu Pro His Ile Asp Asp Val Ala Leu Val Thr
920 925 930

ggt gcg gct cct gag tcg atc gcc ggt gca gtt gcg gct cgc ctg ctg 2947
Gly Ala Ala Pro Glu Ser Ile Ala Gly Ala Val Ala Ala Arg Leu Leu
935 940 945

tcc cag ggc gcg acc gtc att ctc acc gca tcg aac gtc tcc cag gcg 2995
Ser Gln Gly Ala Thr Val Ile Leu Thr Ala Ser Asn Val Ser Gln Ala
950 955 960 965

cgt aag gaa tac gca cgc aag ctc tac gct gcg aac gca acc cct aac 3043
Arg Lys Glu Tyr Ala Arg Lys Leu Tyr Ala Ala Asn Ala Thr Pro Asn
970 975 980

gca aag ctg tgg att gtt cct gcg aac atg tcc tcc tac cgc gat gtt 3091
Ala Lys Leu Trp Ile Val Pro Ala Asn Met Ser Ser Tyr Arg Asp Val
985 990 995

gat gca gtc atc gat tgg atc ggc aac gag cag cgc gtc acc gtc ggc 3139
Asp Ala Val Ile Asp Trp Ile Gly Asn Glu Gln Arg Val Thr Val Gly
1000 1005 1010

agc acc gtc acc gtg acc aag cca gct ctg acc cca acc ctt gcg tac 3187
Ser Thr Val Thr Val Thr Lys Pro Ala Leu Thr Pro Thr Leu Ala Tyr
1015 1020 1025

cca ttc gca gct cca tcc gta tcc ggt acc ttg gcg gat gca ggc cca 3235
Pro Phe Ala Ala Pro Ser Val Ser Gly Thr Leu Ala Asp Ala Gly Pro
1030 1035 1040 1045

cag gct gaa aac cag gca cgc ctg ctc ctc tgg tcc gtg gag cgc acc 3283
Gln Ala Glu Asn Gln Ala Arg Leu Leu Leu Trp Ser Val Glu Arg Thr
1050 1055 1060

atc gca gga ctt gca gat ctt gca tcc cgc ggt gtc gat gga cgc gtc 3331
Ile Ala Gly Leu Ala Asp Leu Ala Ser Arg Gly Val Asp Gly Arg Val
1065 1070 1075

cac gtt gta ctc cca ggt tcc ccg aac cgc gga atg ttc ggt ggc gac 3379
His Val Val Leu Pro Gly Ser Pro Asn Arg Gly Met Phe Gly Gly Asp
1080 1085 1090

ggc gct tac ggc gaa gtc aag gct gct ttc gac gcc atc ctt gcc aag 3427
Gly Ala Tyr Gly Glu Val Lys Ala Ala Phe Asp Ala Ile Leu Ala Lys
1095 1100 1105

tgg ggc tcc gag acc ggc tgg cca cag ttt gtc tcc ctc gca cag gca 3475
Trp Gly Ser Glu Thr Gly Trp Pro Gln Phe Val Ser Leu Ala Gln Ala
1110 1115 1120 1125

cgc atc ggc tgg gtc gca ggc acc ggc ctc atg ggt cgc aac gac gtg 3523
Arg Ile Gly Trp Val Ala Gly Thr Gly Leu Met Gly Arg Asn Asp Val
1130 1135 1140

ctc atc cct gcc gct gaa aag ctg ggc atc cac gtc tac acc cct gaa 3571
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1145 1150 1155

gag atc tct tcc gaa ctg ctg ggt ctt gca tcc gca gaa tcc cgc gaa 3619
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1160 1165 1170

aag gct ctg gaa gca ccg atc gat tac gac ctg acc ggt gga ctt tcc 3667
Lys Ala Leu Glu Ala Pro Ile Asp Tyr Asp Leu Thr Gly Gly Leu Ser
1175 1180 1185

ggt ggc gta tcc atc gca gca ctg gca gca tcc ctc gag tcc gac gca 3715
Gly Gly Val Ser Ile Ala Ala Leu Ala Ala Ser Leu Glu Ser Asp Ala
1190 1195 1200 1205

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Val Glu Thr Thr Ser Ala Ala Glu Asp Thr Ile Lys Ala Leu Pro Ser
1210 1215 1220

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Pro Lys His Pro Glu Gln Pro Val Gly Thr Pro Val Gly Glu Val Lys
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Thr Asp Leu Glu Asp Met Val Val Met Val Gly Val Gly Glu Val Ser
1240 1245 1250

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Arg Asp Gly Ser Val Asp Leu Thr Ala Ala Gly Val Leu Glu Leu Ala
1270 1275 1280 1285

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Trp Met Met Gly Leu Ile Ser Trp Ser Glu Asp Pro Lys Pro Ala Trp
1290 1295 1300

tac gac gct gac ggc acc gaa gtg cct gaa gaa gag atc tac gag cgc 4051
Tyr Asp Ala Asp Gly Thr Glu Val Pro Glu Glu Glu Ile Tyr Glu Arg
1305 1310 1315

ttc cgc gac gaa gtc atc gca cga tgc ggt gtt cgt gag ctt gtc gac 4099
Phe Arg Asp Glu Val Ile Ala Arg Cys Gly Val Arg Glu Leu Val Asp
1320 1325 1330

gac gca ttc ctc gtc gac ggc ggc tcc ctc gac gca gct gaa gtc ttc 4147
Asp Ala Phe Leu Val Asp Gly Gly Ser Leu Asp Ala Ala Glu Val Phe
1335 1340 1345

ctc gac cgc gac atc tcc ttc tcc gta acc tct gct gaa gaa gca cag 4195
Leu Asp Arg Asp Ile Ser Phe Ser Val Thr Ser Ala Glu Glu Ala Gln
1350 1355 1360 1365

gcc tac gtc gat gca gat gct tcc gtg acc gtt gaa gaa gca gac ggc 4243
Ala Tyr Val Asp Ala Asp Ala Ser Val Thr Val Glu Glu Ala Asp Gly
1370 1375 1380

gaa tgg atc gtg acc aag aag aag ggc tcc acc tcc ttc gtg cca cgc 4291

Glu Trp Ile Val Thr Lys Lys Lys Gly Ser Thr Ser Phe Val Pro Arg
1385 1390 1395

aag gca acc ctg acc cgc tcc gta gca ggc cag ctg cca acc gac ttc 4339
Lys Ala Thr Leu Thr Arg Ser Val Ala Gly Gln Leu Pro Thr Asp Phe
1400 1405 1410

gac cct gcc aag tgg ggt atc cca gcc tcc atg atc gat gca ctc gac 4387
Asp Pro Ala Lys Trp Gly Ile Pro Ala Ser Met Ile Asp Ala Leu Asp
1415 1420 1425

aac atc gca gcg tgg aac ctg gtc act gca gtc gac gcc ttc ctg tcc 4435
Asn Ile Ala Ala Trp Asn Leu Val Thr Ala Val Asp Ala Phe Leu Ser
1430 1435 1440 1445

tcc ggc ttc agc cca gca gaa ctc ctg cag tcc atc cac cca gct gac 4483
Ser Gly Phe Ser Pro Ala Glu Leu Leu Gln Ser Ile His Pro Ala Asp
1450 1455 1460

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Val Ser Ser Thr Gln Gly Thr Gly Ile Gly Gly Met Gln Ser Leu Arg
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aag ctg ttc gtc aac cgc ttc ctc ggc cag gat cgt cca tcc gac atc 4579
Lys Leu Phe Val Asn Arg Phe Leu Gly Gln Asp Arg Pro Ser Asp Ile
1480 1485 1490

ctc cag gag acc ctg cca aac gtt gtg gct gca cac acc atg cag tcc 4627
Leu Gln Glu Thr Leu Pro Asn Val Val Ala Ala His Thr Met Gln Ser
1495 1500 1505

tac gtc ggt ggc tac ggc cag atg atc cac cca gtg gca gca tgt gca 4675
Tyr Val Gly Gly Tyr Gly Gln Met Ile His Pro Val Ala Ala Cys Ala
1510 1515 1520 1525

acc gca gct gtc tcc gtg gaa gaa ggc gtg gac aag atc cgc ctc aac 4723
Thr Ala Ala Val Ser Val Glu Glu Gly Val Asp Lys Ile Arg Leu Asn
1530 1535 1540

aag gca gat ttc gtt gtc gcc ggt ggt atc gat gac atc cag gtt gaa 4771
Lys Ala Asp Phe Val Val Ala Gly Gly Ile Asp Asp Ile Gln Val Glu
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tcc ctg acc ggc ttc ggt gac atg aac gcc acc gca gac acc cag gca 4819
Ser Leu Thr Gly Phe Gly Asp Met Asn Ala Thr Ala Asp Thr Gln Ala
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atg ctg gac aag ggc atc gac cca cgc ttc atc tcc cgc gca aac gat 4867
Met Leu Asp Lys Gly Ile Asp Pro Arg Phe Ile Ser Arg Ala Asn Asp
1575 1580 1585

cga cgt cgc gca ggc ttc ctc gaa gca gca ggt ggc ggt acc gtc ctc 4915
Arg Arg Arg Ala Gly Phe Leu Glu Ala Ala Gly Gly Gly Thr Val Leu
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ctg gca cgt gca tcc gtt gct gct gaa ctg gga ctg cca gtt ctc gca 4963
Leu Ala Arg Ala Ser Val Ala Ala Glu Leu Gly Leu Pro Val Leu Ala
1610 1615 1620

gtt gtt gca cac gca cag tcc tac gcc gat ggt gct cac acc tcc atc 5011
Val Val Ala His Ala Gln Ser Tyr Ala Asp Gly Ala His Thr Ser Ile

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            1625                1630                1635

cca gca ccg gga ctt ggc gca ctg ggt gca gca cgt ggt ggc aag aag    5059
Pro Ala Pro Gly Leu Gly Ala Leu Gly Ala Ala Arg Gly Gly Lys Lys
        1640                1645                1650

tcc gta ctt gct cgc gaa ctg aac aaa ttg ggt ctg acc cca gat gac    5107
Ser Val Leu Ala Arg Glu Leu Asn Lys Leu Gly Leu Thr Pro Asp Asp
    1655                1660                1665

gtt cgc gtg gtc tcg aag cac gac acc tcc acc aac gcc aac gat cca    5155
Val Arg Val Val Ser Lys His Asp Thr Ser Thr Asn Ala Asn Asp Pro
1670                1675                1680                1685

aac gag tcc gag ctg cac aac ctg ctg tgg aag acc att gga cgc gaa    5203
Asn Glu Ser Glu Leu His Asn Leu Leu Trp Lys Thr Ile Gly Arg Glu
                1690                1695                1700

gcc gac aac ccg atg ttc gtc gtc tcc cag aag tcc ctt acc gga cac    5251
Ala Asp Asn Pro Met Phe Val Val Ser Gln Lys Ser Leu Thr Gly His
            1705                1710                1715

tca aag ggc ggt gca gca ctc ttc cag atc ggt gga ctt gtc tcc atc    5299
Ser Lys Gly Gly Ala Ala Leu Phe Gln Ile Gly Gly Leu Val Ser Ile
        1720                1725                1730

ctg gaa acc ggc aag ctg cca cag aac gca tcc ctt gac tgc gtt gac    5347
Leu Glu Thr Gly Lys Leu Pro Gln Asn Ala Ser Leu Asp Cys Val Asp
    1735                1740                1745

cca gag atg gaa gca aag ggc gag aac ttc gtc tgg ctg cgc aag cca    5395
Pro Glu Met Glu Ala Lys Gly Glu Asn Phe Val Trp Leu Arg Lys Pro
1750                1755                1760                1765

ctg gat ctc ggc gca ggc tcc att aag gcc ggc gta ctt acc tca ctg    5443
Leu Asp Leu Gly Ala Gly Ser Ile Lys Ala Gly Val Leu Thr Ser Leu
                1770                1775                1780

ggc ttc ggc cac gtg gct gca gtc gtc gtg ctg gca acc agc ggc atc    5491
Gly Phe Gly His Val Ala Ala Val Val Val Leu Ala Thr Ser Gly Ile
            1785                1790                1795

ttc gag cag gca atg cgc aac gca ggc ctc gac gtc gaa gca tgg cgt    5539
Phe Glu Gln Ala Met Arg Asn Ala Gly Leu Asp Val Glu Ala Trp Arg
        1800                1805                1810

gca cgc gca acc cag cgc ctg cgc acc ggt gca aac cgc cta gaa gct    5587
Ala Arg Ala Thr Gln Arg Leu Arg Thr Gly Ala Asn Arg Leu Glu Ala
    1815                1820                1825

ggc atg gtt ggc cga gca cca ttg ttc gag cag gtc gac gga cgt cgc    5635
Gly Met Val Gly Arg Ala Pro Leu Phe Glu Gln Val Asp Gly Arg Arg
1830                1835                1840                1845

ctg cca gag cat ggc gct cac caa gca gag atc aac ttg ctt atc gac    5683
Leu Pro Glu His Gly Ala His Gln Ala Glu Ile Asn Leu Leu Ile Asp
                1850                1855                1860

gct gac gct cgc ctc ggt gct gac ggc atc tac cag ggc taaacgttag     5732
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atagctaaga aag 5745

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Pro Ala Asp Ser Tyr Gly Ala Arg Asp Glu Val Val Glu Ala Thr Pro
        35                  40                  45

Arg Ser Phe Ile Arg Gln Ala Thr Val Ser Ala Pro Ala Asp Met Thr
    50                  55                  60

Pro Phe Ala Met Val Ser Gly Asp Tyr Asn Pro Ile His Thr Ser Asp
65                  70                  75                  80

Asn Ala Ala Lys Leu Val Gly Leu Asp Ala Ala Leu Val His Gly Met
                85                  90                  95

Trp Leu Ser Ala Thr Ala Gln His Leu Ala Gly Leu Gly Ser Glu Val
            100                 105                 110

Ile Gly Trp Thr Tyr Ser Met Tyr Gly Met Val Gln Leu Asn Asp Val
        115                 120                 125

Val Asp Ile Thr Val Glu Arg Val Gly Arg Ala Gly Leu Lys Pro Ala
    130                 135                 140

Tyr Glu Val Thr Cys Arg Ile Asp Gly Asn Val Val Ser Arg Gly Gln
145                 150                 155                 160

Ala Leu Leu Lys Ala Pro Ser Thr Ala Tyr Val Tyr Pro Ser Gln Gly
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Ile Gln Ala Lys Gly Met Gly Gln Gly Asp Arg Thr Ala Ser Ala Glu
            180                 185                 190

Ala Arg Ala Val Trp Glu Arg Ala Asp Ala His Thr Arg Ala Asn Leu
        195                 200                 205

Gly Phe Ser Ile Gln Gln Val Ile Asp Glu Asn Pro Thr Glu Leu Lys
    210                 215                 220

Val Gly Asp Thr Thr Phe Val His Pro Ala Gly Val Leu Asn Leu Thr
225                 230                 235                 240

Gln Phe Thr Gln Val Ala Leu Ala Val Val Ala Tyr Ala Gln Thr Glu
                245                 250                 255

Arg Leu Lys Ala Ala Asn Ala Ile Val Asp Gly Ser Leu Tyr Ala Gly
            260                 265                 270
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His Ser Leu Gly Glu Tyr Thr Ala Leu Ala Ser Leu Gly Asn Ile Phe
275 280 285

Glu Leu Glu Gly Val Ile Asp Val Val Phe Ser Arg Gly Ser Ala Met
290 295 300

His Ser Leu Val Pro Arg Asp Glu Lys Gly Arg Ser Asn Tyr Gly Leu
305 310 315 320

Ala Ala Phe Arg Pro Asn Met Ile Asn Val Ala Ala Thr Glu Val Glu
325 330 335

Asn Trp Val Asp Arg Val Ala Glu Glu Ser Gly Glu Phe Leu Gln Ile
340 345 350

Val Asn Tyr Asn Val Asp Gly Gln Gln Tyr Ala Val Ala Gly Thr Leu
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Ala Gly Leu Lys Ala Leu Lys Ala Ser Ala Ser Ala Asn Pro Arg Ala
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Tyr Val Asn Ile Pro Gly Ile Asp Val Pro Phe His Ser Ser Val Leu
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Arg Pro Gly Val Pro Ala Phe Ala Glu Lys Leu Asp Glu Leu Leu Pro
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Glu Thr Ile Asp Ile Asp Ala Leu Arg Gly Arg Tyr Ile Pro Asn Leu
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Val Ala Arg Pro Phe Glu Leu Thr Gln Ser Phe Val Asp Ala Ile Leu
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Ala Val Val Pro Ser Glu Arg Leu Lys Gly Ile Lys Val Glu Asp Thr
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Asp Glu Asn Thr Leu Ala Arg Leu Leu Leu Ile Glu Leu Leu Ser Trp
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Gln Phe Ala Ser Pro Val Arg Trp Ile Glu Thr Gln Ala Leu Ile Ile
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Asp Thr Val Asp Gln Ile Ile Glu Val Gly Leu Ala Ala Ser Pro Thr
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Leu Thr Asn Leu Ala Leu Arg Thr Met Asp Val Ile Gly Lys Ser Arg
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Pro Val Phe Asn Val Glu Arg Asp Gln Asp Thr Val Met Leu Asn Asp
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Val Arg Gln Ala Pro Val Ala Glu Val Glu Glu Glu Ala Val Glu Glu
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Ala Pro Val Ala Ala Ala Ala Pro Ala Pro Val Gly Asn Ala Pro Glu
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Leu Lys Phe Asn Ala Ala Asn Ala Ile Met Val Leu Phe Ala Val Gln

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Asn Lys Ile Asn Ile Asp Gln Ile Thr Ala Ala Asp Thr Ser Glu Thr
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Ser Thr Glu Leu Ser Val Pro Thr Ile Asp Gly Ala Ala Asp Ala Asp
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Val Ala Thr Leu Gln Gly Arg Val Val Thr Ala Ala Pro Gly Tyr Lys
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Pro Phe Gly Pro Val Leu Ser Glu Thr Val Arg Ala Arg Leu Arg Ala
675 680 685

Leu Thr Gly Ala Ala Gly Leu Lys Thr Ser Tyr Ile Gly Asp Arg Val
690 695 700

Thr Gly Thr Trp Gly Leu Pro Glu Ser Trp Thr Ala His Val Glu Val
705 710 715 720

Glu Leu Leu Leu Gly Thr Arg Glu Gly Glu Ser Val Arg Gly Gly Asn
725 730 735

Leu Gly Ser Leu Pro Ala Asn Ala Ser Ser Lys Gly Asp Val Asp Ala
740 745 750

Leu Ile Asp Ala Ala Val Gln Asn Val Ala Ala Ala Asn Gly Thr Ser
755 760 765

Val Ser Met Ser Ser Gly Gly Ala Ala Ser Gly Gly Gly Val Val Asp
770 775 780

Ser Ala Ala Leu Asp Ala Tyr Ala Ser Thr Val Thr Gly Glu Glu Gly
785 790 795 800

Val Leu Ala Asn Val Ala Arg Gly Ile Leu Ser Gln Leu Gly Leu Asp
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Thr Lys Asp Glu Val Glu Gly Ala Glu Ile Asp Thr Glu Leu Tyr Asp
820 825 830

Ala Val Glu Ala Glu Leu Gly Thr Gly Trp Leu Lys Leu Val Thr Pro
835 840 845

Val Phe Ser Ala Asp Arg Ala Ile Leu Phe Asp Asp Arg Trp Ala Ser
850 855 860

Ala Arg Glu Asp Leu Ala Arg Leu Ala Asn Gly Glu Asp Ile Ala Val
865 870 875 880

Glu Arg Phe Ala Gly Thr Gly Glu Thr Val Val Lys Gln Ala Ala Trp
885 890 895

Trp Ala Glu His Val Glu Asp Thr Ala Leu Ala Ala Thr Leu Lys Gln
900 905 910

Val Ser Glu Val Ala Ala Lys Pro Ala Asn Glu Pro His Ile Asp Asp
915 920 925

Val Ala Leu Val Thr Gly Ala Ala Pro Glu Ser Ile Ala Gly Ala Val
930 935 940

Ala Ala Arg Leu Leu Ser Gln Gly Ala Thr Val Ile Leu Thr Ala Ser
945 950 955 960

Asn Val Ser Gln Ala Arg Lys Glu Tyr Ala Arg Lys Leu Tyr Ala Ala
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Asn Ala Thr Pro Asn Ala Lys Leu Trp Ile Val Pro Ala Asn Met Ser
980 985 990

Ser Tyr Arg Asp Val Asp Ala Val Ile Asp Trp Ile Gly Asn Glu Gln
995 1000 1005

Arg Val Thr Val Gly Ser Thr Val Thr Val Thr Lys Pro Ala Leu Thr
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Ser Val Glu Arg Thr Ile Ala Gly Leu Ala Asp Leu Ala Ser Arg Gly
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Val Asp Gly Arg Val His Val Val Leu Pro Gly Ser Pro Asn Arg Gly
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Met Phe Gly Gly Asp Gly Ala Tyr Gly Glu Val Lys Ala Ala Phe Asp
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Ala Ile Leu Ala Lys Trp Gly Ser Glu Thr Gly Trp Pro Gln Phe Val
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Ser Leu Ala Gln Ala Arg Ile Gly Trp Val Ala Gly Thr Gly Leu Met
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Gly Arg Asn Asp Val Leu Ile Pro Ala Ala Glu Lys Leu Gly Ile His
1140 1145 1150

Val Tyr Thr Pro Glu Glu Ile Ser Ser Glu Leu Leu Gly Leu Ala Ser
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Ala Glu Ser Arg Glu Lys Ala Leu Glu Ala Pro Ile Asp Tyr Asp Leu
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Glu Glu Ala Asp Gly Glu Trp Ile Val Thr Lys Lys Lys Gly Ser Thr
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Met Gln Ser Leu Arg Lys Leu Phe Val Asn Arg Phe Leu Gly Gln Asp
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Arg Pro Ser Asp Ile Leu Gln Glu Thr Leu Pro Asn Val Val Ala Ala
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Lys Ile Arg Leu Asn Lys Ala Asp Phe Val Val Ala Gly Gly Ile Asp
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Asp Ile Gln Val Glu Ser Leu Thr Gly Phe Gly Asp Met Asn Ala Thr
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Ala Asp Thr Gln Ala Met Leu Asp Lys Gly Ile Asp Pro Arg Phe Ile

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Gln Gly

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Ser Thr Val Thr Gly Glu Glu Gly Val Leu Ala Asn Val Ala Arg Gly
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Ile Leu Ser Gln Leu Gly Leu Asp Thr Lys Asp Glu Val Glu Gly Ala
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Glu Ile Asp Thr Glu Leu Tyr Asp Ala Val Glu Ala Glu Leu Gly Thr
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Gly Trp Leu Lys Leu Val Thr Pro Val Phe Ser Ala Asp Arg Ala Ile
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Leu Phe Asp Asp Arg Trp Ala Ser Ala Arg Glu Asp Leu Ala Arg Leu
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Ala Asn Gly Glu Asp Ile Ala Val Glu Arg Phe Ala Gly Thr Gly Glu
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Thr Val Val Lys Gln Ala Ala Trp Trp Ala Glu His Val Glu Asp Thr
115 120 125

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Ala Leu Ala Ala Thr Leu Lys Gln Val Ser Glu Val Ala Ala Lys Pro
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Glu Asp Met Val Val Met Val Gly Val Gly Glu Val Ser Ser Trp Gly
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Ser Val Asp Leu Thr Ala Ala Gly Val Leu Glu Leu Ala Trp Met Met
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Gly Leu Ile Ser Trp Ser Glu Asp Pro Lys Pro Ala Trp Tyr Asp Ala
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    610                 615                 620

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Leu Thr Arg Ser Val Ala Gly Gln Leu Pro Thr Asp Phe Asp Pro Ala
625                 630                 635                 640

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Lys Trp Gly Ile Pro Ala Ser Met Ile Asp Ala Leu Asp Asn Ile Ala
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gcg tgg aac ctg gtc act gca gtc gac gcc ttc ctg tcc tcc ggc ttc    2016
Ala Trp Asn Leu Val Thr Ala Val Asp Ala Phe Leu Ser Ser Gly Phe
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agc cca gca gaa ctc ctg cag tcc atc cac cca gct gac gtg tcc tcc    2064
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acc cag ggc acc ggt atc ggt ggc atg cag tcc cta cgc aag ctg ttc    2112
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690 695 700

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705 710 715 720

acc ctg cca aac gtt gtg gct gca cac acc atg cag tcc tac gtc ggt 2208
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725 730 735

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Gly Tyr Gly Gln Met Ile His Pro Val Ala Ala Cys Ala Thr Ala Ala
740 745 750

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Val Ser Val Glu Glu Gly Val Asp Lys Ile Arg Leu Asn Lys Ala Asp
755 760 765

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785 790 795 800

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835 840 845

cac gca cag tcc tac gcc gat ggt gct cac acc tcc atc cca gca ccg 2592
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850 855 860

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885 890 895

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900 905 910

gag ctg cac aac ctg ctg tgg aag acc att gga cgc gaa gcc gac aac 2784
Glu Leu His Asn Leu Leu Trp Lys Thr Ile Gly Arg Glu Ala Asp Asn
915 920 925

ccg atg ttc gtc gtc tcc cag aag tcc ctt acc gga cac tca aag ggc 2832
Pro Met Phe Val Val Ser Gln Lys Ser Leu Thr Gly His Ser Lys Gly

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    930                  935                  940

ggt gca gca ctc ttc cag atc ggt gga ctt gtc tcc atc ctg gaa acc    2880
Gly Ala Ala Leu Phe Gln Ile Gly Gly Leu Val Ser Ile Leu Glu Thr
945                 950                 955                 960

ggc aag ctg cca cag aac gca tcc ctt gac tgc gtt gac cca gag atg    2928
Gly Lys Leu Pro Gln Asn Ala Ser Leu Asp Cys Val Asp Pro Glu Met
                965                 970                 975

gaa gca aag ggc gag aac ttc gtc tgg ctg cgc aag cca ctg gat ctc    2976
Glu Ala Lys Gly Glu Asn Phe Val Trp Leu Arg Lys Pro Leu Asp Leu
            980                 985                 990

ggc gca ggc tcc att aag gcc ggc gta ctt acc tca ctg ggc ttc ggc    3024
Gly Ala Gly Ser Ile Lys Ala Gly Val Leu Thr Ser Leu Gly Phe Gly
        995                 1000                1005

cac gtg gct gca gtc gtc gtg ctg gca acc agc ggc atc ttc gag cag    3072
His Val Ala Ala Val Val Val Leu Ala Thr Ser Gly Ile Phe Glu Gln
    1010                1015                1020

gca atg cgc aac gca ggc ctc gac gtc gaa gca tgg cgt gca cgc gca    3120
Ala Met Arg Asn Ala Gly Leu Asp Val Glu Ala Trp Arg Ala Arg Ala
1025                1030                1035                1040

acc cag cgc ctg cgc acc ggt gca aac cgc cta gaa gct ggc atg gtt    3168
Thr Gln Arg Leu Arg Thr Gly Ala Asn Arg Leu Glu Ala Gly Met Val
                1045                1050                1055

ggc cga gca cca ttg ttc gag cag gtc gac gga cgt cgc ctg cca gag    3216
Gly Arg Ala Pro Leu Phe Glu Gln Val Asp Gly Arg Arg Leu Pro Glu
            1060                1065                1070

cat ggc gct cac caa gca gag atc aac ttg ctt atc gac gct gac gct    3264
His Gly Ala His Gln Ala Glu Ile Asn Leu Leu Ile Asp Ala Asp Ala
        1075                1080                1085

cgc ctc ggt gct gac ggc atc tac cag ggc taaacgttag atagctaaga      3314
Arg Leu Gly Ala Asp Gly Ile Tyr Gln Gly
    1090                1095

aag                                                                3317


<210> 48
<211> 1098
<212> PRT
<213> Corynebacterium glutamicum

<400> 48
Ala Ser Gly Gly Gly Val Val Asp Ser Ala Ala Leu Asp Ala Tyr Ala
  1               5                  10                  15

Ser Thr Val Thr Gly Glu Glu Gly Val Leu Ala Asn Val Ala Arg Gly
            20                  25                  30

Ile Leu Ser Gln Leu Gly Leu Asp Thr Lys Asp Glu Val Glu Gly Ala
        35                  40                  45

Glu Ile Asp Thr Glu Leu Tyr Asp Ala Val Glu Ala Glu Leu Gly Thr
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50 55 60

Gly Trp Leu Lys Leu Val Thr Pro Val Phe Ser Ala Asp Arg Ala Ile
65 70 75 80

Leu Phe Asp Asp Arg Trp Ala Ser Ala Arg Glu Asp Leu Ala Arg Leu
85 90 95

Ala Asn Gly Glu Asp Ile Ala Val Glu Arg Phe Ala Gly Thr Gly Glu
100 105 110

Thr Val Val Lys Gln Ala Ala Trp Trp Ala Glu His Val Glu Asp Thr
115 120 125

Ala Leu Ala Ala Thr Leu Lys Gln Val Ser Glu Val Ala Ala Lys Pro
130 135 140

Ala Asn Glu Pro His Ile Asp Asp Val Ala Leu Val Thr Gly Ala Ala
145 150 155 160

Pro Glu Ser Ile Ala Gly Ala Val Ala Ala Arg Leu Leu Ser Gln Gly
165 170 175

Ala Thr Val Ile Leu Thr Ala Ser Asn Val Ser Gln Ala Arg Lys Glu
180 185 190

Tyr Ala Arg Lys Leu Tyr Ala Ala Asn Ala Thr Pro Asn Ala Lys Leu
195 200 205

Trp Ile Val Pro Ala Asn Met Ser Ser Tyr Arg Asp Val Asp Ala Val
210 215 220

Ile Asp Trp Ile Gly Asn Glu Gln Arg Val Thr Val Gly Ser Thr Val
225 230 235 240

Thr Val Thr Lys Pro Ala Leu Thr Pro Thr Leu Ala Tyr Pro Phe Ala
245 250 255

Ala Pro Ser Val Ser Gly Thr Leu Ala Asp Ala Gly Pro Gln Ala Glu
260 265 270

Asn Gln Ala Arg Leu Leu Leu Trp Ser Val Glu Arg Thr Ile Ala Gly
275 280 285

Leu Ala Asp Leu Ala Ser Arg Gly Val Asp Gly Arg Val His Val Val
290 295 300

Leu Pro Gly Ser Pro Asn Arg Gly Met Phe Gly Gly Asp Gly Ala Tyr
305 310 315 320

Gly Glu Val Lys Ala Ala Phe Asp Ala Ile Leu Ala Lys Trp Gly Ser
325 330 335

Glu Thr Gly Trp Pro Gln Phe Val Ser Leu Ala Gln Ala Arg Ile Gly
340 345 350

Trp Val Ala Gly Thr Gly Leu Met Gly Arg Asn Asp Val Leu Ile Pro
355 360 365

Ala Ala Glu Lys Leu Gly Ile His Val Tyr Thr Pro Glu Glu Ile Ser
370 375 380

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Ser Glu Leu Leu Gly Leu Ala Ser Ala Glu Ser Arg Glu Lys Ala Leu
385                 390                 395                 400

Glu Ala Pro Ile Asp Tyr Asp Leu Thr Gly Gly Leu Ser Gly Gly Val
                405                 410                 415

Ser Ile Ala Ala Leu Ala Ala Ser Leu Glu Ser Asp Ala Val Glu Thr
            420                 425                 430

Thr Ser Ala Ala Glu Asp Thr Ile Lys Ala Leu Pro Ser Pro Lys His
        435                 440                 445

Pro Glu Gln Pro Val Gly Thr Pro Val Gly Glu Val Lys Thr Asp Leu
    450                 455                 460

Glu Asp Met Val Val Met Val Gly Val Gly Glu Val Ser Ser Trp Gly
465                 470                 475                 480

Ser Gly Arg Thr Arg Phe Glu Ala Glu Tyr Gly Ile Gln Arg Asp Gly
                485                 490                 495

Ser Val Asp Leu Thr Ala Ala Gly Val Leu Glu Leu Ala Trp Met Met
            500                 505                 510

Gly Leu Ile Ser Trp Ser Glu Asp Pro Lys Pro Ala Trp Tyr Asp Ala
        515                 520                 525

Asp Gly Thr Glu Val Pro Glu Glu Glu Ile Tyr Glu Arg Phe Arg Asp
    530                 535                 540

Glu Val Ile Ala Arg Cys Gly Val Arg Glu Leu Val Asp Asp Ala Phe
545                 550                 555                 560

Leu Val Asp Gly Gly Ser Leu Asp Ala Ala Glu Val Phe Leu Asp Arg
                565                 570                 575

Asp Ile Ser Phe Ser Val Thr Ser Ala Glu Glu Ala Gln Ala Tyr Val
            580                 585                 590

Asp Ala Asp Ala Ser Val Thr Val Glu Glu Ala Asp Gly Glu Trp Ile
        595                 600                 605

Val Thr Lys Lys Lys Gly Ser Thr Ser Phe Val Pro Arg Lys Ala Thr
    610                 615                 620

Leu Thr Arg Ser Val Ala Gly Gln Leu Pro Thr Asp Phe Asp Pro Ala
625                 630                 635                 640

Lys Trp Gly Ile Pro Ala Ser Met Ile Asp Ala Leu Asp Asn Ile Ala
                645                 650                 655

Ala Trp Asn Leu Val Thr Ala Val Asp Ala Phe Leu Ser Ser Gly Phe
            660                 665                 670

Ser Pro Ala Glu Leu Leu Gln Ser Ile His Pro Ala Asp Val Ser Ser
        675                 680                 685

Thr Gln Gly Thr Gly Ile Gly Gly Met Gln Ser Leu Arg Lys Leu Phe
    690                 695                 700
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Val Asn Arg Phe Leu Gly Gln Asp Arg Pro Ser Asp Ile Leu Gln Glu
705 710 715 720

Thr Leu Pro Asn Val Val Ala Ala His Thr Met Gln Ser Tyr Val Gly
725 730 735

Gly Tyr Gly Gln Met Ile His Pro Val Ala Ala Cys Ala Thr Ala Ala
740 745 750

Val Ser Val Glu Glu Gly Val Asp Lys Ile Arg Leu Asn Lys Ala Asp
755 760 765

Phe Val Val Ala Gly Gly Ile Asp Asp Ile Gln Val Glu Ser Leu Thr
770 775 780

Gly Phe Gly Asp Met Asn Ala Thr Ala Asp Thr Gln Ala Met Leu Asp
785 790 795 800

Lys Gly Ile Asp Pro Arg Phe Ile Ser Arg Ala Asn Asp Arg Arg Arg
805 810 815

Ala Gly Phe Leu Glu Ala Ala Gly Gly Gly Thr Val Leu Leu Ala Arg
820 825 830

Ala Ser Val Ala Ala Glu Leu Gly Leu Pro Val Leu Ala Val Val Ala
835 840 845

His Ala Gln Ser Tyr Ala Asp Gly Ala His Thr Ser Ile Pro Ala Pro
850 855 860

Gly Leu Gly Ala Leu Gly Ala Ala Arg Gly Gly Lys Lys Ser Val Leu
865 870 875 880

Ala Arg Glu Leu Asn Lys Leu Gly Leu Thr Pro Asp Asp Val Arg Val
885 890 895

Val Ser Lys His Asp Thr Ser Thr Asn Ala Asn Asp Pro Asn Glu Ser
900 905 910

Glu Leu His Asn Leu Leu Trp Lys Thr Ile Gly Arg Glu Ala Asp Asn
915 920 925

Pro Met Phe Val Val Ser Gln Lys Ser Leu Thr Gly His Ser Lys Gly
930 935 940

Gly Ala Ala Leu Phe Gln Ile Gly Gly Leu Val Ser Ile Leu Glu Thr
945 950 955 960

Gly Lys Leu Pro Gln Asn Ala Ser Leu Asp Cys Val Asp Pro Glu Met
965 970 975

Glu Ala Lys Gly Glu Asn Phe Val Trp Leu Arg Lys Pro Leu Asp Leu
980 985 990

Gly Ala Gly Ser Ile Lys Ala Gly Val Leu Thr Ser Leu Gly Phe Gly
995 1000 1005

His Val Ala Ala Val Val Val Leu Ala Thr Ser Gly Ile Phe Glu Gln
1010 1015 1020

Ala Met Arg Asn Ala Gly Leu Asp Val Glu Ala Trp Arg Ala Arg Ala

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1025                1030                1035                1040

Thr Gln Arg Leu Arg Thr Gly Ala Asn Arg Leu Glu Ala Gly Met Val
                1045                1050                1055

Gly Arg Ala Pro Leu Phe Glu Gln Val Asp Gly Arg Arg Leu Pro Glu
            1060                1065                1070

His Gly Ala His Gln Ala Glu Ile Asn Leu Leu Ile Asp Ala Asp Ala
        1075                1080                1085

Arg Leu Gly Ala Asp Gly Ile Tyr Gln Gly
    1090                1095


&lt;210&gt; 49
&lt;211&gt; 6136
&lt;212&gt; DNA
&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (101)..(6136)
&lt;223&gt; RXN03111

&lt;400&gt; 49
cgtgaccgaa ttgagcagga acttcggggc cagccgactg attaaccgct ttggccagga 60

gccttttgcc ttcgctttcg ccggccaagg atatgactgg ttg aag acc ctt cgt   115
                                            Leu Lys Thr Leu Arg
                                             1               5

gcc gcg gtt gcc gca ggt gca ggc acc aat gtt agt gac atc gtc gag   163
Ala Ala Val Ala Ala Gly Ala Gly Thr Asn Val Ser Asp Ile Val Glu
                10                  15                  20

cgc gca aat gcg ctg ctt gca cta gtt gca gat gat ctc att ggc acc   211
Arg Ala Asn Ala Leu Leu Ala Leu Val Ala Asp Asp Leu Ile Gly Thr
            25                  30                  35

ctt cca ttt ggt ttc gat cca gtg gct tgg gct aac aac tcc gaa gat   259
Leu Pro Phe Gly Phe Asp Pro Val Ala Trp Ala Asn Asn Ser Glu Asp
        40                  45                  50

cca gct ttc gat act gca caa tct gca gtg agc gtg ccg ggt atc ttt   307
Pro Ala Phe Asp Thr Ala Gln Ser Ala Val Ser Val Pro Gly Ile Phe
    55                  60                  65

gtc tcc cag atc gca acc ctg gat tcc ctt gag gcg cag cgc ctt gat   355
Val Ser Gln Ile Ala Thr Leu Asp Ser Leu Glu Ala Gln Arg Leu Asp
70                  75                  80                  85

gtg gat cag gct gtg tcc agc att ggt cat tcc cag ggc gta ttg ggc   403
Val Asp Gln Ala Val Ser Ser Ile Gly His Ser Gln Gly Val Leu Gly
                90                  95                  100

gtg cac ctg ctc aat gat gcg act cgt gct gat gaa ctc gtt gcc att   451
Val His Leu Leu Asn Asp Ala Thr Arg Ala Asp Glu Leu Val Ala Ile
            105                 110                 115

gcg cag ttg atc ggt gca gcg atc acc cgc acc gca cgc atg acg ggc   499
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Ala Gln Leu Ile Gly Ala Ala Ile Thr Arg Thr Ala Arg Met Thr Gly
120 125 130

ctg atc gcg cag ggc gac aac atg ccg atg ctg tcg atc gcc gga att 547
Leu Ile Ala Gln Gly Asp Asn Met Pro Met Leu Ser Ile Ala Gly Ile
135 140 145

tcc cgc gaa cag ctt cag caa gct atc gac gcg gcc tgc gcc gaa gtc 595
Ser Arg Glu Gln Leu Gln Gln Ala Ile Asp Ala Ala Cys Ala Glu Val
150 155 160 165

cct gcg gag atc cgc ccg gtt atc ggt ctg cgc aac tca cgc gat tct 643
Pro Ala Glu Ile Arg Pro Val Ile Gly Leu Arg Asn Ser Arg Asp Ser
170 175 180

tat gtt ttg gtt ggc cgc cca gac gac aac gct cgc gtt gtt aag gtc 691
Tyr Val Leu Val Gly Arg Pro Asp Asp Asn Ala Arg Val Val Lys Val
185 190 195

att gag gca atg gct gcc aag gat aag aag gcc att gaa gat aag ctg 739
Ile Glu Ala Met Ala Ala Lys Asp Lys Lys Ala Ile Glu Asp Lys Leu
200 205 210

cgc ggc ggt tcc gcg ttc agc ccc cgt att act ccg ctg aag gtg cag 787
Arg Gly Gly Ser Ala Phe Ser Pro Arg Ile Thr Pro Leu Lys Val Gln
215 220 225

gct gct ttc cat cac cca gct atg aac atg gct gtg gag cag acc gtg 835
Ala Ala Phe His His Pro Ala Met Asn Met Ala Val Glu Gln Thr Val
230 235 240 245

gcg tgg gca acc act gct ggt ttg gat gtg gaa ctc acc cgc gag atc 883
Ala Trp Ala Thr Thr Ala Gly Leu Asp Val Glu Leu Thr Arg Glu Ile
250 255 260

gcc gct gat gtt ttg gtt aac cct gtc gat tgg gta gca cgc gtc aac 931
Ala Ala Asp Val Leu Val Asn Pro Val Asp Trp Val Ala Arg Val Asn
265 270 275

gaa gcg tat gag gct ggc gct cgc tgg ttc ctc gac gtt gga cca gat 979
Glu Ala Tyr Glu Ala Gly Ala Arg Trp Phe Leu Asp Val Gly Pro Asp
280 285 290

ggt ggc atc gtt aag ctg act gcc aac atc ctt gag ggc cgc ggc gcg 1027
Gly Gly Ile Val Lys Leu Thr Ala Asn Ile Leu Glu Gly Arg Gly Ala
295 300 305

gat tcc ttc tat gtt ggt gac gcc gca ggc cag gcc aag ata ttt gat 1075
Asp Ser Phe Tyr Val Gly Asp Ala Ala Gly Gln Ala Lys Ile Phe Asp
310 315 320 325

gct ggc atg gca cct gaa ctt cca gtg gat tac cag gag ttc gca cca 1123
Ala Gly Met Ala Pro Glu Leu Pro Val Asp Tyr Gln Glu Phe Ala Pro
330 335 340

cgc gtt gag cac gtt gat gga acc cca cgc ctg gtt acc aag ttc act 1171
Arg Val Glu His Val Asp Gly Thr Pro Arg Leu Val Thr Lys Phe Thr
345 350 355

gag ctg acc ggc cgc acc cca atg atg ctg gct ggc atg acc cca acc 1219
Glu Leu Thr Gly Arg Thr Pro Met Met Leu Ala Gly Met Thr Pro Thr

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        360                 365                 370

acc gtt gac cct gcc att gtt gca gcc gct gca aac ggt gga cac tgg      1267
Thr Val Asp Pro Ala Ile Val Ala Ala Ala Ala Asn Gly Gly His Trp
    375                 380                 385

gct gag ctc gct ggt ggc gga cag gtt acc cca gag ctg ctg gaa acc      1315
Ala Glu Leu Ala Gly Gly Gly Gln Val Thr Pro Glu Leu Leu Glu Thr
390                 395                 400                 405

cac atc gca cag ctc acc gac atg ctt gag cca ggt atc aac gcc cag      1363
His Ile Ala Gln Leu Thr Asp Met Leu Glu Pro Gly Ile Asn Ala Gln
                410                 415                 420

ttc aac tcc atg ttc ttg gat cca tac ctg tgg aag atg cag att ggt      1411
Phe Asn Ser Met Phe Leu Asp Pro Tyr Leu Trp Lys Met Gln Ile Gly
            425                 430                 435

ggc aag cgc ctt gtt cct aag gcc cgc gct aat ggt gca tcc atc gac      1459
Gly Lys Arg Leu Val Pro Lys Ala Arg Ala Asn Gly Ala Ser Ile Asp
        440                 445                 450

ggc atc gtc atc acc gcc ggc att cct gaa aag gat gaa gct gtt gca      1507
Gly Ile Val Ile Thr Ala Gly Ile Pro Glu Lys Asp Glu Ala Val Ala
    455                 460                 465

ttg gtc aag gaa ctg atg cgt gat ggt ttc cct tgg atc gca ttc aag      1555
Leu Val Lys Glu Leu Met Arg Asp Gly Phe Pro Trp Ile Ala Phe Lys
470                 475                 480                 485

cca ggt gcc atc aag cag gtt aac tct gtg ttg gct atc gct aag gaa      1603
Pro Gly Ala Ile Lys Gln Val Asn Ser Val Leu Ala Ile Ala Lys Glu
                490                 495                 500

gtt cca gaa ctc ccc atc atc att cag att gag ggt ggc gtt gca ggt      1651
Val Pro Glu Leu Pro Ile Ile Ile Gln Ile Glu Gly Gly Val Ala Gly
            505                 510                 515

gga cac cac tct tgg gaa gac ctc gat gag ctg ctg atc gcc acc tac      1699
Gly His His Ser Trp Glu Asp Leu Asp Glu Leu Leu Ile Ala Thr Tyr
        520                 525                 530

ggc aag gtc cgc gca ctg gat aac gtg gtg ctg tgt gtc ggc ggt ggc      1747
Gly Lys Val Arg Ala Leu Asp Asn Val Val Leu Cys Val Gly Gly Gly
    535                 540                 545

att ggc tca cct gag cgc gct gct gat tac gtc acc ggt tcc tgg tcc      1795
Ile Gly Ser Pro Glu Arg Ala Ala Asp Tyr Val Thr Gly Ser Trp Ser
550                 555                 560                 565

act tcc tac ggc ctg cca gct atg cct gtt gat ggc atc ttg gtg ggt      1843
Thr Ser Tyr Gly Leu Pro Ala Met Pro Val Asp Gly Ile Leu Val Gly
                570                 575                 580

acc gct gcg atg gca acc aag gaa gca acc acc tcc cag gcc gtc aag      1891
Thr Ala Ala Met Ala Thr Lys Glu Ala Thr Thr Ser Gln Ala Val Lys
            585                 590                 595

gaa ctt ctt gtt tcc acc cag ggc tct gat gaa tgg gtt cct gct ggt      1939
Glu Leu Leu Val Ser Thr Gln Gly Ser Asp Glu Trp Val Pro Ala Gly
        600                 605                 610
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ggc gca aag aac gga atg gca tct ggc cgt tcc cag ctt ggc gca gac    1987
Gly Ala Lys Asn Gly Met Ala Ser Gly Arg Ser Gln Leu Gly Ala Asp
    615                 620                 625

atc cac gag atc gac aac tcc ttt gct aag gct gga cgc ctt ctt gat    2035
Ile His Glu Ile Asp Asn Ser Phe Ala Lys Ala Gly Arg Leu Leu Asp
630                 635                 640                 645

gag gtt gca ggc gat gag acg gct gtg cag gcg cgc cgg gat gag atc    2083
Glu Val Ala Gly Asp Glu Thr Ala Val Gln Ala Arg Arg Asp Glu Ile
                650                 655                 660

att gaa gcg att ggc aag acc gcc aag gtg tac ttc ggt gac atc gga    2131
Ile Glu Ala Ile Gly Lys Thr Ala Lys Val Tyr Phe Gly Asp Ile Gly
            665                 670                 675

tcc atg act tac gag cag tgg ctc aac cgc tac ctc gag ctg tct ggc    2179
Ser Met Thr Tyr Glu Gln Trp Leu Asn Arg Tyr Leu Glu Leu Ser Gly
        680                 685                 690

cct gtt gat ggt cag tgg att gat gct tcc tgg gct gca cgt ttt gcc    2227
Pro Val Asp Gly Gln Trp Ile Asp Ala Ser Trp Ala Ala Arg Phe Ala
    695                 700                 705

cag atg ctg gag cgt gcc gag gcg cgt ttg atc gag cag gat cat ggc    2275
Gln Met Leu Glu Arg Ala Glu Ala Arg Leu Ile Glu Gln Asp His Gly
710                 715                 720                 725

caa ttt gag cca agc ctg acg gtg gag gat ggc gtc gac aag ctt gtt    2323
Gln Phe Glu Pro Ser Leu Thr Val Glu Asp Gly Val Asp Lys Leu Val
                730                 735                 740

gct gct tac ccg cat gcc gca acc gac ctg ctc acc ccg gct gat gtc    2371
Ala Ala Tyr Pro His Ala Ala Thr Asp Leu Leu Thr Pro Ala Asp Val
            745                 750                 755

gcc tgg ttc ttg ggc ctg tgc cgc acg ccg ggc aag cct gtg aac ttt    2419
Ala Trp Phe Leu Gly Leu Cys Arg Thr Pro Gly Lys Pro Val Asn Phe
        760                 765                 770

gtg ccc gtc att gat aag gac gtg cgt cgc tgg tgg cgc tcg gac tcc    2467
Val Pro Val Ile Asp Lys Asp Val Arg Arg Trp Trp Arg Ser Asp Ser
    775                 780                 785

ctg tgg cag tcc cac gat gat cgc tac acc gct gat cag gtg gct att    2515
Leu Trp Gln Ser His Asp Asp Arg Tyr Thr Ala Asp Gln Val Ala Ile
790                 795                 800                 805

atc cct ggt gtc gtc gcc gtt gct ggc atc acc aag gcc aac gaa cct    2563
Ile Pro Gly Val Val Ala Val Ala Gly Ile Thr Lys Ala Asn Glu Pro
                810                 815                 820

gtc gct gac ctg ctt gat cgc ttt gtc gac gcc acc atc gag cgc atc    2611
Val Ala Asp Leu Leu Asp Arg Phe Val Asp Ala Thr Ile Glu Arg Ile
            825                 830                 835

gat gag cac gat tcc cgc tcc cgc gac atc atg ggc aaa gtg ctt tcc    2659
Asp Glu His Asp Ser Arg Ser Arg Asp Ile Met Gly Lys Val Leu Ser
        840                 845                 850
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tca cct ggc aca ttc tgg gct ggc cgc aac atc cca tcg gtg atc cac    2707
Ser Pro Gly Thr Phe Trp Ala Gly Arg Asn Ile Pro Ser Val Ile His
    855                 860                 865

agc ctt ggg cat gct gac aag tgg tcc cgc tcc gaa ttc gaa gca ttc    2755
Ser Leu Gly His Ala Asp Lys Trp Ser Arg Ser Glu Phe Glu Ala Phe
870                 875                 880                 885

cat agc cca acc ggc gcc aac ttg gtg tac gaa gac gcc gag cac gcg    2803
His Ser Pro Thr Gly Ala Asn Leu Val Tyr Glu Asp Ala Glu His Ala
                890                 895                 900

atg ctg act gtg cct ttg gcg ggt tcc acc gca ttc ggc acc acc gct    2851
Met Leu Thr Val Pro Leu Ala Gly Ser Thr Ala Phe Gly Thr Thr Ala
            905                 910                 915

gag ctg aaa atc cgt ttc acc agc ccc atc gac gct ctg cca agc gct    2899
Glu Leu Lys Ile Arg Phe Thr Ser Pro Ile Asp Ala Leu Pro Ser Ala
        920                 925                 930

gtc cca ctg gtc acc cag gaa gac gct gaa gcc gcg atg ggt gaa ctg    2947
Val Pro Leu Val Thr Gln Glu Asp Ala Glu Ala Ala Met Gly Glu Leu
    935                 940                 945

acc cgc atc gca gct ggc ggc acc ctg gca act gtg aac aat ggc acc    2995
Thr Arg Ile Ala Ala Gly Gly Thr Leu Ala Thr Val Asn Asn Gly Thr
950                 955                 960                 965

gct acc tgg gaa acc tcc gtc gat gcc ggc gtc atc gct gac tac aac    3043
Ala Thr Trp Glu Thr Ser Val Asp Ala Gly Val Ile Ala Asp Tyr Asn
                970                 975                 980

aac gtc acc gca ggc tac ctg cca gca tcc gtt gtt cct gca cac acc    3091
Asn Val Thr Ala Gly Tyr Leu Pro Ala Ser Val Val Pro Ala His Thr
            985                 990                 995

gca cct gac gtg ctg gtt ggc cgc gca tgg cca gca gtt ttc gct gcc    3139
Ala Pro Asp Val Leu Val Gly Arg Ala Trp Pro Ala Val Phe Ala Ala
        1000                1005                1010

gta aag tcc gca gtc atc cca ggc acc gat tcc gca tcc gtt gtg gaa    3187
Val Lys Ser Ala Val Ile Pro Gly Thr Asp Ser Ala Ser Val Val Glu
    1015                1020                1025

ggc atg ctg tcc ctg gtt cac ctg gag cac cac att gtg ctc aag tcc    3235
Gly Met Leu Ser Leu Val His Leu Glu His His Ile Val Leu Lys Ser
1030                1035                1040                1045

gat gtc cca acc gac ggc gcg ctg aag gtt tcc gcg act gcc gat gag    3283
Asp Val Pro Thr Asp Gly Ala Leu Lys Val Ser Ala Thr Ala Asp Glu
                1050                1055                1060

gta gtc gat acc gac ctg ggt cgc ctc gtg atc gtg cgc gca gaa atc    3331
Val Val Asp Thr Asp Leu Gly Arg Leu Val Ile Val Arg Ala Glu Ile
            1065                1070                1075

gcc gac gca gaa ggc aac ctg att gct acg ttg gct gag cgt ttc gcg    3379
Ala Asp Ala Glu Gly Asn Leu Ile Ala Thr Leu Ala Glu Arg Phe Ala
        1080                1085                1090

atc cgc gga cgc aag ggc aac gct gtc gca cgc acc aac acc tcc gca    3427
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Ile Arg Gly Arg Lys Gly Asn Ala Val Ala Arg Thr Asn Thr Ser Ala
    1095                1100                1105

ctg cca acc acc gtg gac acc cca cgc tca gct cgc gca gtg gca acc   3475
Leu Pro Thr Thr Val Asp Thr Pro Arg Ser Ala Arg Ala Val Ala Thr
1110                1115                1120                1125

gtt gtt gca cct gaa tcc atg cgc cca ttc gct gtg atc tcc ggt gac   3523
Val Val Ala Pro Glu Ser Met Arg Pro Phe Ala Val Ile Ser Gly Asp
                1130                1135                1140

cgc aac cca att cac gtc tct gat gtt gcg gct tcc ctg gct ggt ctg   3571
Arg Asn Pro Ile His Val Ser Asp Val Ala Ala Ser Leu Ala Gly Leu
            1145                1150                1155

cca ggt gtg atc gtg cac ggc atg tgg acc tct gcc atc ggt gaa ctg   3619
Pro Gly Val Ile Val His Gly Met Trp Thr Ser Ala Ile Gly Glu Leu
        1160                1165                1170

atc gcc ggt gca gca ttc aac gat gag cag atc caa act ccc gca gcc   3667
Ile Ala Gly Ala Ala Phe Asn Asp Glu Gln Ile Gln Thr Pro Ala Ala
    1175                1180                1185

aag gtc gtg gaa tac acc gca acc atg ctg gca cca gtt ctt cca ggt   3715
Lys Val Val Glu Tyr Thr Ala Thr Met Leu Ala Pro Val Leu Pro Gly
1190                1195                1200                1205

gaa gaa att gag ttc agc gtt gag cgc tcc gca gtg gac aac cgc cca   3763
Glu Glu Ile Glu Phe Ser Val Glu Arg Ser Ala Val Asp Asn Arg Pro
                1210                1215                1220

gga atg gga gag gtc cgc acc gtt acc gca acc gtc aac ggc aac tta   3811
Gly Met Gly Glu Val Arg Thr Val Thr Ala Thr Val Asn Gly Asn Leu
            1225                1230                1235

gtg ctt acc gcc acc gct gtt gtg gca gct cca tct act ttc tac gca   3859
Val Leu Thr Ala Thr Ala Val Val Ala Ala Pro Ser Thr Phe Tyr Ala
        1240                1245                1250

ttc cca ggc cag ggc att cag tcc cag ggc atg ggt atg gaa gca cgc   3907
Phe Pro Gly Gln Gly Ile Gln Ser Gln Gly Met Gly Met Glu Ala Arg
    1255                1260                1265

cgt aac tct cag gca gct cgc gct atc tgg gac cgc gcc gat gca cac   3955
Arg Asn Ser Gln Ala Ala Arg Ala Ile Trp Asp Arg Ala Asp Ala His
1270                1275                1280                1285

acc cgc aat aag ctg ggc ttc tcc atc gtg gaa atc gtg gaa aac aac   4003
Thr Arg Asn Lys Leu Gly Phe Ser Ile Val Glu Ile Val Glu Asn Asn
                1290                1295                1300

cca cgc gaa gta acc gtg gca ggg gag aag ttc ttc cac cca gac ggc   4051
Pro Arg Glu Val Thr Val Ala Gly Glu Lys Phe Phe His Pro Asp Gly
            1305                1310                1315

gtt ttg tac ctc acc cag ttc acc cag gtg ggc atg gca act ctg ggc   4099
Val Leu Tyr Leu Thr Gln Phe Thr Gln Val Gly Met Ala Thr Leu Gly
        1320                1325                1330

gtt gct cag atc gct gaa atg cgt gaa gca cat gcc ttg aac cag cgt   4147
Val Ala Gln Ile Ala Glu Met Arg Glu Ala His Ala Leu Asn Gln Arg
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1335                1340                1345

gca tac ttt gct gga cac tcc gtt ggt gag tac aac gcg ctt gct gca    4195
Ala Tyr Phe Ala Gly His Ser Val Gly Glu Tyr Asn Ala Leu Ala Ala
1350                1355                1360                1365

tat gct ggt gtg ctg tcc ctg gaa tcc gtt ctg gag atc gtt tac cgt    4243
Tyr Ala Gly Val Leu Ser Leu Glu Ser Val Leu Glu Ile Val Tyr Arg
                1370                1375                1380

cgt ggc ttg acc atg cac cgc ttg gtg gat cgc gat gaa aac ggt ctg    4291
Arg Gly Leu Thr Met His Arg Leu Val Asp Arg Asp Glu Asn Gly Leu
            1385                1390                1395

tcc aac tac gcg ctc gca gct ctt cgc ccc aac aag atg ggt ctg acc    4339
Ser Asn Tyr Ala Leu Ala Ala Leu Arg Pro Asn Lys Met Gly Leu Thr
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gca gac aac gtt ttc gat tac gtt gcg tct gtt tcc gaa gct tcc ggt    4387
Ala Asp Asn Val Phe Asp Tyr Val Ala Ser Val Ser Glu Ala Ser Gly
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gaa ttc ctg gag atc gtt aac tac aac ttg gct ggc ctg cag tac gca    4435
Glu Phe Leu Glu Ile Val Asn Tyr Asn Leu Ala Gly Leu Gln Tyr Ala
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gtt gct gga acc cag gct ggt ctt gcc gcc ctt cgt gcc gat gtt gag    4483
Val Ala Gly Thr Gln Ala Gly Leu Ala Ala Leu Arg Ala Asp Val Glu
                1450                1455                1460

aac cgt gca cca ggt cag cgt gcc ttc att ttg atc cct ggc att gac    4531
Asn Arg Ala Pro Gly Gln Arg Ala Phe Ile Leu Ile Pro Gly Ile Asp
            1465                1470                1475

gtg cca ttc cac tcc tcc aag ctg cgc gac ggt gtg ggc gcg ttc cgt    4579
Val Pro Phe His Ser Ser Lys Leu Arg Asp Gly Val Gly Ala Phe Arg
        1480                1485                1490

gag cac ctt gat tcc ctg atc cca gct gag ctg gat ctg gat gtg ctg    4627
Glu His Leu Asp Ser Leu Ile Pro Ala Glu Leu Asp Leu Asp Val Leu
    1495                1500                1505

gtt ggc cgc tac att cca aac ttg gtg gct cgc cca ttc gaa ctc act    4675
Val Gly Arg Tyr Ile Pro Asn Leu Val Ala Arg Pro Phe Glu Leu Thr
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gaa gag ttc gtg gca tcc atg gca gaa gtg gtg gag tcc acc tat gtc    4723
Glu Glu Phe Val Ala Ser Met Ala Glu Val Val Glu Ser Thr Tyr Val
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aat gag atc ttg gct gat ttc aag gct gct tcc gcc gat aag cag aag    4771
Asn Glu Ile Leu Ala Asp Phe Lys Ala Ala Ser Ala Asp Lys Gln Lys
            1545                1550                1555

ctt gcc cgc acg ttg ctt att gag ctg ctt gca tgg cag ttc gca tca    4819
Leu Ala Arg Thr Leu Leu Ile Glu Leu Leu Ala Trp Gln Phe Ala Ser
        1560                1565                1570

cct gtg cgc tgg atc gag act cag gat ctg ttg atc aag ggc ctt caa    4867
Pro Val Arg Trp Ile Glu Thr Gln Asp Leu Leu Ile Lys Gly Leu Gln
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gct gag cgt ttc gtg gag gtc ggt gtt ggc tct gct cca acg ctt gcc    4915
Ala Glu Arg Phe Val Glu Val Gly Val Gly Ser Ala Pro Thr Leu Ala
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aac atg atg ggc cag acc ctg cgc ctt cct cag tac gcg gac gcc acc    4963
Asn Met Met Gly Gln Thr Leu Arg Leu Pro Gln Tyr Ala Asp Ala Thr
                1610                1615                1620

att gag gtg tta aac att gag cgc gat cgc cca gtt gtg ttc gct acc    5011
Ile Glu Val Leu Asn Ile Glu Arg Asp Arg Pro Val Val Phe Ala Thr
            1625                1630                1635

gat gag gtt gtg cgt gaa gtg gcg gtt gaa gag acc cca gca gct cct    5059
Asp Glu Val Val Arg Glu Val Ala Val Glu Glu Thr Pro Ala Ala Pro
        1640                1645                1650

gca gaa acc act gaa acc cca gca acc cca gca acc cca gcc cct gtt    5107
Ala Glu Thr Thr Glu Thr Pro Ala Thr Pro Ala Thr Pro Ala Pro Val
    1655                1660                1665

gca gct gca gcc cct gcc acc ggc ggc cct cgc cca gat gac atc agc    5155
Ala Ala Ala Ala Pro Ala Thr Gly Gly Pro Arg Pro Asp Asp Ile Ser
1670                1675                1680                1685

ttc act cct tct gat gcc act gaa atg ctc atc gct atc tgg acc aag    5203
Phe Thr Pro Ser Asp Ala Thr Glu Met Leu Ile Ala Ile Trp Thr Lys
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Val Arg Pro Asp Gln Met Gly Ala Thr Asp Ser Ile Glu Thr Leu Val
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gag ggc gtg tcc tct cgc cgt aac cag ctc ctg ctg gat ctt ggt gtg    5299
Glu Gly Val Ser Ser Arg Arg Asn Gln Leu Leu Leu Asp Leu Gly Val
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gag ttc ggc ctc ggc gca att gac gga gca gcc gat gct gag ctc ggt    5347
Glu Phe Gly Leu Gly Ala Ile Asp Gly Ala Ala Asp Ala Glu Leu Gly
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gat cta aag gtc acc gtg tcc aag atg gct aag ggc tac aag gcg ttt    5395
Asp Leu Lys Val Thr Val Ser Lys Met Ala Lys Gly Tyr Lys Ala Phe
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ggc cct gtg ctc tcc gat gct gca gct gat gcc ctg cgt cgc ctc act    5443
Gly Pro Val Leu Ser Asp Ala Ala Ala Asp Ala Leu Arg Arg Leu Thr
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ggt cct acc ggt aag cgc ccg gga tac atc gca gag cgc gtc acc ggc    5491
Gly Pro Thr Gly Lys Arg Pro Gly Tyr Ile Ala Glu Arg Val Thr Gly
            1785                1790                1795

acg tgg gaa ttg ggc cag ggc tgg gct gac cac gtg gtc gct gaa gtt    5539
Thr Trp Glu Leu Gly Gln Gly Trp Ala Asp His Val Val Ala Glu Val
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gtg atc ggc gcc cgc gaa ggc gca tcc ctg cgc ggc ggc gac ctg gcg    5587
Val Ile Gly Ala Arg Glu Gly Ala Ser Leu Arg Gly Gly Asp Leu Ala
    1815                1820                1825
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Ser Leu Ser Pro Ala Ser Pro Ala Ser Ala Ser Asp Leu Asp Ser Leu
1830 1835 1840 1845

atc gac gca gcc gtc cag gcc gta gcc tcc cgc cgc ggc gtt gcg gtc 5683
Ile Asp Ala Ala Val Gln Ala Val Ala Ser Arg Arg Gly Val Ala Val
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Ser Leu Pro Ser Ala Gly Gly Ala Ala Gly Gly Val Val Asp Ser Ala
1865 1870 1875

gct ctt ggc gag ttt gca gag cag gtc acc gga cac gat ggt gtg ctt 5779
Ala Leu Gly Glu Phe Ala Glu Gln Val Thr Gly His Asp Gly Val Leu
1880 1885 1890

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Ala Gln Ala Ala Arg Thr Ile Leu Thr Gln Leu Gly Leu Asp Lys Pro
1895 1900 1905

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Ala Thr Val Ser Val Glu Asp Thr Ala Glu Glu Asp Leu Tyr Glu Leu
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Val Ser Lys Glu Leu Gly Ser Asp Trp Pro Arg Gln Val Ala Pro Ser
1930 1935 1940

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Phe Asp Glu Glu Lys Val Val Leu Leu Asp Asp Arg Trp Ala Ser Ala
1945 1950 1955

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Ala Gln Arg Leu Asp Val Asp Gln Ala Val Ser Ser Ile Gly His Ser
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Gln Gly Val Leu Gly Val His Leu Leu Asn Asp Ala Thr Arg Ala Asp
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Glu Leu Val Ala Ile Ala Gln Leu Ile Gly Ala Ala Ile Thr Arg Thr
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Ala Arg Met Thr Gly Leu Ile Ala Gln Gly Asp Asn Met Pro Met Leu
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Ser Ile Ala Gly Ile Ser Arg Glu Gln Leu Gln Gln Ala Ile Asp Ala
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Ala Cys Ala Glu Val Pro Ala Glu Ile Arg Pro Val Ile Gly Leu Arg
                165                 170                 175

Asn Ser Arg Asp Ser Tyr Val Leu Val Gly Arg Pro Asp Asp Asn Ala
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Arg Val Val Lys Val Ile Glu Ala Met Ala Ala Lys Asp Lys Lys Ala
        195                 200                 205

Ile Glu Asp Lys Leu Arg Gly Gly Ser Ala Phe Ser Pro Arg Ile Thr
    210                 215                 220

Pro Leu Lys Val Gln Ala Ala Phe His His Pro Ala Met Asn Met Ala
225                 230                 235                 240

Val Glu Gln Thr Val Ala Trp Ala Thr Thr Ala Gly Leu Asp Val Glu
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Leu Thr Arg Glu Ile Ala Ala Asp Val Leu Val Asn Pro Val Asp Trp
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Val Ala Arg Val Asn Glu Ala Tyr Glu Ala Gly Ala Arg Trp Phe Leu
        275                 280                 285

Asp Val Gly Pro Asp Gly Gly Ile Val Lys Leu Thr Ala Asn Ile Leu
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Glu Gly Arg Gly Ala Asp Ser Phe Tyr Val Gly Asp Ala Ala Gly Gln
305                 310                 315                 320

Ala Lys Ile Phe Asp Ala Gly Met Ala Pro Glu Leu Pro Val Asp Tyr
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Gln Glu Phe Ala Pro Arg Val Glu His Val Asp Gly Thr Pro Arg Leu
            340                 345                 350

Val Thr Lys Phe Thr Glu Leu Thr Gly Arg Thr Pro Met Met Leu Ala
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Gly Met Thr Pro Thr Thr Val Asp Pro Ala Ile Val Ala Ala Ala Ala
370 375 380

Asn Gly Gly His Trp Ala Glu Leu Ala Gly Gly Gly Gln Val Thr Pro
385 390 395 400

Glu Leu Leu Glu Thr His Ile Ala Gln Leu Thr Asp Met Leu Glu Pro
405 410 415

Gly Ile Asn Ala Gln Phe Asn Ser Met Phe Leu Asp Pro Tyr Leu Trp
420 425 430

Lys Met Gln Ile Gly Gly Lys Arg Leu Val Pro Lys Ala Arg Ala Asn
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Gly Ala Ser Ile Asp Gly Ile Val Ile Thr Ala Gly Ile Pro Glu Lys
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Asp Glu Ala Val Ala Leu Val Lys Glu Leu Met Arg Asp Gly Phe Pro
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Trp Ile Ala Phe Lys Pro Gly Ala Ile Lys Gln Val Asn Ser Val Leu
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Ala Ile Ala Lys Glu Val Pro Glu Leu Pro Ile Ile Ile Gln Ile Glu
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Gly Gly Val Ala Gly Gly His His Ser Trp Glu Asp Leu Asp Glu Leu
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Cys Val Gly Gly Gly Ile Gly Ser Pro Glu Arg Ala Ala Asp Tyr Val
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Thr Gly Ser Trp Ser Thr Ser Tyr Gly Leu Pro Ala Met Pro Val Asp
565 570 575

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Ser Gln Ala Val Lys Glu Leu Leu Val Ser Thr Gln Gly Ser Asp Glu
595 600 605

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690 695 700

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705 710 715 720

Glu Gln Asp His Gly Gln Phe Glu Pro Ser Leu Thr Val Glu Asp Gly
725 730 735

Val Asp Lys Leu Val Ala Ala Tyr Pro His Ala Ala Thr Asp Leu Leu
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Thr Pro Ala Asp Val Ala Trp Phe Leu Gly Leu Cys Arg Thr Pro Gly
755 760 765

Lys Pro Val Asn Phe Val Pro Val Ile Asp Lys Asp Val Arg Arg Trp
770 775 780

Trp Arg Ser Asp Ser Leu Trp Gln Ser His Asp Asp Arg Tyr Thr Ala
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Asp Gln Val Ala Ile Ile Pro Gly Val Val Ala Val Ala Gly Ile Thr
805 810 815

Lys Ala Asn Glu Pro Val Ala Asp Leu Leu Asp Arg Phe Val Asp Ala
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Thr Ile Glu Arg Ile Asp Glu His Asp Ser Arg Ser Arg Asp Ile Met
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Gly Lys Val Leu Ser Ser Pro Gly Thr Phe Trp Ala Gly Arg Asn Ile
850 855 860

Pro Ser Val Ile His Ser Leu Gly His Ala Asp Lys Trp Ser Arg Ser
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Glu Phe Glu Ala Phe His Ser Pro Thr Gly Ala Asn Leu Val Tyr Glu
885 890 895

Asp Ala Glu His Ala Met Leu Thr Val Pro Leu Ala Gly Ser Thr Ala
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Val Pro Ala His Thr Ala Pro Asp Val Leu Val Gly Arg Ala Trp Pro
995 1000 1005

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Ala Ser Val Val Glu Gly Met Leu Ser Leu Val His Leu Glu His His
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Val Ile Ser Gly Asp Arg Asn Pro Ile His Val Ser Asp Val Ala Ala
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Ser Leu Ala Gly Leu Pro Gly Val Ile Val His Gly Met Trp Thr Ser
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Gln Thr Pro Ala Ala Lys Val Val Glu Tyr Thr Ala Thr Met Leu Ala
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Phe His Pro Asp Gly Val Leu Tyr Leu Thr Gln Phe Thr Gln Val Gly
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Glu Ile Val Tyr Arg Arg Gly Leu Thr Met His Arg Leu Val Asp Arg
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Lys Met Gly Leu Thr Ala Asp Asn Val Phe Asp Tyr Val Ala Ser Val
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Gly Leu Gln Tyr Ala Val Ala Gly Thr Gln Ala Gly Leu Ala Ala Leu
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Arg Ala Asp Val Glu Asn Arg Ala Pro Gly Gln Arg Ala Phe Ile Leu
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Ile Pro Gly Ile Asp Val Pro Phe His Ser Ser Lys Leu Arg Asp Gly
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Val Gly Ala Phe Arg Glu His Leu Asp Ser Leu Ile Pro Ala Glu Leu
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Asp Leu Asp Val Leu Val Gly Arg Tyr Ile Pro Asn Leu Val Ala Arg
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Glu Ser Thr Tyr Val Asn Glu Ile Leu Ala Asp Phe Lys Ala Ala Ser
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1555 1560 1565

Trp Gln Phe Ala Ser Pro Val Arg Trp Ile Glu Thr Gln Asp Leu Leu
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Ile Lys Gly Leu Gln Ala Glu Arg Phe Val Glu Val Gly Val Gly Ser
1585 1590 1595 1600

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1810 1815 1820

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1825 1830 1835 1840

Asp Leu Asp Ser Leu Ile Asp Ala Ala Val Gln Ala Val Ala Ser Arg
1845 1850 1855

Arg Gly Val Ala Val Ser Leu Pro Ser Ala Gly Gly Ala Ala Gly Gly
1860 1865 1870

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1875 1880 1885

His Asp Gly Val Leu Ala Gln Ala Ala Arg Thr Ile Leu Thr Gln Leu
1890 1895 1900

Gly Leu Asp Lys Pro Ala Thr Val Ser Val Glu Asp Thr Ala Glu Glu
1905 1910 1915 1920

Asp Leu Tyr Glu Leu Val Ser Lys Glu Leu Gly Ser Asp Trp Pro Arg
1925 1930 1935

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Ser Tyr Val Leu Val Gly Arg Pro Asp Asp Asn Ala Arg Val Val Lys
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Val Ile Glu Ala Met Ala Ala Lys Asp Lys Lys Ala Ile Glu Asp Lys
230                 235                 240                 245

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Leu Arg Gly Gly Ser Ala Phe Ser Pro Arg Ile Thr Pro Leu Lys Val
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Gln Ala Ala Phe His His Pro Ala Met Asn Met Ala Val Glu Gln Thr
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gtg gcg tgg gca acc act gct ggt ttg gat gtg gaa ctc acc cgc gag     979
Val Ala Trp Ala Thr Thr Ala Gly Leu Asp Val Glu Leu Thr Arg Glu
        280                 285                 290

atc gcc gct gat gtt ttg gtt aac cct gtc gat tgg gta gca cgc gtc     1027
Ile Ala Ala Asp Val Leu Val Asn Pro Val Asp Trp Val Ala Arg Val
    295                 300                 305

aac gaa gcg tat gag gct ggc gct cgc tgg ttc ctc gac gtt gga cca     1075
Asn Glu Ala Tyr Glu Ala Gly Ala Arg Trp Phe Leu Asp Val Gly Pro
310                 315                 320                 325

gat ggt ggc atc gtt aag ctg act gcc aac atc ctt gag ggc cgc ggc     1123
Asp Gly Gly Ile Val Lys Leu Thr Ala Asn Ile Leu Glu Gly Arg Gly
                330                 335                 340

gcg gat tcc ttc tat gtt ggt gac gcc gca ggc cag gcc aag ata ttt     1171
Ala Asp Ser Phe Tyr Val Gly Asp Ala Ala Gly Gln Ala Lys Ile Phe
            345                 350                 355

gat gct ggc atg gca cct gaa ctt cca gtg gat tac cag gag ttc gca     1219
Asp Ala Gly Met Ala Pro Glu Leu Pro Val Asp Tyr Gln Glu Phe Ala
        360                 365                 370

cca cgc gtt gag cac gtt gat gga acc cca cgc ctg gtt acc aag ttc     1267
Pro Arg Val Glu His Val Asp Gly Thr Pro Arg Leu Val Thr Lys Phe
    375                 380                 385

act gag ctg acc ggc cgc acc cca atg atg ctg gct ggc atg acc cca     1315
Thr Glu Leu Thr Gly Arg Thr Pro Met Met Leu Ala Gly Met Thr Pro
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390                 395                      400                      405

acc acc gtt gac cct gcc att gtt gca gcc gct gca aac ggt gga cac     1363
Thr Thr Val Asp Pro Ala Ile Val Ala Ala Ala Ala Asn Gly Gly His
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tgg gct gag ctc gct ggt ggc gga cag gtt acc cca gag ctg ctg gaa     1411
Trp Ala Glu Leu Ala Gly Gly Gly Gln Val Thr Pro Glu Leu Leu Glu
            425                      430                      435

acc cac atc gca cag ctc acc gac atg ctt gag cca ggt atc aac gcc     1459
Thr His Ile Ala Gln Leu Thr Asp Met Leu Glu Pro Gly Ile Asn Ala
        440                      445                      450

cag ttc aac tcc atg ttc ttg gat cca tac ctg tgg aag atg cag att     1507
Gln Phe Asn Ser Met Phe Leu Asp Pro Tyr Leu Trp Lys Met Gln Ile
    455                      460                      465

ggt ggc aag cgc ctt gtt cct aag gcc cgc gct aat ggt gca tcc atc     1555
Gly Gly Lys Arg Leu Val Pro Lys Ala Arg Ala Asn Gly Ala Ser Ile
470                 475                      480                      485

gac ggc atc gtc atc acc gcc ggc att cct gaa aag gat gaa gct gtt     1603
Asp Gly Ile Val Ile Thr Ala Gly Ile Pro Glu Lys Asp Glu Ala Val
                490                      495                      500

gca ttg gtc aag gaa ctg atg cgt gat ggt ttc cct tgg atc gca ttc     1651
Ala Leu Val Lys Glu Leu Met Arg Asp Gly Phe Pro Trp Ile Ala Phe
            505                      510                      515

aag cca ggt gcc atc aag cag gtt aac tct gtg ttg gct atc gct aag     1699
Lys Pro Gly Ala Ile Lys Gln Val Asn Ser Val Leu Ala Ile Ala Lys
        520                      525                      530

gaa gtt cca gaa ctc ccc atc atc att cag att gag ggt ggc gtt gca     1747
Glu Val Pro Glu Leu Pro Ile Ile Ile Gln Ile Glu Gly Gly Val Ala
    535                      540                      545

ggt gga cac cac tct tgg gaa gac ctc gat gag ctg ctg atc gcc acc     1795
Gly Gly His His Ser Trp Glu Asp Leu Asp Glu Leu Leu Ile Ala Thr
550                 555                      560                      565

tac ggc aag gtc cgc gca ctg gat aac gtg gtg ctg tgt gtc ggc ggt     1843
Tyr Gly Lys Val Arg Ala Leu Asp Asn Val Val Leu Cys Val Gly Gly
                570                      575                      580

ggc att ggc tca cct gag cgc gct gct gat tac gtc acc ggt tcc tgg     1891
Gly Ile Gly Ser Pro Glu Arg Ala Ala Asp Tyr Val Thr Gly Ser Trp
            585                      590                      595

tcc act tcc tac ggc ctg cca gct atg cct gtt gat ggc atc ttg gtg     1939
Ser Thr Ser Tyr Gly Leu Pro Ala Met Pro Val Asp Gly Ile Leu Val
        600                      605                      610

ggt acc gct gcg atg gca acc aag gaa gca acc acc tcc cag gcc gtc     1987
Gly Thr Ala Ala Met Ala Thr Lys Glu Ala Thr Thr Ser Gln Ala Val
    615                      620                      625

aag gaa ctt ctt gtt tcc acc cag ggc tct gat gaa tgg gtt cct gct     2035
Lys Glu Leu Leu Val Ser Thr Gln Gly Ser Asp Glu Trp Val Pro Ala
630                 635                      640                      645
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Gly Gly Ala Lys Asn Gly Met Ala Tyr Gly Arg Ser Gln Leu Gly Ala
650 655 660

gac atc cac gag atc gac aac tcc ttt gct aag gct gga cgc ctt ctt 2131
Asp Ile His Glu Ile Asp Asn Ser Phe Ala Lys Ala Gly Arg Leu Leu
665 670 675

gat gag gtt gca ggc cat gaa acg gat ttg caa gcg cgc ccg gat gag 2179
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35 40 45

Val Ser Asp Ile Val Glu Arg Ala Asn Ala Leu Leu Ala Leu Val Ala
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Asp Asp Leu Ile Gly Thr Leu Pro Phe Gly Phe Asp Pro Val Ala Trp
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Ala Asn Asn Ser Glu Asp Pro Ala Phe Asp Thr Ala Gln Ser Ala Val
85 90 95

Ser Val Pro Gly Ile Phe Val Ser Gln Ile Ala Thr Leu Asp Ser Leu
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Glu Ala Gln Arg Leu Asp Val Asp Gln Ala Val Ser Ser Ile Gly His
115 120 125

Ser Gln Gly Val Leu Gly Val His Leu Leu Asn Asp Ala Thr Arg Ala
130 135 140

Asp Glu Leu Val Ala Ile Ala Gln Leu Ile Gly Ala Ala Ile Thr Arg
145 150 155 160

Thr Ala Arg Met Thr Gly Leu Ile Ala Gln Gly Asp Asn Met Pro Met
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Leu Ser Ile Ala Gly Ile Ser Arg Glu Gln Leu Gln Gln Ala Ile Asp
180 185 190

Ala Ala Cys Ala Glu Val Pro Ala Glu Ile Arg Pro Val Ile Gly Leu

195 200 205

Arg Asn Ser Arg Asp Ser Tyr Val Leu Val Gly Arg Pro Asp Asp Asn
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Ala Arg Val Val Lys Val Ile Glu Ala Met Ala Ala Lys Asp Lys Lys
225 230 235 240

Ala Ile Glu Asp Lys Leu Arg Gly Gly Ser Ala Phe Ser Pro Arg Ile
245 250 255

Thr Pro Leu Lys Val Gln Ala Ala Phe His His Pro Ala Met Asn Met
260 265 270

Ala Val Glu Gln Thr Val Ala Trp Ala Thr Thr Ala Gly Leu Asp Val
275 280 285

Glu Leu Thr Arg Glu Ile Ala Ala Asp Val Leu Val Asn Pro Val Asp
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Trp Val Ala Arg Val Asn Glu Ala Tyr Glu Ala Gly Ala Arg Trp Phe
305 310 315 320

Leu Asp Val Gly Pro Asp Gly Gly Ile Val Lys Leu Thr Ala Asn Ile
325 330 335

Leu Glu Gly Arg Gly Ala Asp Ser Phe Tyr Val Gly Asp Ala Ala Gly
340 345 350

Gln Ala Lys Ile Phe Asp Ala Gly Met Ala Pro Glu Leu Pro Val Asp
355 360 365

Tyr Gln Glu Phe Ala Pro Arg Val Glu His Val Asp Gly Thr Pro Arg
370 375 380

Leu Val Thr Lys Phe Thr Glu Leu Thr Gly Arg Thr Pro Met Met Leu
385 390 395 400

Ala Gly Met Thr Pro Thr Thr Val Asp Pro Ala Ile Val Ala Ala Ala
405 410 415

Ala Asn Gly Gly His Trp Ala Glu Leu Ala Gly Gly Gly Gln Val Thr
420 425 430

Pro Glu Leu Leu Glu Thr His Ile Ala Gln Leu Thr Asp Met Leu Glu
435 440 445

Pro Gly Ile Asn Ala Gln Phe Asn Ser Met Phe Leu Asp Pro Tyr Leu
450 455 460

Trp Lys Met Gln Ile Gly Gly Lys Arg Leu Val Pro Lys Ala Arg Ala
465 470 475 480

Asn Gly Ala Ser Ile Asp Gly Ile Val Ile Thr Ala Gly Ile Pro Glu
485 490 495

Lys Asp Glu Ala Val Ala Leu Val Lys Glu Leu Met Arg Asp Gly Phe
500 505 510

Pro Trp Ile Ala Phe Lys Pro Gly Ala Ile Lys Gln Val Asn Ser Val
515 520 525

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Leu Ala Ile Ala Lys Glu Val Pro Glu Leu Pro Ile Ile Ile Gln Ile
    530                 535                 540

Glu Gly Gly Val Ala Gly Gly His His Ser Trp Glu Asp Leu Asp Glu
545                 550                 555                 560

Leu Leu Ile Ala Thr Tyr Gly Lys Val Arg Ala Leu Asp Asn Val Val
                565                 570                 575

Leu Cys Val Gly Gly Gly Ile Gly Ser Pro Glu Arg Ala Ala Asp Tyr
            580                 585                 590

Val Thr Gly Ser Trp Ser Thr Ser Tyr Gly Leu Pro Ala Met Pro Val
        595                 600                 605

Asp Gly Ile Leu Val Gly Thr Ala Ala Met Ala Thr Lys Glu Ala Thr
    610                 615                 620

Thr Ser Gln Ala Val Lys Glu Leu Leu Val Ser Thr Gln Gly Ser Asp
625                 630                 635                 640

Glu Trp Val Pro Ala Gly Gly Ala Lys Asn Gly Met Ala Tyr Gly Arg
                645                 650                 655

Ser Gln Leu Gly Ala Asp Ile His Glu Ile Asp Asn Ser Phe Ala Lys
            660                 665                 670

Ala Gly Arg Leu Leu Asp Glu Val Ala Gly His Glu Thr Asp Leu Gln
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Ala Arg Pro Asp Glu Ile Ile
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Gln Trp Leu Asn Arg Tyr Leu Glu Leu Ser Gly Pro Val Asp Gly Gln
  1               5                  10                  15

tgg att gat gct tcc tgg gct gca cgt ttt gcc cag atg ctg gag cgt      96
Trp Ile Asp Ala Ser Trp Ala Ala Arg Phe Ala Gln Met Leu Glu Arg
             20                  25                  30

gcc gag gcg cgt ttg atc gag cag gat cat ggc caa ttt gag cca agc     144
Ala Glu Ala Arg Leu Ile Glu Gln Asp His Gly Gln Phe Glu Pro Ser
         35                  40                  45

ctg acg gtg gag gat ggc gtc gac aag ctt gtt gct gct tac ccg cat     192
Leu Thr Val Glu Asp Gly Val Asp Lys Leu Val Ala Ala Tyr Pro His
     50                  55                  60
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gcc gca acc gac ctg ctc acc ccg gct gat gtc gcc tgg ttc ttg ggc     240
Ala Ala Thr Asp Leu Leu Thr Pro Ala Asp Val Ala Trp Phe Leu Gly
 65                  70                  75                  80

ctg tgc cgc acg ccg ggc aag cct gtg aac ttt gtg ccc gtc att gat     288
Leu Cys Arg Thr Pro Gly Lys Pro Val Asn Phe Val Pro Val Ile Asp
                 85                  90                  95

aag gac gtg cgt cgc tgg tgg cgc tcg gac tcc ctg tgg cag tcc cac     336
Lys Asp Val Arg Arg Trp Trp Arg Ser Asp Ser Leu Trp Gln Ser His
            100                 105                 110

gat gat cgc tac acc gct gat cag gtg gct att atc cct ggt gtc gtc     384
Asp Asp Arg Tyr Thr Ala Asp Gln Val Ala Ile Ile Pro Gly Val Val
        115                 120                 125

gcc gtt gct ggc atc acc aag gcc aac gaa cct gtc gct gac ctg ctt     432
Ala Val Ala Gly Ile Thr Lys Ala Asn Glu Pro Val Ala Asp Leu Leu
    130                 135                 140

gat cgc ttt gtc gac gcc acc atc gag cgc atc gat gag cac gat tcc     480
Asp Arg Phe Val Asp Ala Thr Ile Glu Arg Ile Asp Glu His Asp Ser
145                 150                 155                 160

cgc tcc cgc gac atc atg ggc aaa gtg ctt tcc tca cct ggc aca ttc     528
Arg Ser Arg Asp Ile Met Gly Lys Val Leu Ser Ser Pro Gly Thr Phe
                165                 170                 175

tgg gct ggc cgc aac atc cca tcg gtg atc cac agc ctt ggg cat gct     576
Trp Ala Gly Arg Asn Ile Pro Ser Val Ile His Ser Leu Gly His Ala
            180                 185                 190

gac aag tgg tcc cgc tcc gaa ttc gaa gca ttc cat agc cca acc ggc     624
Asp Lys Trp Ser Arg Ser Glu Phe Glu Ala Phe His Ser Pro Thr Gly
        195                 200                 205

gcc aac ttg gtg tac gaa gac gcc gag cac gcg atg ctg act gtg cct     672
Ala Asn Leu Val Tyr Glu Asp Ala Glu His Ala Met Leu Thr Val Pro
    210                 215                 220

ttg gcg ggt tcc acc gca ttc ggc acc acc gct gag ctg aaa atc cgt     720
Leu Ala Gly Ser Thr Ala Phe Gly Thr Thr Ala Glu Leu Lys Ile Arg
225                 230                 235                 240

ttc acc agc ccc atc gac gct ctg cca agc gct gtc cca ctg gtc acc     768
Phe Thr Ser Pro Ile Asp Ala Leu Pro Ser Ala Val Pro Leu Val Thr
                245                 250                 255

cag gaa gac gct gaa gcc gcg atg ggt gaa ctg acc cgc atc gca gct     816
Gln Glu Asp Ala Glu Ala Ala Met Gly Glu Leu Thr Arg Ile Ala Ala
            260                 265                 270

ggc ggc acc ctg gca act gtg aac aat ggc acc gct acc tgg gaa acc     864
Gly Gly Thr Leu Ala Thr Val Asn Asn Gly Thr Ala Thr Trp Glu Thr
        275                 280                 285

tcc gtc gat gcc ggc gtc atc gct gac tac aac aac gtc acc gca ggc     912
Ser Val Asp Ala Gly Val Ile Ala Asp Tyr Asn Asn Val Thr Ala Gly
    290                 295                 300
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tac ctg cca gca tcc gtt gtt cct gca cac acc gca cct gac gtg ctg    960
Tyr Leu Pro Ala Ser Val Val Pro Ala His Thr Ala Pro Asp Val Leu
305                 310                 315                 320

gtt ggc cgc gca tgg cca gca gtt ttc gct gcc gta aag tcc gca gtc    1008
Val Gly Arg Ala Trp Pro Ala Val Phe Ala Ala Val Lys Ser Ala Val
                325                 330                 335

atc cca ggc acc gat tcc gca tcc gtt gtg gaa ggc atg ctg tcc ctg    1056
Ile Pro Gly Thr Asp Ser Ala Ser Val Val Glu Gly Met Leu Ser Leu
            340                 345                 350

gtt cac ctg gag cac cac att gtg ctc aag tcc gat gtc cca acc gac    1104
Val His Leu Glu His His Ile Val Leu Lys Ser Asp Val Pro Thr Asp
        355                 360                 365

ggc gcg ctg aag gtt tcc gcg act gcc gat gag gta gtc gat acc gac    1152
Gly Ala Leu Lys Val Ser Ala Thr Ala Asp Glu Val Val Asp Thr Asp
    370                 375                 380

ctg ggt cgc ctc gtg atc gtg cgc gca gaa atc gcc gac gca gaa ggc    1200
Leu Gly Arg Leu Val Ile Val Arg Ala Glu Ile Ala Asp Ala Glu Gly
385                 390                 395                 400

aac ctg att gct acg ttg gct gag cgt ttc gcg atc cgc gga cgc aag    1248
Asn Leu Ile Ala Thr Leu Ala Glu Arg Phe Ala Ile Arg Gly Arg Lys
                405                 410                 415

ggc aac gct gtc gca cgc acc aac acc tcc gca ctg cca acc acc gtg    1296
Gly Asn Ala Val Ala Arg Thr Asn Thr Ser Ala Leu Pro Thr Thr Val
            420                 425                 430

gac acc cca cgc tca gct cgc gca gtg gca acc gtt gtt gca cct gaa    1344
Asp Thr Pro Arg Ser Ala Arg Ala Val Ala Thr Val Val Ala Pro Glu
        435                 440                 445

tcc atg cgc cca ttc gct gtg atc tcc ggt gac cgc aac cca att cac    1392
Ser Met Arg Pro Phe Ala Val Ile Ser Gly Asp Arg Asn Pro Ile His
    450                 455                 460

gtc tct gat gtt gcg gct tcc ctg gct ggt ctg cca ggt gtg atc gtg    1440
Val Ser Asp Val Ala Ala Ser Leu Ala Gly Leu Pro Gly Val Ile Val
465                 470                 475                 480

cac ggc atg tgg acc tct gcc atc ggt gaa ctg atc gcc ggt gca gca    1488
His Gly Met Trp Thr Ser Ala Ile Gly Glu Leu Ile Ala Gly Ala Ala
                485                 490                 495

ttc aac gat gag cag atc caa act ccc gca gcc aag gtc gtg gaa tac    1536
Phe Asn Asp Glu Gln Ile Gln Thr Pro Ala Ala Lys Val Val Glu Tyr
            500                 505                 510

acc gca acc atg ctg gca cca gtt ctt cca ggt gaa gaa att gag ttc    1584
Thr Ala Thr Met Leu Ala Pro Val Leu Pro Gly Glu Glu Ile Glu Phe
        515                 520                 525

agc gtt gag cgc tcc gca gtg gac aac cgc cca gga atg gga gag gtc    1632
Ser Val Glu Arg Ser Ala Val Asp Asn Arg Pro Gly Met Gly Glu Val
    530                 535                 540

cgc acc gtt acc gca acc gtc aac ggc aac tta gtg ctt acc gcc acc    1680
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Arg Thr Val Thr Ala Thr Val Asn Gly Asn Leu Val Leu Thr Ala Thr
545                 550                 555                 560

gct gtt gtg gca gct cca tct act ttc tac gca ttc cca ggc cag ggc    1728
Ala Val Val Ala Ala Pro Ser Thr Phe Tyr Ala Phe Pro Gly Gln Gly
                565                 570                 575

att cag tcc cag ggc atg ggt atg gaa gca cgc cgt aac tct cag gca    1776
Ile Gln Ser Gln Gly Met Gly Met Glu Ala Arg Arg Asn Ser Gln Ala
            580                 585                 590

gct cgc gct atc tgg gac cgc gcc gat gca cac acc cgc aat aag ctg    1824
Ala Arg Ala Ile Trp Asp Arg Ala Asp Ala His Thr Arg Asn Lys Leu
        595                 600                 605

ggc ttc tcc atc gtg gaa atc gtg gaa aac aac cca cgc gaa gta acc    1872
Gly Phe Ser Ile Val Glu Ile Val Glu Asn Asn Pro Arg Glu Val Thr
    610                 615                 620

gtg gca ggg gag aag ttc ttc cac cca gac ggc gtt ttg tac ctc acc    1920
Val Ala Gly Glu Lys Phe Phe His Pro Asp Gly Val Leu Tyr Leu Thr
625                 630                 635                 640

cag ttc acc cag gtg ggc atg gca act ctg ggc gtt gct cag atc gct    1968
Gln Phe Thr Gln Val Gly Met Ala Thr Leu Gly Val Ala Gln Ile Ala
                645                 650                 655

gaa atg cgt gaa gca cat gcc ttg aac cag cgt gca tac ttt gct gga    2016
Glu Met Arg Glu Ala His Ala Leu Asn Gln Arg Ala Tyr Phe Ala Gly
            660                 665                 670

cac tcc gtt ggt gag tac aac gcg ctt gct gca tat gct ggt gtg ctg    2064
His Ser Val Gly Glu Tyr Asn Ala Leu Ala Ala Tyr Ala Gly Val Leu
        675                 680                 685

tcc ctg gaa tcc gtt ctg gag atc gtt tac cgt cgt ggc ttg acc atg    2112
Ser Leu Glu Ser Val Leu Glu Ile Val Tyr Arg Arg Gly Leu Thr Met
    690                 695                 700

cac cgc ttg gtg gat cgc gat gaa aac ggt ctg tcc aac tac gcg ctc    2160
His Arg Leu Val Asp Arg Asp Glu Asn Gly Leu Ser Asn Tyr Ala Leu
705                 710                 715                 720

gca gct ctt cgc ccc aac aag atg ggt ctg acc gca gac aac gtt ttc    2208
Ala Ala Leu Arg Pro Asn Lys Met Gly Leu Thr Ala Asp Asn Val Phe
                725                 730                 735

gat tac gtt gcg tct gtt tcc gaa gct tcc ggt gaa ttc ctg gag atc    2256
Asp Tyr Val Ala Ser Val Ser Glu Ala Ser Gly Glu Phe Leu Glu Ile
            740                 745                 750

gtt aac tac aac ttg gct ggc ctg cag tac gca gtt gct gga acc cag    2304
Val Asn Tyr Asn Leu Ala Gly Leu Gln Tyr Ala Val Ala Gly Thr Gln
        755                 760                 765

gct ggt ctt gcc gcc ctt cgt gcc gat gtt gag aac cgt gca cca ggt    2352
Ala Gly Leu Ala Ala Leu Arg Ala Asp Val Glu Asn Arg Ala Pro Gly
    770                 775                 780

cag cgt gcc ttc att ttg atc cct ggc att gac gtg cca ttc cac tcc    2400
Gln Arg Ala Phe Ile Leu Ile Pro Gly Ile Asp Val Pro Phe His Ser
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785                 790                 795                 800

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Ser Lys Leu Arg Asp Gly Val Gly Ala Phe Arg Glu His Leu Asp Ser
                805                 810                 815

ctg atc cca gct gag ctg gat ctg gat gtg ctg gtt ggc cgc tac att      2496
Leu Ile Pro Ala Glu Leu Asp Leu Asp Val Leu Val Gly Arg Tyr Ile
            820                 825                 830

cca aac ttg gtg gct cgc cca ttc gaa ctc act gaa gag ttc gtg gca      2544
Pro Asn Leu Val Ala Arg Pro Phe Glu Leu Thr Glu Glu Phe Val Ala
        835                 840                 845

tcc atg gca gaa gtg gtg gag tcc acc tat gtc aat gag atc ttg gct      2592
Ser Met Ala Glu Val Val Glu Ser Thr Tyr Val Asn Glu Ile Leu Ala
    850                 855                 860

gat ttc aag gct gct tcc gcc gat aag cag aag ctt gcc cgc acg ttg      2640
Asp Phe Lys Ala Ala Ser Ala Asp Lys Gln Lys Leu Ala Arg Thr Leu
865                 870                 875                 880

ctt att gag ctg ctt gca tgg cag ttc gca tca cct gtg cgc tgg atc      2688
Leu Ile Glu Leu Leu Ala Trp Gln Phe Ala Ser Pro Val Arg Trp Ile
                885                 890                 895

gag act cag gat ctg ttg atc aag ggc ctt caa gct gag cgt ttc gtg      2736
Glu Thr Gln Asp Leu Leu Ile Lys Gly Leu Gln Ala Glu Arg Phe Val
            900                 905                 910

gag gtc ggt gtt ggc tct gct cca acg ctt gcc aac atg atg ggc cag      2784
Glu Val Gly Val Gly Ser Ala Pro Thr Leu Ala Asn Met Met Gly Gln
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acc ctg cgc ctt cct cag tac gcg gac gcc acc att gag gtg tta aac      2832
Thr Leu Arg Leu Pro Gln Tyr Ala Asp Ala Thr Ile Glu Val Leu Asn
    930                 935                 940

att gag cgc gat cgc cca gtt gtg ttc gct acc gat gag gtt gtg cgt      2880
Ile Glu Arg Asp Arg Pro Val Val Phe Ala Thr Asp Glu Val Val Arg
945                 950                 955                 960

gaa gtg gcg gtt gaa gag acc cca gca gct cct gca gaa acc act gaa      2928
Glu Val Ala Val Glu Glu Thr Pro Ala Ala Pro Ala Glu Thr Thr Glu
                965                 970                 975

acc cca gca acc cca gca acc cca gcc cct gtt gca gct gca gcc cct      2976
Thr Pro Ala Thr Pro Ala Thr Pro Ala Pro Val Ala Ala Ala Ala Pro
            980                 985                 990

gcc acc ggc ggc cct cgc cca gat gac atc agc ttc act cct tct gat      3024
Ala Thr Gly Gly Pro Arg Pro Asp Asp Ile Ser Phe Thr Pro Ser Asp
        995                 1000                1005

gcc act gaa atg ctc atc gct atc tgg acc aag gtt cgc cca gat cag      3072
Ala Thr Glu Met Leu Ile Ala Ile Trp Thr Lys Val Arg Pro Asp Gln
    1010                1015                1020

atg ggt gcc act gat tcc atc gag acc ctg gtt gag ggc gtg tcc tct      3120
Met Gly Ala Thr Asp Ser Ile Glu Thr Leu Val Glu Gly Val Ser Ser
1025                1030                1035                1040
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gca att gac gga gca gcc gat gct gag ctc ggt gat cta aag gtc acc 3216
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Val Ser Lys Met Ala Lys Gly Tyr Lys Ala Phe Gly Pro Val Leu Ser
1075 1080 1085

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1105 1110 1115 1120

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Ser Pro Ala Ser Ala Ser Asp Leu Asp Ser Leu Ile Asp Ala Ala Val
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cag gcc gta gcc tcc cgc cgc ggc gtt gcg gtc tcc ctg cct tca gca 3552
Gln Ala Val Ala Ser Arg Arg Gly Val Ala Val Ser Leu Pro Ser Ala
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Gly Gly Ala Ala Gly Gly Val Val Asp Ser Ala Ala Leu Gly Glu Phe
1185 1190 1195 1200

gca gag cag gtc acc gga cac gat ggt gtg ctt gct cag gca gcc cgc 3648
Ala Glu Gln Val Thr Gly His Asp Gly Val Leu Ala Gln Ala Ala Arg
1205 1210 1215

acc atc ttg acc cag ttg ggt ctt gat aag cca gca acc gtt tcc gtg 3696
Thr Ile Leu Thr Gln Leu Gly Leu Asp Lys Pro Ala Thr Val Ser Val
1220 1225 1230

gaa gac acc gca gag gaa gac ctc tac gag ttg gtc tcc aag gaa ctc 3744
Glu Asp Thr Ala Glu Glu Asp Leu Tyr Glu Leu Val Ser Lys Glu Leu
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Gly Ser Asp Trp Pro Arg Gln Val Ala Pro Ser Phe Asp Glu Glu Lys
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Trp Ile Asp Ala Ser Trp Ala Ala Arg Phe Ala Gln Met Leu Glu Arg
            20   25   30

Ala Glu Ala Arg Leu Ile Glu Gln Asp His Gly Gln Phe Glu Pro Ser
        35   40   45

Leu Thr Val Glu Asp Gly Val Asp Lys Leu Val Ala Ala Tyr Pro His
    50   55   60

Ala Ala Thr Asp Leu Leu Thr Pro Ala Asp Val Ala Trp Phe Leu Gly
65   70   75   80

Leu Cys Arg Thr Pro Gly Lys Pro Val Asn Phe Val Pro Val Ile Asp
                85   90   95

Lys Asp Val Arg Arg Trp Trp Arg Ser Asp Ser Leu Trp Gln Ser His
            100   105   110

Asp Asp Arg Tyr Thr Ala Asp Gln Val Ala Ile Ile Pro Gly Val Val
        115   120   125

Ala Val Ala Gly Ile Thr Lys Ala Asn Glu Pro Val Ala Asp Leu Leu
    130   135   140

Asp Arg Phe Val Asp Ala Thr Ile Glu Arg Ile Asp Glu His Asp Ser
145   150   155   160

Arg Ser Arg Asp Ile Met Gly Lys Val Leu Ser Ser Pro Gly Thr Phe
                165   170   175

Trp Ala Gly Arg Asn Ile Pro Ser Val Ile His Ser Leu Gly His Ala
            180   185   190

Asp Lys Trp Ser Arg Ser Glu Phe Glu Ala Phe His Ser Pro Thr Gly
        195   200   205

Ala Asn Leu Val Tyr Glu Asp Ala Glu His Ala Met Leu Thr Val Pro
    210   215   220

Leu Ala Gly Ser Thr Ala Phe Gly Thr Thr Ala Glu Leu Lys Ile Arg
225   230   235   240

Phe Thr Ser Pro Ile Asp Ala Leu Pro Ser Ala Val Pro Leu Val Thr
                245   250   255

Gln Glu Asp Ala Glu Ala Ala Met Gly Glu Leu Thr Arg Ile Ala Ala
            260   265   270

Gly Gly Thr Leu Ala Thr Val Asn Asn Gly Thr Ala Thr Trp Glu Thr
        275   280   285

Ser Val Asp Ala Gly Val Ile Ala Asp Tyr Asn Asn Val Thr Ala Gly
290 295 300

Tyr Leu Pro Ala Ser Val Val Pro Ala His Thr Ala Pro Asp Val Leu
305 310 315 320

Val Gly Arg Ala Trp Pro Ala Val Phe Ala Ala Val Lys Ser Ala Val
325 330 335

Ile Pro Gly Thr Asp Ser Ala Ser Val Val Glu Gly Met Leu Ser Leu
340 345 350

Val His Leu Glu His His Ile Val Leu Lys Ser Asp Val Pro Thr Asp
355 360 365

Gly Ala Leu Lys Val Ser Ala Thr Ala Asp Glu Val Val Asp Thr Asp
370 375 380

Leu Gly Arg Leu Val Ile Val Arg Ala Glu Ile Ala Asp Ala Glu Gly
385 390 395 400

Asn Leu Ile Ala Thr Leu Ala Glu Arg Phe Ala Ile Arg Gly Arg Lys
405 410 415

Gly Asn Ala Val Ala Arg Thr Asn Thr Ser Ala Leu Pro Thr Thr Val
420 425 430

Asp Thr Pro Arg Ser Ala Arg Ala Val Ala Thr Val Val Ala Pro Glu
435 440 445

Ser Met Arg Pro Phe Ala Val Ile Ser Gly Asp Arg Asn Pro Ile His
450 455 460

Val Ser Asp Val Ala Ala Ser Leu Ala Gly Leu Pro Gly Val Ile Val
465 470 475 480

His Gly Met Trp Thr Ser Ala Ile Gly Glu Leu Ile Ala Gly Ala Ala
485 490 495

Phe Asn Asp Glu Gln Ile Gln Thr Pro Ala Ala Lys Val Val Glu Tyr
500 505 510

Thr Ala Thr Met Leu Ala Pro Val Leu Pro Gly Glu Glu Ile Glu Phe
515 520 525

Ser Val Glu Arg Ser Ala Val Asp Asn Arg Pro Gly Met Gly Glu Val
530 535 540

Arg Thr Val Thr Ala Thr Val Asn Gly Asn Leu Val Leu Thr Ala Thr
545 550 555 560

Ala Val Val Ala Ala Pro Ser Thr Phe Tyr Ala Phe Pro Gly Gln Gly
565 570 575

Ile Gln Ser Gln Gly Met Gly Met Glu Ala Arg Arg Asn Ser Gln Ala
580 585 590

Ala Arg Ala Ile Trp Asp Arg Ala Asp Ala His Thr Arg Asn Lys Leu
595 600 605

Gly Phe Ser Ile Val Glu Ile Val Glu Asn Asn Pro Arg Glu Val Thr

610 615 620

Val Ala Gly Glu Lys Phe Phe His Pro Asp Gly Val Leu Tyr Leu Thr
625 630 635 640

Gln Phe Thr Gln Val Gly Met Ala Thr Leu Gly Val Ala Gln Ile Ala
645 650 655

Glu Met Arg Glu Ala His Ala Leu Asn Gln Arg Ala Tyr Phe Ala Gly
660 665 670

His Ser Val Gly Glu Tyr Asn Ala Leu Ala Ala Tyr Ala Gly Val Leu
675 680 685

Ser Leu Glu Ser Val Leu Glu Ile Val Tyr Arg Arg Gly Leu Thr Met
690 695 700

His Arg Leu Val Asp Arg Asp Glu Asn Gly Leu Ser Asn Tyr Ala Leu
705 710 715 720

Ala Ala Leu Arg Pro Asn Lys Met Gly Leu Thr Ala Asp Asn Val Phe
725 730 735

Asp Tyr Val Ala Ser Val Ser Glu Ala Ser Gly Glu Phe Leu Glu Ile
740 745 750

Val Asn Tyr Asn Leu Ala Gly Leu Gln Tyr Ala Val Ala Gly Thr Gln
755 760 765

Ala Gly Leu Ala Ala Leu Arg Ala Asp Val Glu Asn Arg Ala Pro Gly
770 775 780

Gln Arg Ala Phe Ile Leu Ile Pro Gly Ile Asp Val Pro Phe His Ser
785 790 795 800

Ser Lys Leu Arg Asp Gly Val Gly Ala Phe Arg Glu His Leu Asp Ser
805 810 815

Leu Ile Pro Ala Glu Leu Asp Leu Asp Val Leu Val Gly Arg Tyr Ile
820 825 830

Pro Asn Leu Val Ala Arg Pro Phe Glu Leu Thr Glu Glu Phe Val Ala
835 840 845

Ser Met Ala Glu Val Val Glu Ser Thr Tyr Val Asn Glu Ile Leu Ala
850 855 860

Asp Phe Lys Ala Ala Ser Ala Asp Lys Gln Lys Leu Ala Arg Thr Leu
865 870 875 880

Leu Ile Glu Leu Leu Ala Trp Gln Phe Ala Ser Pro Val Arg Trp Ile
885 890 895

Glu Thr Gln Asp Leu Leu Ile Lys Gly Leu Gln Ala Glu Arg Phe Val
900 905 910

Glu Val Gly Val Gly Ser Ala Pro Thr Leu Ala Asn Met Met Gly Gln
915 920 925

Thr Leu Arg Leu Pro Gln Tyr Ala Asp Ala Thr Ile Glu Val Leu Asn
930 935 940

Ile Glu Arg Asp Arg Pro Val Val Phe Ala Thr Asp Glu Val Val Arg
945 950 955 960

Glu Val Ala Val Glu Glu Thr Pro Ala Ala Pro Ala Glu Thr Thr Glu
965 970 975

Thr Pro Ala Thr Pro Ala Thr Pro Ala Pro Val Ala Ala Ala Ala Pro
980 985 990

Ala Thr Gly Gly Pro Arg Pro Asp Asp Ile Ser Phe Thr Pro Ser Asp
995 1000 1005

Ala Thr Glu Met Leu Ile Ala Ile Trp Thr Lys Val Arg Pro Asp Gln
1010 1015 1020

Met Gly Ala Thr Asp Ser Ile Glu Thr Leu Val Glu Gly Val Ser Ser
1025 1030 1035 1040

Arg Arg Asn Gln Leu Leu Leu Asp Leu Gly Val Glu Phe Gly Leu Gly
1045 1050 1055

Ala Ile Asp Gly Ala Ala Asp Ala Glu Leu Gly Asp Leu Lys Val Thr
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Val Ser Lys Met Ala Lys Gly Tyr Lys Ala Phe Gly Pro Val Leu Ser
1075 1080 1085

Asp Ala Ala Ala Asp Ala Leu Arg Arg Leu Thr Gly Pro Thr Gly Lys
1090 1095 1100

Arg Pro Gly Tyr Ile Ala Glu Arg Val Thr Gly Thr Trp Glu Leu Gly
1105 1110 1115 1120

Gln Gly Trp Ala Asp His Val Val Ala Glu Val Val Ile Gly Ala Arg
1125 1130 1135

Glu Gly Ala Ser Leu Arg Gly Gly Asp Leu Ala Ser Leu Ser Pro Ala
1140 1145 1150

Ser Pro Ala Ser Ala Ser Asp Leu Asp Ser Leu Ile Asp Ala Ala Val
1155 1160 1165

Gln Ala Val Ala Ser Arg Arg Gly Val Ala Val Ser Leu Pro Ser Ala
1170 1175 1180

Gly Gly Ala Ala Gly Gly Val Val Asp Ser Ala Ala Leu Gly Glu Phe
1185 1190 1195 1200

Ala Glu Gln Val Thr Gly His Asp Gly Val Leu Ala Gln Ala Ala Arg
1205 1210 1215

Thr Ile Leu Thr Gln Leu Gly Leu Asp Lys Pro Ala Thr Val Ser Val
1220 1225 1230

Glu Asp Thr Ala Glu Glu Asp Leu Tyr Glu Leu Val Ser Lys Glu Leu
1235 1240 1245

Gly Ser Asp Trp Pro Arg Gln Val Ala Pro Ser Phe Asp Glu Glu Lys
1250 1255 1260

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Val Val Leu Leu Asp Asp Arg Trp Ala Ser Ala Arg Glu
1265                1270                1275


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                                           Met Glu Gln Ser Gln
                                           1               5

tcg tcg gat cag aag atg acc gtt gaa cag gtt cgc acc tgg ctc cgt   163
Ser Ser Asp Gln Lys Met Thr Val Glu Gln Val Arg Thr Trp Leu Arg
                10                  15                  20

gat tgg gtt gtc cgc acc acg ggt att ccg gtg gag gaa gtt acg gat   211
Asp Trp Val Val Arg Thr Thr Gly Ile Pro Val Glu Glu Val Thr Asp
            25                  30                  35

gac aag gca atg gag acc ttt ggc ctt tcc tct cgc gat gtt gtt gtg   259
Asp Lys Ala Met Glu Thr Phe Gly Leu Ser Ser Arg Asp Val Val Val
        40                  45                  50

ttg tct ggt gag ctg gaa aac ctg ctg gac acc tcc ttg gat gcc acc   307
Leu Ser Gly Glu Leu Glu Asn Leu Leu Asp Thr Ser Leu Asp Ala Thr
    55                  60                  65

atc gct tat gag tac cca acg atc cgt agt ttg gcg cag cgc ctt gtt   355
Ile Ala Tyr Glu Tyr Pro Thr Ile Arg Ser Leu Ala Gln Arg Leu Val
70                  75                  80                  85

gag ggc gag cct cgt cgt gca cat acc cag cgt gaa ttg aat ttc tcc   403
Glu Gly Glu Pro Arg Arg Ala His Thr Gln Arg Glu Leu Asn Phe Ser
                90                  95                  100

gcg gtg agc gat tcc cca ggt tcc cac gat att gcg gtt gtc ggt atg   451
Ala Val Ser Asp Ser Pro Gly Ser His Asp Ile Ala Val Val Gly Met
            105                 110                 115

gct gcg cgt tac cca ggc gct gag agc ctg gag gat atg tgg aag cta   499
Ala Ala Arg Tyr Pro Gly Ala Glu Ser Leu Glu Asp Met Trp Lys Leu
        120                 125                 130

ctc gtc gag ggc cgt gac ggt atc tcg gat cta ccg att ggc cgt tgg   547
Leu Val Glu Gly Arg Asp Gly Ile Ser Asp Leu Pro Ile Gly Arg Trp
    135                 140                 145

tct gag tat gca ggc gat gag gtt atg tct cgg aag atg gaa gag ttt   595
Ser Glu Tyr Ala Gly Asp Glu Val Met Ser Arg Lys Met Glu Glu Phe
150                 155                 160                 165
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tct acc atc ggt ggc tac ctg tca gat atc tct agc ttt gat gcg gag     643
Ser Thr Ile Gly Gly Tyr Leu Ser Asp Ile Ser Ser Phe Asp Ala Glu
                170                 175                 180

ttc ttt ggt ctg tct ccg ctc gag gcc gcc aac atg gat cct cag cag     691
Phe Phe Gly Leu Ser Pro Leu Glu Ala Ala Asn Met Asp Pro Gln Gln
            185                 190                 195

cgt att ttg ctg gag cta acg tgg gag gct ttg gag tac gct cgc atc     739
Arg Ile Leu Leu Glu Leu Thr Trp Glu Ala Leu Glu Tyr Ala Arg Ile
        200                 205                 210

gca cca aac act ttg cgt ggc gaa gcc gtg ggc gtg ttc ata ggt tcc     787
Ala Pro Asn Thr Leu Arg Gly Glu Ala Val Gly Val Phe Ile Gly Ser
    215                 220                 225

tcc aac aac gat tac ggc atg atg atc gct gcc gat cca gca gaa gca     835
Ser Asn Asn Asp Tyr Gly Met Met Ile Ala Ala Asp Pro Ala Glu Ala
230                 235                 240                 245

cat cct tat gcg ctg act ggt act tct agt gcg att gtc gct aac cgc     883
His Pro Tyr Ala Leu Thr Gly Thr Ser Ser Ala Ile Val Ala Asn Arg
                250                 255                 260

att aac tac gct ttc gat ttc cgc ggt cct tcc gtc aac gtg gat acc     931
Ile Asn Tyr Ala Phe Asp Phe Arg Gly Pro Ser Val Asn Val Asp Thr
            265                 270                 275

gca tgt tct tct tct ctg gta gcg gtt cac cag gct gtc cgt gcg ctg     979
Ala Cys Ser Ser Ser Leu Val Ala Val His Gln Ala Val Arg Ala Leu
        280                 285                 290

cgt aat ggc gaa gcg gat cac gct atc gct ggt gga gtg aac att ttg     1027
Arg Asn Gly Glu Ala Asp His Ala Ile Ala Gly Gly Val Asn Ile Leu
    295                 300                 305

gca tct cca ttt gtc aca act gca ttc gct gag ctc ggt gtg atc agc     1075
Ala Ser Pro Phe Val Thr Thr Ala Phe Ala Glu Leu Gly Val Ile Ser
310                 315                 320                 325

cca acc ggc aag atc cac gca ttc tct gat gat gcc gat ggt ttc gtg     1123
Pro Thr Gly Lys Ile His Ala Phe Ser Asp Asp Ala Asp Gly Phe Val
                330                 335                 340

cgt tcc gac ggc gcc gga gtc gtt gtg ctg aag cgc gtg gat gac gca     1171
Arg Ser Asp Gly Ala Gly Val Val Val Leu Lys Arg Val Asp Asp Ala
            345                 350                 355

atc cgc gac ggc gac aag atc atc ggt gtg atc aag ggt tct gca gtg     1219
Ile Arg Asp Gly Asp Lys Ile Ile Gly Val Ile Lys Gly Ser Ala Val
        360                 365                 370

aac tcc gat ggt cac tcc aac gga ctg acc gct cca aac cct gac gca     1267
Asn Ser Asp Gly His Ser Asn Gly Leu Thr Ala Pro Asn Pro Asp Ala
    375                 380                 385

cag gtt gat gtg ctg cag cgt gca tat gtt gac gct cag gtt gat ccc     1315
Gln Val Asp Val Leu Gln Arg Ala Tyr Val Asp Ala Gln Val Asp Pro
390                 395                 400                 405

acc acc gtg gat tac gtt gag gct cac ggc acc ggc acc atc ctg ggt     1363
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Thr Thr Val Asp Tyr Val Glu Ala His Gly Thr Gly Thr Ile Leu Gly
                410                 415                 420

gac ccc att gaa gca act gcc ctg ggt gct gtt ttg ggc tat ggc cgt     1411
Asp Pro Ile Glu Ala Thr Ala Leu Gly Ala Val Leu Gly Tyr Gly Arg
            425                 430                 435

gac gca tcc acc cca act ctt ctg ggc tct gca aag tcc aac ttc ggc     1459
Asp Ala Ser Thr Pro Thr Leu Leu Gly Ser Ala Lys Ser Asn Phe Gly
        440                 445                 450

cac act gag tca gct gcg ggt att gca ggt gtc atc aag gtg ctg ctt     1507
His Thr Glu Ser Ala Ala Gly Ile Ala Gly Val Ile Lys Val Leu Leu
    455                 460                 465

gct ttg cag aac aag act ctg cca cca acc gtg aac ttt gca ggt cca     1555
Ala Leu Gln Asn Lys Thr Leu Pro Pro Thr Val Asn Phe Ala Gly Pro
470                 475                 480                 485

aac cgc tac atc gat ttc gat gct gag cgt ttg gaa gtt gtg gaa gat     1603
Asn Arg Tyr Ile Asp Phe Asp Ala Glu Arg Leu Glu Val Val Glu Asp
                490                 495                 500

cca cgt gaa tgg ccg gaa tac aac ggt cac gca gta gct ggt gtg tct     1651
Pro Arg Glu Trp Pro Glu Tyr Asn Gly His Ala Val Ala Gly Val Ser
            505                 510                 515

gcg ttc ggg ttc ggt gga acc aac gcg cac gtg gtg atc tct gag tac     1699
Ala Phe Gly Phe Gly Gly Thr Asn Ala His Val Val Ile Ser Glu Tyr
        520                 525                 530

aac gca gaa gac tac gaa acc cgt gcc ccg aag gag gcg ttg ctt cct     1747
Asn Ala Glu Asp Tyr Glu Thr Arg Ala Pro Lys Glu Ala Leu Leu Pro
    535                 540                 545

gac cag cag gtt gcc ctg ccg gtg tct ggt cac ctg cca tcc agg cgt     1795
Asp Gln Gln Val Ala Leu Pro Val Ser Gly His Leu Pro Ser Arg Arg
550                 555                 560                 565

cga caa gca gct gct gac ttg gcg gac ttc ttg gag ggc cgc aaa gat     1843
Arg Gln Ala Ala Ala Asp Leu Ala Asp Phe Leu Glu Gly Arg Lys Asp
                570                 575                 580

tgc gac cta acc cca gta gcc cgc gcg ctg gca ggc cgc aat cat ggc     1891
Cys Asp Leu Thr Pro Val Ala Arg Ala Leu Ala Gly Arg Asn His Gly
            585                 590                 595

cgc tcc cgc gca gtc gtg ctt gca agc act atc gag gaa gcc gta aag     1939
Arg Ser Arg Ala Val Val Leu Ala Ser Thr Ile Glu Glu Ala Val Lys
        600                 605                 610

cgc ctg cgc cag gtc gca gaa ggc aag gtc agc gtc ggt atc tcc gca     1987
Arg Leu Arg Gln Val Ala Glu Gly Lys Val Ser Val Gly Ile Ser Ala
    615                 620                 625

gct gat tcc cca gcg gcc aac ggt cct gtg ttt gtg tac tcc ggt ttc     2035
Ala Asp Ser Pro Ala Ala Asn Gly Pro Val Phe Val Tyr Ser Gly Phe
630                 635                 640                 645

gga tcc cag cac cgc ctc atg atc aag gaa ttg tgc tca att tcg cca     2083
Gly Ser Gln His Arg Leu Met Ile Lys Glu Leu Cys Ser Ile Ser Pro
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                650                 655                 660

cag ttc cgc gag cgc atc gaa gag ctc gat gaa atg gtt aag ttc gag    2131
Gln Phe Arg Glu Arg Ile Glu Glu Leu Asp Glu Met Val Lys Phe Glu
            665                 670                 675

tcc ggc tgg tcc atc atg aaa ctt gtt ttg gat gat gag caa act tac    2179
Ser Gly Trp Ser Ile Met Lys Leu Val Leu Asp Asp Glu Gln Thr Tyr
        680                 685                 690

gac acc gag acc gcg cag gtt gtg atc acc gca atc cag atc gca ctg    2227
Asp Thr Glu Thr Ala Gln Val Val Ile Thr Ala Ile Gln Ile Ala Leu
    695                 700                 705

act gac ctg ttg gca agc ttc ggt gta aag cca gct gcc gtc atg ggc    2275
Thr Asp Leu Leu Ala Ser Phe Gly Val Lys Pro Ala Ala Val Met Gly
710                 715                 720                 725

atg tcg atg ggt gag atc gct gcc gct tac gct gcc ggt gga ctc agc    2323
Met Ser Met Gly Glu Ile Ala Ala Ala Tyr Ala Ala Gly Gly Leu Ser
                730                 735                 740

gac cgc gat acc atg ctc att gcc agc cac cgt tcc cgc cta atg ggc    2371
Asp Arg Asp Thr Met Leu Ile Ala Ser His Arg Ser Arg Leu Met Gly
            745                 750                 755

gag ggc gag aag tcc ctg gct gag gat cag ctg ggt gcc atg gct gtg    2419
Glu Gly Glu Lys Ser Leu Ala Glu Asp Gln Leu Gly Ala Met Ala Val
        760                 765                 770

gtg gaa ttc gcc gct gcg gac ctg gat aag ttc atc gaa gaa aac cct    2467
Val Glu Phe Ala Ala Ala Asp Leu Asp Lys Phe Ile Glu Glu Asn Pro
    775                 780                 785

gag tac aag ggc att gag cct gct gtt tat gca ggc cca ggc atg act    2515
Glu Tyr Lys Gly Ile Glu Pro Ala Val Tyr Ala Gly Pro Gly Met Thr
790                 795                 800                 805

acc gtg ggt gga cct cgc gac gcc gtg gtt cag ttc gta gag aag ctg    2563
Thr Val Gly Gly Pro Arg Asp Ala Val Val Gln Phe Val Glu Lys Leu
                810                 815                 820

gaa tct gaa gac aag ttt gcc cgc ctg ctc aac gtc aag ggc gct ggc    2611
Glu Ser Glu Asp Lys Phe Ala Arg Leu Leu Asn Val Lys Gly Ala Gly
            825                 830                 835

cac acc tct gct gtg gaa cca ctt ctt ggt gag ctc gct ggc gaa atc    2659
His Thr Ser Ala Val Glu Pro Leu Leu Gly Glu Leu Ala Gly Glu Ile
        840                 845                 850

gct ggc atc gag cca ctt ccg ctg cag atc ccg ttg ttc agc tct gtc    2707
Ala Gly Ile Glu Pro Leu Pro Leu Gln Ile Pro Leu Phe Ser Ser Val
    855                 860                 865

gat cag ggt gtt acc tac cca gtt gga gca gtg gtc cac gac gcc gat    2755
Asp Gln Gly Val Thr Tyr Pro Val Gly Ala Val Val His Asp Ala Asp
870                 875                 880                 885

tac atg ctc cgc tgt acc cgc cag tcc gtg tac ttc cag gac tcc acc    2803
Tyr Met Leu Arg Cys Thr Arg Gln Ser Val Tyr Phe Gln Asp Ser Thr
                890                 895                 900
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gaa gct gca ttc gct gca ggc cac aac acc ttg gtg gaa att tcc ccg 2851
Glu Ala Ala Phe Ala Ala Gly His Asn Thr Leu Val Glu Ile Ser Pro
905 910 915

aac cca gtt gca ctc atg ggc atg atg aac acc gcg ttc acc gtg ggc 2899
Asn Pro Val Ala Leu Met Gly Met Met Asn Thr Ala Phe Thr Val Gly
920 925 930

aag cct gat gca cag ctg ctg ttc agc ctg aag cga aaa gtc cca gag 2947
Lys Pro Asp Ala Gln Leu Leu Phe Ser Leu Lys Arg Lys Val Pro Glu
935 940 945

gca gaa tcc ctc cgc gac ctt ctg gcg aag ctg tac gtc aac ggc gca 2995
Ala Glu Ser Leu Arg Asp Leu Leu Ala Lys Leu Tyr Val Asn Gly Ala
950 955 960 965

aac gtt gat ttc tcc gcg ctg tac ggc gaa ggt gaa acc atc gat ccg 3043
Asn Val Asp Phe Ser Ala Leu Tyr Gly Glu Gly Glu Thr Ile Asp Pro
970 975 980

cca cac atc acc tgg aag cac cag cgc ttc tgg act tcc gca cgc cca 3091
Pro His Ile Thr Trp Lys His Gln Arg Phe Trp Thr Ser Ala Arg Pro
985 990 995

tcc tct ggc gca tcc ctg gat ctg ccg ggc ttc cgc gtg aat ctg cca 3139
Ser Ser Gly Ala Ser Leu Asp Leu Pro Gly Phe Arg Val Asn Leu Pro
1000 1005 1010

aac aac act gtg gcg ttt tcc acc gca gcc gaa ctg gca cca tcc gca 3187
Asn Asn Thr Val Ala Phe Ser Thr Ala Ala Glu Leu Ala Pro Ser Ala
1015 1020 1025

gtg gca atc atg gaa gca gcc gcc atg gct gtc acc cca ggt tcc tcc 3235
Val Ala Ile Met Glu Ala Ala Ala Met Ala Val Thr Pro Gly Ser Ser
1030 1035 1040 1045

gtc gac gca gtg gac gag cgc gac atg ctg cca cca agc ggc gaa atc 3283
Val Asp Ala Val Asp Glu Arg Asp Met Leu Pro Pro Ser Gly Glu Ile
1050 1055 1060

acc acc atc gtg act cgc tcc ttg ggc ggt ttg agc ctg tcc gta tac 3331
Thr Thr Ile Val Thr Arg Ser Leu Gly Gly Leu Ser Leu Ser Val Tyr
1065 1070 1075

aag att gag gga acc acc agc act ctt gtc gcc gaa ggt ttc gca gcc 3379
Lys Ile Glu Gly Thr Thr Ser Thr Leu Val Ala Glu Gly Phe Ala Ala
1080 1085 1090

aac cca gga ttc gcc gca gca tct tcc ttc gac ggt cca ggc tac gac 3427
Asn Pro Gly Phe Ala Ala Ala Ser Ser Phe Asp Gly Pro Gly Tyr Asp
1095 1100 1105

gga ttc aac acc gat tac agc gac cag cca gac cct cgc tcc gac ctg 3475
Gly Phe Asn Thr Asp Tyr Ser Asp Gln Pro Asp Pro Arg Ser Asp Leu
1110 1115 1120 1125

cct ttg gac atc gaa gca gtc cgc tgg gac cca gcg acc gaa acc gtc 3523
Pro Leu Asp Ile Glu Ala Val Arg Trp Asp Pro Ala Thr Glu Thr Val
1130 1135 1140

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gaa gag cgc atg cgc gcc atc gtc tcc gaa gca atg ggc tac gac gtg    3571
Glu Glu Arg Met Arg Ala Ile Val Ser Glu Ala Met Gly Tyr Asp Val
            1145                1150                1155

gat gac ctc cca cgc gaa ctc cca ctg att gac ctc ggc ctc gac tcc    3619
Asp Asp Leu Pro Arg Glu Leu Pro Leu Ile Asp Leu Gly Leu Asp Ser
        1160                1165                1170

ctc atg ggc atg cgc atc aaa aac cgc atc gaa aat gac ttc cag atc    3667
Leu Met Gly Met Arg Ile Lys Asn Arg Ile Glu Asn Asp Phe Gln Ile
    1175                1180                1185

cca cca ctc cag gtc caa gcg ctc cgc gat gca tcc gtc gct gac gtg    3715
Pro Pro Leu Gln Val Gln Ala Leu Arg Asp Ala Ser Val Ala Asp Val
1190                1195                1200                1205

gta atc atg gtg gaa aac atg gtc gct ggc cgc tcc tct gag acg ctt    3763
Val Ile Met Val Glu Asn Met Val Ala Gly Arg Ser Ser Glu Thr Leu
                1210                1215                1220

gtc gac gcc acc ccg cag gtg cca gct gag gca gca ggg gag gct caa    3811
Val Asp Ala Thr Pro Gln Val Pro Ala Glu Ala Ala Gly Glu Ala Gln
            1225                1230                1235

gct gct gag tct tct gct tcg ggc gag gac gtg cag ggc gtt ggc gtt    3859
Ala Ala Glu Ser Ser Ala Ser Gly Glu Asp Val Gln Gly Val Gly Val
        1240                1245                1250

gca ccg cga gat gcg tcg gaa cgc atg gtc ttt ggt act tgg gca ggc    3907
Ala Pro Arg Asp Ala Ser Glu Arg Met Val Phe Gly Thr Trp Ala Gly
    1255                1260                1265

ctg act ggc gct gcg gca gct ggc gtg acc agc aag ttg cca cag atc    3955
Leu Thr Gly Ala Ala Ala Ala Gly Val Thr Ser Lys Leu Pro Gln Ile
1270                1275                1280                1285

gat gtc gat act gca acc gca att gcc gag cgc ctc acc gag cgt tcc    4003
Asp Val Asp Thr Ala Thr Ala Ile Ala Glu Arg Leu Thr Glu Arg Ser
                1290                1295                1300

gga att gaa atc agc act gaa cag gtg ttg gct gca gaa acc ctc gaa    4051
Gly Ile Glu Ile Ser Thr Glu Gln Val Leu Ala Ala Glu Thr Leu Glu
            1305                1310                1315

cca ctg tct gac ctg gtg cgt gaa ggc ctc gaa act gaa gtt cag ggc    4099
Pro Leu Ser Asp Leu Val Arg Glu Gly Leu Glu Thr Glu Val Gln Gly
        1320                1325                1330

aac att cgt gtg ctg cgt gga cgt gca gaa ggc tcc acc aag cct gca    4147
Asn Ile Arg Val Leu Arg Gly Arg Ala Glu Gly Ser Thr Lys Pro Ala
    1335                1340                1345

gtg ttc atg ttc cac cca gct ggc ggt tct tcc gtg gtc tac caa cca    4195
Val Phe Met Phe His Pro Ala Gly Gly Ser Ser Val Val Tyr Gln Pro
1350                1355                1360                1365

cta atg cgt cgt ctg cct gaa gat gtc cct gtc tat ggc gtt gag cgt    4243
Leu Met Arg Arg Leu Pro Glu Asp Val Pro Val Tyr Gly Val Glu Arg
                1370                1375                1380

ctg gaa ggc gat ctc gct gac cgc gcg gca gca tat gtt gat gac atc    4291
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Leu Glu Gly Asp Leu Ala Asp Arg Ala Ala Ala Tyr Val Asp Asp Ile
          1385                1390                1395

aag aag tac tcc gat ggc ttc cca gta gtt ttg ggt ggc tgg agc ttc    4339
Lys Lys Tyr Ser Asp Gly Phe Pro Val Val Leu Gly Gly Trp Ser Phe
      1400                1405                1410

ggc ggt gcc gtt gcc ttc gag gtt gcc cac caa ctg gtt ggc tcc gat    4387
Gly Gly Ala Val Ala Phe Glu Val Ala His Gln Leu Val Gly Ser Asp
  1415                1420                1425

gtt gag gta gct acc gtg gcg ttg ctg gat act gtg cag cct tca aac    4435
Val Glu Val Ala Thr Val Ala Leu Leu Asp Thr Val Gln Pro Ser Asn
1430                1435                1440                1445

cca gca cca gat acc gct gag gaa act cgt gca cgc tgg act cgc tac    4483
Pro Ala Pro Asp Thr Ala Glu Glu Thr Arg Ala Arg Trp Thr Arg Tyr
                1450                1455                1460

gcg gac ttc gcc aag aag acc tac ggc ctt gat ttc gag gta cct ttt    4531
Ala Asp Phe Ala Lys Lys Thr Tyr Gly Leu Asp Phe Glu Val Pro Phe
            1465                1470                1475

gaa atc ttg gac acc atc ggt gaa gac gga atg ctg tcc atg atg acc    4579
Glu Ile Leu Asp Thr Ile Gly Glu Asp Gly Met Leu Ser Met Met Thr
        1480                1485                1490

gac ttc ctg gcc aac acc gac gcc tcc gag cac gga ttg tcc gca ggt    4627
Asp Phe Leu Ala Asn Thr Asp Ala Ser Glu His Gly Leu Ser Ala Gly
    1495                1500                1505

gtg ctt gaa cac cag cgc gct tct ttt gtg gac aac cgc atc ctg gct    4675
Val Leu Glu His Gln Arg Ala Ser Phe Val Asp Asn Arg Ile Leu Ala
1510                1515                1520                1525

aaa ctt aat ttt gca gac tgg gcc aac gtt gaa gcc cct gtc atc ctg    4723
Lys Leu Asn Phe Ala Asp Trp Ala Asn Val Glu Ala Pro Val Ile Leu
                1530                1535                1540

ttc cgc gcg gaa cgc atg cat gat gga gct atc gaa ctt gaa cca aac    4771
Phe Arg Ala Glu Arg Met His Asp Gly Ala Ile Glu Leu Glu Pro Asn
            1545                1550                1555

tat gcc aag att gat caa gat gga gga tgg tcc gga att gtc aac gat    4819
Tyr Ala Lys Ile Asp Gln Asp Gly Gly Trp Ser Gly Ile Val Asn Asp
        1560                1565                1570

ttg gaa att gtt cag ctg aat ggt gac cac ctg gca gtt gtc gat gaa    4867
Leu Glu Ile Val Gln Leu Asn Gly Asp His Leu Ala Val Val Asp Glu
    1575                1580                1585

cca gaa atc ggc aca gtc gga gct cat ttg agt cgc cgc att gat gag    4915
Pro Glu Ile Gly Thr Val Gly Ala His Leu Ser Arg Arg Ile Asp Glu
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att tct cgg aag aat tagtaacgga gagctgacgg aag                      4953
Ile Ser Arg Lys Asn
                1610
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Arg Thr Trp Leu Arg Asp Trp Val Val Arg Thr Thr Gly Ile Pro Val
            20   25   30

Glu Glu Val Thr Asp Asp Lys Ala Met Glu Thr Phe Gly Leu Ser Ser
        35   40   45

Arg Asp Val Val Val Leu Ser Gly Glu Leu Glu Asn Leu Leu Asp Thr
    50   55   60

Ser Leu Asp Ala Thr Ile Ala Tyr Glu Tyr Pro Thr Ile Arg Ser Leu
65   70   75   80

Ala Gln Arg Leu Val Glu Gly Glu Pro Arg Arg Ala His Thr Gln Arg
                85   90   95

Glu Leu Asn Phe Ser Ala Val Ser Asp Ser Pro Gly Ser His Asp Ile
            100   105   110

Ala Val Val Gly Met Ala Ala Arg Tyr Pro Gly Ala Glu Ser Leu Glu
        115   120   125

Asp Met Trp Lys Leu Leu Val Glu Gly Arg Asp Gly Ile Ser Asp Leu
    130   135   140

Pro Ile Gly Arg Trp Ser Glu Tyr Ala Gly Asp Glu Val Met Ser Arg
145   150   155   160

Lys Met Glu Glu Phe Ser Thr Ile Gly Gly Tyr Leu Ser Asp Ile Ser
                165   170   175

Ser Phe Asp Ala Glu Phe Phe Gly Leu Ser Pro Leu Glu Ala Ala Asn
            180   185   190

Met Asp Pro Gln Gln Arg Ile Leu Leu Glu Leu Thr Trp Glu Ala Leu
        195   200   205

Glu Tyr Ala Arg Ile Ala Pro Asn Thr Leu Arg Gly Glu Ala Val Gly
    210   215   220

Val Phe Ile Gly Ser Ser Asn Asn Asp Tyr Gly Met Met Ile Ala Ala
225   230   235   240

Asp Pro Ala Glu Ala His Pro Tyr Ala Leu Thr Gly Thr Ser Ser Ala
                245   250   255

Ile Val Ala Asn Arg Ile Asn Tyr Ala Phe Asp Phe Arg Gly Pro Ser
            260   265   270

Val Asn Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Val His Gln
        275   280   285

Ala Val Arg Ala Leu Arg Asn Gly Glu Ala Asp His Ala Ile Ala Gly
    290   295   300

Gly Val Asn Ile Leu Ala Ser Pro Phe Val Thr Thr Ala Phe Ala Glu
305 310 315 320

Leu Gly Val Ile Ser Pro Thr Gly Lys Ile His Ala Phe Ser Asp Asp
325 330 335

Ala Asp Gly Phe Val Arg Ser Asp Gly Ala Gly Val Val Val Leu Lys
340 345 350

Arg Val Asp Asp Ala Ile Arg Asp Gly Asp Lys Ile Ile Gly Val Ile
355 360 365

Lys Gly Ser Ala Val Asn Ser Asp Gly His Ser Asn Gly Leu Thr Ala
370 375 380

Pro Asn Pro Asp Ala Gln Val Asp Val Leu Gln Arg Ala Tyr Val Asp
385 390 395 400

Ala Gln Val Asp Pro Thr Thr Val Asp Tyr Val Glu Ala His Gly Thr
405 410 415

Gly Thr Ile Leu Gly Asp Pro Ile Glu Ala Thr Ala Leu Gly Ala Val
420 425 430

Leu Gly Tyr Gly Arg Asp Ala Ser Thr Pro Thr Leu Leu Gly Ser Ala
435 440 445

Lys Ser Asn Phe Gly His Thr Glu Ser Ala Ala Gly Ile Ala Gly Val
450 455 460

Ile Lys Val Leu Leu Ala Leu Gln Asn Lys Thr Leu Pro Pro Thr Val
465 470 475 480

Asn Phe Ala Gly Pro Asn Arg Tyr Ile Asp Phe Asp Ala Glu Arg Leu
485 490 495

Glu Val Val Glu Asp Pro Arg Glu Trp Pro Glu Tyr Asn Gly His Ala
500 505 510

Val Ala Gly Val Ser Ala Phe Gly Phe Gly Gly Thr Asn Ala His Val
515 520 525

Val Ile Ser Glu Tyr Asn Ala Glu Asp Tyr Glu Thr Arg Ala Pro Lys
530 535 540

Glu Ala Leu Leu Pro Asp Gln Gln Val Ala Leu Pro Val Ser Gly His
545 550 555 560

Leu Pro Ser Arg Arg Arg Gln Ala Ala Ala Asp Leu Ala Asp Phe Leu
565 570 575

Glu Gly Arg Lys Asp Cys Asp Leu Thr Pro Val Ala Arg Ala Leu Ala
580 585 590

Gly Arg Asn His Gly Arg Ser Arg Ala Val Val Leu Ala Ser Thr Ile
595 600 605

Glu Glu Ala Val Lys Arg Leu Arg Gln Val Ala Glu Gly Lys Val Ser
610 615 620

Val Gly Ile Ser Ala Ala Asp Ser Pro Ala Ala Asn Gly Pro Val Phe
625 630 635 640

Val Tyr Ser Gly Phe Gly Ser Gln His Arg Leu Met Ile Lys Glu Leu
645 650 655

Cys Ser Ile Ser Pro Gln Phe Arg Glu Arg Ile Glu Glu Leu Asp Glu
660 665 670

Met Val Lys Phe Glu Ser Gly Trp Ser Ile Met Lys Leu Val Leu Asp
675 680 685

Asp Glu Gln Thr Tyr Asp Thr Glu Thr Ala Gln Val Val Ile Thr Ala
690 695 700

Ile Gln Ile Ala Leu Thr Asp Leu Leu Ala Ser Phe Gly Val Lys Pro
705 710 715 720

Ala Ala Val Met Gly Met Ser Met Gly Glu Ile Ala Ala Ala Tyr Ala
725 730 735

Ala Gly Gly Leu Ser Asp Arg Asp Thr Met Leu Ile Ala Ser His Arg
740 745 750

Ser Arg Leu Met Gly Glu Gly Glu Lys Ser Leu Ala Glu Asp Gln Leu
755 760 765

Gly Ala Met Ala Val Val Glu Phe Ala Ala Ala Asp Leu Asp Lys Phe
770 775 780

Ile Glu Glu Asn Pro Glu Tyr Lys Gly Ile Glu Pro Ala Val Tyr Ala
785 790 795 800

Gly Pro Gly Met Thr Thr Val Gly Gly Pro Arg Asp Ala Val Val Gln
805 810 815

Phe Val Glu Lys Leu Glu Ser Glu Asp Lys Phe Ala Arg Leu Leu Asn
820 825 830

Val Lys Gly Ala Gly His Thr Ser Ala Val Glu Pro Leu Leu Gly Glu
835 840 845

Leu Ala Gly Glu Ile Ala Gly Ile Glu Pro Leu Pro Leu Gln Ile Pro
850 855 860

Leu Phe Ser Ser Val Asp Gln Gly Val Thr Tyr Pro Val Gly Ala Val
865 870 875 880

Val His Asp Ala Asp Tyr Met Leu Arg Cys Thr Arg Gln Ser Val Tyr
885 890 895

Phe Gln Asp Ser Thr Glu Ala Ala Phe Ala Ala Gly His Asn Thr Leu
900 905 910

Val Glu Ile Ser Pro Asn Pro Val Ala Leu Met Gly Met Met Asn Thr
915 920 925

Ala Phe Thr Val Gly Lys Pro Asp Ala Gln Leu Leu Phe Ser Leu Lys
930 935 940

Arg Lys Val Pro Glu Ala Glu Ser Leu Arg Asp Leu Leu Ala Lys Leu

945 950 955 960

Tyr Val Asn Gly Ala Asn Val Asp Phe Ser Ala Leu Tyr Gly Glu Gly
965 970 975

Glu Thr Ile Asp Pro Pro His Ile Thr Trp Lys His Gln Arg Phe Trp
980 985 990

Thr Ser Ala Arg Pro Ser Ser Gly Ala Ser Leu Asp Leu Pro Gly Phe
995 1000 1005

Arg Val Asn Leu Pro Asn Asn Thr Val Ala Phe Ser Thr Ala Ala Glu
1010 1015 1020

Leu Ala Pro Ser Ala Val Ala Ile Met Glu Ala Ala Ala Met Ala Val
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Thr Pro Gly Ser Ser Val Asp Ala Val Asp Glu Arg Asp Met Leu Pro
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Pro Ser Gly Glu Ile Thr Thr Ile Val Thr Arg Ser Leu Gly Gly Leu
1060 1065 1070

Ser Leu Ser Val Tyr Lys Ile Glu Gly Thr Thr Ser Thr Leu Val Ala
1075 1080 1085

Glu Gly Phe Ala Ala Asn Pro Gly Phe Ala Ala Ala Ser Ser Phe Asp
1090 1095 1100

Gly Pro Gly Tyr Asp Gly Phe Asn Thr Asp Tyr Ser Asp Gln Pro Asp
1105 1110 1115 1120

Pro Arg Ser Asp Leu Pro Leu Asp Ile Glu Ala Val Arg Trp Asp Pro
1125 1130 1135

Ala Thr Glu Thr Val Glu Glu Arg Met Arg Ala Ile Val Ser Glu Ala
1140 1145 1150

Met Gly Tyr Asp Val Asp Asp Leu Pro Arg Glu Leu Pro Leu Ile Asp
1155 1160 1165

Leu Gly Leu Asp Ser Leu Met Gly Met Arg Ile Lys Asn Arg Ile Glu
1170 1175 1180

Asn Asp Phe Gln Ile Pro Pro Leu Gln Val Gln Ala Leu Arg Asp Ala
1185 1190 1195 1200

Ser Val Ala Asp Val Val Ile Met Val Glu Asn Met Val Ala Gly Arg
1205 1210 1215

Ser Ser Glu Thr Leu Val Asp Ala Thr Pro Gln Val Pro Ala Glu Ala
1220 1225 1230

Ala Gly Glu Ala Gln Ala Ala Glu Ser Ser Ala Ser Gly Glu Asp Val
1235 1240 1245

Gln Gly Val Gly Val Ala Pro Arg Asp Ala Ser Glu Arg Met Val Phe
1250 1255 1260

Gly Thr Trp Ala Gly Leu Thr Gly Ala Ala Ala Ala Gly Val Thr Ser
1265 1270 1275 1280

Lys Leu Pro Gln Ile Asp Val Asp Thr Ala Thr Ala Ile Ala Glu Arg
1285 1290 1295

Leu Thr Glu Arg Ser Gly Ile Glu Ile Ser Thr Glu Gln Val Leu Ala
1300 1305 1310

Ala Glu Thr Leu Glu Pro Leu Ser Asp Leu Val Arg Glu Gly Leu Glu
1315 1320 1325

Thr Glu Val Gln Gly Asn Ile Arg Val Leu Arg Gly Arg Ala Glu Gly
1330 1335 1340

Ser Thr Lys Pro Ala Val Phe Met Phe His Pro Ala Gly Gly Ser Ser
1345 1350 1355 1360

Val Val Tyr Gln Pro Leu Met Arg Arg Leu Pro Glu Asp Val Pro Val
1365 1370 1375

Tyr Gly Val Glu Arg Leu Glu Gly Asp Leu Ala Asp Arg Ala Ala Ala
1380 1385 1390

Tyr Val Asp Asp Ile Lys Lys Tyr Ser Asp Gly Phe Pro Val Val Leu
1395 1400 1405

Gly Gly Trp Ser Phe Gly Gly Ala Val Ala Phe Glu Val Ala His Gln
1410 1415 1420

Leu Val Gly Ser Asp Val Glu Val Ala Thr Val Ala Leu Leu Asp Thr
1425 1430 1435 1440

Val Gln Pro Ser Asn Pro Ala Pro Asp Thr Ala Glu Glu Thr Arg Ala
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Arg Trp Thr Arg Tyr Ala Asp Phe Ala Lys Lys Thr Tyr Gly Leu Asp
1460 1465 1470

Phe Glu Val Pro Phe Glu Ile Leu Asp Thr Ile Gly Glu Asp Gly Met
1475 1480 1485

Leu Ser Met Met Thr Asp Phe Leu Ala Asn Thr Asp Ala Ser Glu His
1490 1495 1500

Gly Leu Ser Ala Gly Val Leu Glu His Gln Arg Ala Ser Phe Val Asp
1505 1510 1515 1520

Asn Arg Ile Leu Ala Lys Leu Asn Phe Ala Asp Trp Ala Asn Val Glu
1525 1530 1535

Ala Pro Val Ile Leu Phe Arg Ala Glu Arg Met His Asp Gly Ala Ile
1540 1545 1550

Glu Leu Glu Pro Asn Tyr Ala Lys Ile Asp Gln Asp Gly Gly Trp Ser
1555 1560 1565

Gly Ile Val Asn Asp Leu Glu Ile Val Gln Leu Asn Gly Asp His Leu
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Ala Val Val Asp Glu Pro Glu Ile Gly Thr Val Gly Ala His Leu Ser
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Arg Arg Ile Asp Glu Ile Ser Arg Lys Asn
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Met Asn Thr Met Pro
1 5

gac caa ccg ctc aac cag gac gga ttc cct acc gca tcc aaa ggg gtg 163
Asp Gln Pro Leu Asn Gln Asp Gly Phe Pro Thr Ala Ser Lys Gly Val
10 15 20

gaa ccc gac aac ctc ccc gac cgc gtt ctc gtg gac ggc ctt aaa cca 211
Glu Pro Asp Asn Leu Pro Asp Arg Val Leu Val Asp Gly Leu Lys Pro
25 30 35

aag cat cag cag ctt cgt gaa att ttg gag gaa atc tgc acc acc cag 259
Lys His Gln Gln Leu Arg Glu Ile Leu Glu Glu Ile Cys Thr Thr Gln
40 45 50

ctt cag cct ggg gac atg ctg cct ggt gag cgc atc ctg gaa gaa aag 307
Leu Gln Pro Gly Asp Met Leu Pro Gly Glu Arg Ile Leu Glu Glu Lys
55 60 65

tat ggc gtc agc cga att acg gtt cgt cgg gcg att ggt gat ctg gtc 355
Tyr Gly Val Ser Arg Ile Thr Val Arg Arg Ala Ile Gly Asp Leu Val
70 75 80 85

gcg tcc ggc agg ttg aag cga gct cgc ggc aaa ggt acc ttc gtg gcc 403
Ala Ser Gly Arg Leu Lys Arg Ala Arg Gly Lys Gly Thr Phe Val Ala
90 95 100

cac tcg ccg ttg att tcc cgc ctg cat ttg gcc tcg ttt tcc gca gag 451
His Ser Pro Leu Ile Ser Arg Leu His Leu Ala Ser Phe Ser Ala Glu
105 110 115

atg gcc gcc cag aag cta tcg gct acc agc agg att ttg agt tct tcc 499
Met Ala Ala Gln Lys Leu Ser Ala Thr Ser Arg Ile Leu Ser Ser Ser
120 125 130

cgc ggt ccc gcc cca gat gat att gct gat ttc ttt ggt acc gat cgc 547
Arg Gly Pro Ala Pro Asp Asp Ile Ala Asp Phe Phe Gly Thr Asp Arg
135 140 145

gcg gcc cag cac atc acg ttg cgc cgc ctg cgc ttt gga aat ggt cga 595
Ala Ala Gln His Ile Thr Leu Arg Arg Leu Arg Phe Gly Asn Gly Arg
150 155 160 165

ccc tat gcc att gac aac ggt tgg tac aac tcc gaa ttc gca cct gac 643
Pro Tyr Ala Ile Asp Asn Gly Trp Tyr Asn Ser Glu Phe Ala Pro Asp
170 175 180

ctg ctg gaa aat gat gtg tac aac tcc gtg tac tcc atc ctg gac cgc 691
Leu Leu Glu Asn Asp Val Tyr Asn Ser Val Tyr Ser Ile Leu Asp Arg
185 190 195

gtc tat ggc gtc ccc gtc acc cag gcc gag caa acg gtc acc gcc gta 739
Val Tyr Gly Val Pro Val Thr Gln Ala Glu Gln Thr Val Thr Ala Val
200 205 210

gca gcc gac gaa gac acc gca cgg ctt ctg gac gtc acc ccc ggc gcc 787
Ala Ala Asp Glu Asp Thr Ala Arg Leu Leu Asp Val Thr Pro Gly Ala
215 220 225

cca ctc ctt cgt atc ctt cga cag tca ctt tct ggc gat aag ccc gtg 835
Pro Leu Leu Arg Ile Leu Arg Gln Ser Leu Ser Gly Asp Lys Pro Val
230 235 240 245

gaa tgg tgc gtt tcc ttg tac cga acc gac cga tat tct tta aaa aca 883
Glu Trp Cys Val Ser Leu Tyr Arg Thr Asp Arg Tyr Ser Leu Lys Thr
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ttg gtt aca cgc tcc gaa gat ctc tgacgtgaac ccattttggt ggc 930
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35 40 45

Ile Cys Thr Thr Gln Leu Gln Pro Gly Asp Met Leu Pro Gly Glu Arg
50 55 60

Ile Leu Glu Glu Lys Tyr Gly Val Ser Arg Ile Thr Val Arg Arg Ala
65 70 75 80

Ile Gly Asp Leu Val Ala Ser Gly Arg Leu Lys Arg Ala Arg Gly Lys
85 90 95

Gly Thr Phe Val Ala His Ser Pro Leu Ile Ser Arg Leu His Leu Ala
100 105 110

Ser Phe Ser Ala Glu Met Ala Ala Gln Lys Leu Ser Ala Thr Ser Arg
115 120 125

Ile Leu Ser Ser Ser Arg Gly Pro Ala Pro Asp Asp Ile Ala Asp Phe
130 135 140

Phe Gly Thr Asp Arg Ala Ala Gln His Ile Thr Leu Arg Arg Leu Arg
145 150 155 160

Phe Gly Asn Gly Arg Pro Tyr Ala Ile Asp Asn Gly Trp Tyr Asn Ser
165 170 175

Glu Phe Ala Pro Asp Leu Leu Glu Asn Asp Val Tyr Asn Ser Val Tyr
180 185 190

Ser Ile Leu Asp Arg Val Tyr Gly Val Pro Val Thr Gln Ala Glu Gln
195 200 205

Thr Val Thr Ala Val Ala Ala Asp Glu Asp Thr Ala Arg Leu Leu Asp
210 215 220

Val Thr Pro Gly Ala Pro Leu Leu Arg Ile Leu Arg Gln Ser Leu Ser
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<223> RXA00880

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Met Thr Ser Pro Asn
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acc ctg cag gaa tac act gaa cct gcc aag tac acc atc gga gaa tct 163
Thr Leu Gln Glu Tyr Thr Glu Pro Ala Lys Tyr Thr Ile Gly Glu Ser
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gaa acc tgc ctg acc gcc ctt cta gat cag att aag act cga cct tac 211
Glu Thr Cys Leu Thr Ala Leu Leu Asp Gln Ile Lys Thr Arg Pro Tyr
25 30 35

gga gtt ttg ttc agc aag cct gcc aac tat gag tgg gtg aat gta act 259
Gly Val Leu Phe Ser Lys Pro Ala Asn Tyr Glu Trp Val Asn Val Thr
40 45 50

gcc aaa gaa ttt cag gac gag gtt ttt gcg gtt gca aaa gga att att 307
Ala Lys Glu Phe Gln Asp Glu Val Phe Ala Val Ala Lys Gly Ile Ile
55 60 65

tca gtc ggc gta gag cag gga gac cgt gtc gcg ctg ctg tcc aat act 355
Ser Val Gly Val Glu Gln Gly Asp Arg Val Ala Leu Leu Ser Asn Thr

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70                  75                  80                  85

cgc tat gag tgg gct gtg ctt gat ttc gct atc tgg gcc gct ggc gca    403
Arg Tyr Glu Trp Ala Val Leu Asp Phe Ala Ile Trp Ala Ala Gly Ala
                90                  95                  100

gtg agc gtg cct atc tac agc tcc tct tca ctg tcc caa att gag tgg    451
Val Ser Val Pro Ile Tyr Ser Ser Ser Ser Leu Ser Gln Ile Glu Trp
            105                 110                 115

atc att gag gat tcc ggc gct gtt ttg gcc att acc gaa acc cct gat    499
Ile Ile Glu Asp Ser Gly Ala Val Leu Ala Ile Thr Glu Thr Pro Asp
        120                 125                 130

cat acc gac ttg atg aag aac ctg gtc atc ggt gaa gac gga act cca    547
His Thr Asp Leu Met Lys Asn Leu Val Ile Gly Glu Asp Gly Thr Pro
    135                 140                 145

gcg att aag ggt tca cct tcc aag ctg cgc cgc att cta gag atc aac    595
Ala Ile Lys Gly Ser Pro Ser Lys Leu Arg Arg Ile Leu Glu Ile Asn
150                 155                 160                 165

tct tcg gcg ttg gag acc ttg aag ttt gag ggc cgc gag ctt tct gat    643
Ser Ser Ala Leu Glu Thr Leu Lys Phe Glu Gly Arg Glu Leu Ser Asp
                170                 175                 180

gag ctg gtg tgg gaa cgc att cat gca acc aag gcc gct gac ctg gcg    691
Glu Leu Val Trp Glu Arg Ile His Ala Thr Lys Ala Ala Asp Leu Ala
            185                 190                 195

tct ttg gtg tac acc tct ggc aca act ggt agg ccg aag ggc tgc gag    739
Ser Leu Val Tyr Thr Ser Gly Thr Thr Gly Arg Pro Lys Gly Cys Glu
        200                 205                 210

ttg tcc cac tac cac tgg ttg gct gag gtc cga gcg ctg atc acc aat    787
Leu Ser His Tyr His Trp Leu Ala Glu Val Arg Ala Leu Ile Thr Asn
    215                 220                 225

gac atc gga gcg atc gcg atg cca ggt tca agg ttg ctc acc ttc ctt    835
Asp Ile Gly Ala Ile Ala Met Pro Gly Ser Arg Leu Leu Thr Phe Leu
230                 235                 240                 245

cct ttg gcg cac gtt ctt gct cgc gca gtg cac ttg gcc ttc gct gtc    883
Pro Leu Ala His Val Leu Ala Arg Ala Val His Leu Ala Phe Ala Val
                250                 255                 260

acc ggt gca acc cag tcc cac tgg tct gat ttc agc acc ctt act ttg    931
Thr Gly Ala Thr Gln Ser His Trp Ser Asp Phe Ser Thr Leu Thr Leu
            265                 270                 275

gaa ctg cag cgt tcc cgc ccg aac ctg att ttg ggt gtt cca cgc gtg    979
Glu Leu Gln Arg Ser Arg Pro Asn Leu Ile Leu Gly Val Pro Arg Val
        280                 285                 290

ttt gaa aag gtc cgc aac gcc gct gct gct aat gct gct gac ggt ggc    1027
Phe Glu Lys Val Arg Asn Ala Ala Ala Ala Asn Ala Ala Asp Gly Gly
    295                 300                 305

gca atc aag cgc atc atg ttt gag cgt gcc gaa aag gcg gcc att gaa    1075
Ala Ile Lys Arg Ile Met Phe Glu Arg Ala Glu Lys Ala Ala Ile Glu
310                 315                 320                 325
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tac tcc atg gct ctt gat act gca gaa ggc cca agc aag tcc cag gtt 1123
Tyr Ser Met Ala Leu Asp Thr Ala Glu Gly Pro Ser Lys Ser Gln Val
330 335 340

atg gca cat aaa gcg ttt gac aag ctg gtg tac tcc aag atc cgt gca 1171
Met Ala His Lys Ala Phe Asp Lys Leu Val Tyr Ser Lys Ile Arg Ala
345 350 355

gct gtc ggt ggc gat gtg cag tac gcc atc acc ggt ggt tca gcg atg 1219
Ala Val Gly Gly Asp Val Gln Tyr Ala Ile Thr Gly Gly Ser Ala Met
360 365 370

ggg cag gag ctg ctg cac ttc ttc cgc ggt gtg ggc atg acc atc tac 1267
Gly Gln Glu Leu Leu His Phe Phe Arg Gly Val Gly Met Thr Ile Tyr
375 380 385

gaa ggt tat ggt ctg acg gaa tct gcg gct gct gca gcg gtg gac ttc 1315
Glu Gly Tyr Gly Leu Thr Glu Ser Ala Ala Ala Ala Ala Val Asp Phe
390 395 400 405

act gat caa aag atc ggc act gtg ggt aag ccg atg ggt ggc atg acc 1363
Thr Asp Gln Lys Ile Gly Thr Val Gly Lys Pro Met Gly Gly Met Thr
410 415 420

atc aag atc aat gaa gat ggc gaa atc atg cta aaa ggc gag atg ttg 1411
Ile Lys Ile Asn Glu Asp Gly Glu Ile Met Leu Lys Gly Glu Met Leu
425 430 435

ttc cag gga tat tgg aac aac cca gaa gcc aca gca gaa gcc ctc cac 1459
Phe Gln Gly Tyr Trp Asn Asn Pro Glu Ala Thr Ala Glu Ala Leu His
440 445 450

gac ggt tgg ttc aac acc ggc gat ctg ggt gag ctg ttg gag tct gga 1507
Asp Gly Trp Phe Asn Thr Gly Asp Leu Gly Glu Leu Leu Glu Ser Gly
455 460 465

cac ctg gtg atc acc gga cgt aag aaa gat ctg atc gtg acc gcg ggc 1555
His Leu Val Ile Thr Gly Arg Lys Lys Asp Leu Ile Val Thr Ala Gly
470 475 480 485

ggc aag aac gtt tcc cca gga ccc atg gaa gac atc atc cgc gca cac 1603
Gly Lys Asn Val Ser Pro Gly Pro Met Glu Asp Ile Ile Arg Ala His
490 495 500

cca ctg gtc agc cag gcc atg gtg gtg ggc gat ggt aaa cca ttc gtt 1651
Pro Leu Val Ser Gln Ala Met Val Val Gly Asp Gly Lys Pro Phe Val
505 510 515

ggc ctg ctg gtg acc ttg gat cca gat atg ttg aag cgg tgg aag ctg 1699
Gly Leu Leu Val Thr Leu Asp Pro Asp Met Leu Lys Arg Trp Lys Leu
520 525 530

aac cac aac att gcg gaa tcc cgc acg gtt tct gag att gct act gat 1747
Asn His Asn Ile Ala Glu Ser Arg Thr Val Ser Glu Ile Ala Thr Asp
535 540 545

cct gca ctg cgt gcg gaa atc cag gat gca gtc aac aac gct aat gcc 1795
Pro Ala Leu Arg Ala Glu Ile Gln Asp Ala Val Asn Asn Ala Asn Ala
550 555 560 565

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acg gtg tct cat tca gag gcg atc aag cgg ttc tac atc ctt gat cgc    1843
Thr Val Ser His Ser Glu Ala Ile Lys Arg Phe Tyr Ile Leu Asp Arg
                570                 575                 580

gac ctg acc gag gaa gcc gac gag ctg acc cca acg ctg aag gtc aag    1891
Asp Leu Thr Glu Glu Ala Asp Glu Leu Thr Pro Thr Leu Lys Val Lys
            585                 590                 595

cgc aac gtt gtt gtt cgc cgt tac gca gac gcc atc gac cac atc tac    1939
Arg Asn Val Val Val Arg Arg Tyr Ala Asp Ala Ile Asp His Ile Tyr
        600                 605                 610

aac cga tgagtaacac agagacccaa ttt                                  1968
Asn Arg
    615


&lt;210&gt; 60
&lt;211&gt; 615
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 60
Met Thr Ser Pro Asn Thr Leu Gln Glu Tyr Thr Glu Pro Ala Lys Tyr
  1               5                  10                  15

Thr Ile Gly Glu Ser Glu Thr Cys Leu Thr Ala Leu Leu Asp Gln Ile
             20                  25                  30

Lys Thr Arg Pro Tyr Gly Val Leu Phe Ser Lys Pro Ala Asn Tyr Glu
         35                  40                  45

Trp Val Asn Val Thr Ala Lys Glu Phe Gln Asp Glu Val Phe Ala Val
     50                  55                  60

Ala Lys Gly Ile Ile Ser Val Gly Val Glu Gln Gly Asp Arg Val Ala
 65                  70                  75                  80

Leu Leu Ser Asn Thr Arg Tyr Glu Trp Ala Val Leu Asp Phe Ala Ile
                 85                  90                  95

Trp Ala Ala Gly Ala Val Ser Val Pro Ile Tyr Ser Ser Ser Ser Leu
            100                 105                 110

Ser Gln Ile Glu Trp Ile Ile Glu Asp Ser Gly Ala Val Leu Ala Ile
        115                 120                 125

Thr Glu Thr Pro Asp His Thr Asp Leu Met Lys Asn Leu Val Ile Gly
    130                 135                 140

Glu Asp Gly Thr Pro Ala Ile Lys Gly Ser Pro Ser Lys Leu Arg Arg
145                 150                 155                 160

Ile Leu Glu Ile Asn Ser Ser Ala Leu Glu Thr Leu Lys Phe Glu Gly
                165                 170                 175

Arg Glu Leu Ser Asp Glu Leu Val Trp Glu Arg Ile His Ala Thr Lys
            180                 185                 190

Ala Ala Asp Leu Ala Ser Leu Val Tyr Thr Ser Gly Thr Thr Gly Arg
        195                 200                 205
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Pro Lys Gly Cys Glu Leu Ser His Tyr His Trp Leu Ala Glu Val Arg
    210                 215                 220

Ala Leu Ile Thr Asn Asp Ile Gly Ala Ile Ala Met Pro Gly Ser Arg
225                 230                 235                 240

Leu Leu Thr Phe Leu Pro Leu Ala His Val Leu Ala Arg Ala Val His
                245                 250                 255

Leu Ala Phe Ala Val Thr Gly Ala Thr Gln Ser His Trp Ser Asp Phe
            260                 265                 270

Ser Thr Leu Thr Leu Glu Leu Gln Arg Ser Arg Pro Asn Leu Ile Leu
        275                 280                 285

Gly Val Pro Arg Val Phe Glu Lys Val Arg Asn Ala Ala Ala Ala Asn
    290                 295                 300

Ala Ala Asp Gly Gly Ala Ile Lys Arg Ile Met Phe Glu Arg Ala Glu
305                 310                 315                 320

Lys Ala Ala Ile Glu Tyr Ser Met Ala Leu Asp Thr Ala Glu Gly Pro
                325                 330                 335

Ser Lys Ser Gln Val Met Ala His Lys Ala Phe Asp Lys Leu Val Tyr
            340                 345                 350

Ser Lys Ile Arg Ala Ala Val Gly Gly Asp Val Gln Tyr Ala Ile Thr
        355                 360                 365

Gly Gly Ser Ala Met Gly Gln Glu Leu Leu His Phe Phe Arg Gly Val
    370                 375                 380

Gly Met Thr Ile Tyr Glu Gly Tyr Gly Leu Thr Glu Ser Ala Ala Ala
385                 390                 395                 400

Ala Ala Val Asp Phe Thr Asp Gln Lys Ile Gly Thr Val Gly Lys Pro
                405                 410                 415

Met Gly Gly Met Thr Ile Lys Ile Asn Glu Asp Gly Glu Ile Met Leu
            420                 425                 430

Lys Gly Glu Met Leu Phe Gln Gly Tyr Trp Asn Asn Pro Glu Ala Thr
        435                 440                 445

Ala Glu Ala Leu His Asp Gly Trp Phe Asn Thr Gly Asp Leu Gly Glu
    450                 455                 460

Leu Leu Glu Ser Gly His Leu Val Ile Thr Gly Arg Lys Lys Asp Leu
465                 470                 475                 480

Ile Val Thr Ala Gly Gly Lys Asn Val Ser Pro Gly Pro Met Glu Asp
                485                 490                 495

Ile Ile Arg Ala His Pro Leu Val Ser Gln Ala Met Val Val Gly Asp
            500                 505                 510

Gly Lys Pro Phe Val Gly Leu Leu Val Thr Leu Asp Pro Asp Met Leu
        515                 520                 525
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Lys Arg Trp Lys Leu Asn His Asn Ile Ala Glu Ser Arg Thr Val Ser
    530                 535                 540

Glu Ile Ala Thr Asp Pro Ala Leu Arg Ala Glu Ile Gln Asp Ala Val
545                 550                 555                 560

Asn Asn Ala Asn Ala Thr Val Ser His Ser Glu Ala Ile Lys Arg Phe
                565                 570                 575

Tyr Ile Leu Asp Arg Asp Leu Thr Glu Glu Ala Asp Glu Leu Thr Pro
            580                 585                 590

Thr Leu Lys Val Lys Arg Asn Val Val Val Arg Arg Tyr Ala Asp Ala
        595                 600                 605

Ile Asp His Ile Tyr Asn Arg
    610                 615


<210> 61
<211> 1047
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1024)
<223> RXA01060

<400> 61
ttccatttac acatctgttc gactcgcgcc cgaatgatgt cgcatcaaca tgagaagcta 60

cttccatact tttactgatt gataagaatg gacaaagaca atg aac cgc aca ctc    115
                                          Met Asn Arg Thr Leu
                                           1               5

cga aca ctt ggc tgg ctt gct gcc gta att caa gaa gat ccg gag ccc    163
Arg Thr Leu Gly Trp Leu Ala Ala Val Ile Gln Glu Asp Pro Glu Pro
                10                  15                  20

tgg ttc acc act gat ccc gac acc gat tat gtc cct tat gta aat agt    211
Trp Phe Thr Thr Asp Pro Asp Thr Asp Tyr Val Pro Tyr Val Asn Ser
            25                  30                  35

ttc tca ttt gaa tcc ctt tcc ctc gtt cca gat gct ctg atg ctg ctc    259
Phe Ser Phe Glu Ser Leu Ser Leu Val Pro Asp Ala Leu Met Leu Leu
        40                  45                  50

aaa cgt tct ctt cac ctt gcg atg gag caa cag gac ctc cca gtg aag    307
Lys Arg Ser Leu His Leu Ala Met Glu Gln Gln Asp Leu Pro Val Lys
    55                  60                  65

gat cta caa gaa gca ctg agg cac gta cta gtt ttc aaa ttc cac ttc    355
Asp Leu Gln Glu Ala Leu Arg His Val Leu Val Phe Lys Phe His Phe
70                  75                  80                  85

agg gaa gaa tgg gag ctg gaa tta gca tgg gac tcc gag cgg acc aag    403
Arg Glu Glu Trp Glu Leu Glu Leu Ala Trp Asp Ser Glu Arg Thr Lys
                90                  95                  100

tct gcg gtg aga att att gag agc aca aaa gaa tct ctt gcc gat caa    451
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Ser Ala Val Arg Ile Ile Glu Ser Thr Lys Glu Ser Leu Ala Asp Gln
            105                 110                 115

tac aga gat tac aaa tac gca ttc ttg cct gag cta att ttc cag gaa     499
Tyr Arg Asp Tyr Lys Tyr Ala Phe Leu Pro Glu Leu Ile Phe Gln Glu
        120                 125                 130

tca cgc ggg atc ttt gac ttt gag ctg gag gga tac acc ctc aaa gta     547
Ser Arg Gly Ile Phe Asp Phe Glu Leu Glu Gly Tyr Thr Leu Lys Val
    135                 140                 145

gga caa agc acg ctt tcc att cct tgg gac atg atc gcc aat ggt tat     595
Gly Gln Ser Thr Leu Ser Ile Pro Trp Asp Met Ile Ala Asn Gly Tyr
150                 155                 160                 165

gtc cct gca agt ctt cgg aat ttt gga gaa tta atg gac cgt gac acc     643
Val Pro Ala Ser Leu Arg Asn Phe Gly Glu Leu Met Asp Arg Asp Thr
                170                 175                 180

gga gat ctt gat gca gat ccc att ctg aga cct cga gaa ctc aaa ttt     691
Gly Asp Leu Asp Ala Asp Pro Ile Leu Arg Pro Arg Glu Leu Lys Phe
            185                 190                 195

gag atc cat aat tgt cca gat ctt aat cct tgg ata atg cgg gaa act     739
Glu Ile His Asn Cys Pro Asp Leu Asn Pro Trp Ile Met Arg Glu Thr
        200                 205                 210

ttt gat ttc atg atg gaa atc gca act gaa aca gga tgg ttc cat gct     787
Phe Asp Phe Met Met Glu Ile Ala Thr Glu Thr Gly Trp Phe His Ala
    215                 220                 225

ctc aac ccc gca tat aat tcc gtc tac acc tac gat ctt att tct cgc     835
Leu Asn Pro Ala Tyr Asn Ser Val Tyr Thr Tyr Asp Leu Ile Ser Arg
230                 235                 240                 245

atg cca gat ttc ctt gtt gaa ggg agc ttt cgt ccg cat tca gtg aaa     883
Met Pro Asp Phe Leu Val Glu Gly Ser Phe Arg Pro His Ser Val Lys
                250                 255                 260

cga tct tgg gaa aaa att caa aag ata gct aaa gct gtt gag tct tat     931
Arg Ser Trp Glu Lys Ile Gln Lys Ile Ala Lys Ala Val Glu Ser Tyr
            265                 270                 275

gca tct cac gat tac tgc atg tca acg ctg aca cat gac tac agg gca     979
Ala Ser His Asp Tyr Cys Met Ser Thr Leu Thr His Asp Tyr Arg Ala
        280                 285                 290

atc gag tta tcc ctg acg cct aca aaa act gag gaa cca agc aca        1024
Ile Glu Leu Ser Leu Thr Pro Thr Lys Thr Glu Glu Pro Ser Thr
    295                 300                 305

taagaaaacc tcgcctgccc act                                          1047


<210> 62
<211> 308
<212> PRT
<213> Corynebacterium glutamicum

<400> 62
Met Asn Arg Thr Leu Arg Thr Leu Gly Trp Leu Ala Ala Val Ile Gln
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1 5 10 15

Glu Asp Pro Glu Pro Trp Phe Thr Thr Asp Pro Asp Thr Asp Tyr Val
20 25 30

Pro Tyr Val Asn Ser Phe Ser Phe Glu Ser Leu Ser Leu Val Pro Asp
35 40 45

Ala Leu Met Leu Leu Lys Arg Ser Leu His Leu Ala Met Glu Gln Gln
50 55 60

Asp Leu Pro Val Lys Asp Leu Gln Glu Ala Leu Arg His Val Leu Val
65 70 75 80

Phe Lys Phe His Phe Arg Glu Glu Trp Glu Leu Glu Leu Ala Trp Asp
85 90 95

Ser Glu Arg Thr Lys Ser Ala Val Arg Ile Ile Glu Ser Thr Lys Glu
100 105 110

Ser Leu Ala Asp Gln Tyr Arg Asp Tyr Lys Tyr Ala Phe Leu Pro Glu
115 120 125

Leu Ile Phe Gln Glu Ser Arg Gly Ile Phe Asp Phe Glu Leu Glu Gly
130 135 140

Tyr Thr Leu Lys Val Gly Gln Ser Thr Leu Ser Ile Pro Trp Asp Met
145 150 155 160

Ile Ala Asn Gly Tyr Val Pro Ala Ser Leu Arg Asn Phe Gly Glu Leu
165 170 175

Met Asp Arg Asp Thr Gly Asp Leu Asp Ala Asp Pro Ile Leu Arg Pro
180 185 190

Arg Glu Leu Lys Phe Glu Ile His Asn Cys Pro Asp Leu Asn Pro Trp
195 200 205

Ile Met Arg Glu Thr Phe Asp Phe Met Met Glu Ile Ala Thr Glu Thr
210 215 220

Gly Trp Phe His Ala Leu Asn Pro Ala Tyr Asn Ser Val Tyr Thr Tyr
225 230 235 240

Asp Leu Ile Ser Arg Met Pro Asp Phe Leu Val Glu Gly Ser Phe Arg
245 250 255

Pro His Ser Val Lys Arg Ser Trp Glu Lys Ile Gln Lys Ile Ala Lys
260 265 270

Ala Val Glu Ser Tyr Ala Ser His Asp Tyr Cys Met Ser Thr Leu Thr
275 280 285

His Asp Tyr Arg Ala Ile Glu Leu Ser Leu Thr Pro Thr Lys Thr Glu
290 295 300

Glu Pro Ser Thr
305

<210> 63

<211> 1848
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1825)
<223> RXN01722

<400> 63
ctcattcccc tcgctaaaag ctgcataaag tttcgacgtt ttcaaagttg attgcttgca 60

ctgtcgttgc gtgtcgcatg ccccggctat tgttgattgc atg ctc agc acg atg 115
Met Leu Ser Thr Met
1 5

cag gac gtc cca ctg tca tta acc aga atc ctc gag tac ggg tcc act 163
Gln Asp Val Pro Leu Ser Leu Thr Arg Ile Leu Glu Tyr Gly Ser Thr
10 15 20

gtt cac ggt gat act ttg atc acc acg tgg ggc ggt gcc gat ggc att 211
Val His Gly Asp Thr Leu Ile Thr Thr Trp Gly Gly Ala Asp Gly Ile
25 30 35

gaa caa gca cag caa act ttt agt gct gtg ggg gct aga gct gcg gct 259
Glu Gln Ala Gln Gln Thr Phe Ser Ala Val Gly Ala Arg Ala Ala Ala
40 45 50

ttg gct cat gcg ctg cat gat tct tta ggt att act ggg gat cag cga 307
Leu Ala His Ala Leu His Asp Ser Leu Gly Ile Thr Gly Asp Gln Arg
55 60 65

gtg gcg tcg atg ctc tat aac tgc gcg gaa cac atg gaa act atg ttt 355
Val Ala Ser Met Leu Tyr Asn Cys Ala Glu His Met Glu Thr Met Phe
70 75 80 85

gca gtc gca tgc atg ggt gcc gtg ttt aat ccg ctg aac aag cag ttg 403
Ala Val Ala Cys Met Gly Ala Val Phe Asn Pro Leu Asn Lys Gln Leu
90 95 100

atg aat gat cag att gtg ttc att ctc aat cac tct gaa gct gaa gtg 451
Met Asn Asp Gln Ile Val Phe Ile Leu Asn His Ser Glu Ala Glu Val
105 110 115

gtt atc gct gat ccg cgc atg gct gaa caa ttg ggt gag atc tta aaa 499
Val Ile Ala Asp Pro Arg Met Ala Glu Gln Leu Gly Glu Ile Leu Lys
120 125 130

gaa aca cca aaa gtt cgt gcc gtg gtg ttt att gga ccg aat gat ttc 547
Glu Thr Pro Lys Val Arg Ala Val Val Phe Ile Gly Pro Asn Asp Phe
135 140 145

tct agc gcg gcg gcc cac atg ccg gag gga atg aag ctg tat tcc tat 595
Ser Ser Ala Ala Ala His Met Pro Glu Gly Met Lys Leu Tyr Ser Tyr
150 155 160 165

gaa gcg ctc ctt gac ggc cgt tcc act gtt tac aac tgg ccc gag cag 643
Glu Ala Leu Leu Asp Gly Arg Ser Thr Val Tyr Asn Trp Pro Glu Gln
170 175 180

gat gaa cgc act gct gct gca att tgc tat tcc acc ggt aca tcg gga 691

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Asp Glu Arg Thr Ala Ala Ala Ile Cys Tyr Ser Thr Gly Thr Ser Gly
            185                 190                 195

ccg ccg aag ggt gtg gtg tat tcc cac cgc tcg ctt tat tta cag tcg    739
Pro Pro Lys Gly Val Val Tyr Ser His Arg Ser Leu Tyr Leu Gln Ser
        200                 205                 210

ttg agc ttg cgc acc acg gat tcc ctc gca gtg gaa cac ggc gaa acg    787
Leu Ser Leu Arg Thr Thr Asp Ser Leu Ala Val Glu His Gly Glu Thr
    215                 220                 225

ttc ctg tgc tgt gtg ccg att tac cac gtc ctc agc tgg ggc gtg ccg    835
Phe Leu Cys Cys Val Pro Ile Tyr His Val Leu Ser Trp Gly Val Pro
230                 235                 240                 245

atc gca gcg ttt atg tcc ggc act ccc ctg gtg ctt cct gga ccg gat    883
Ile Ala Ala Phe Met Ser Gly Thr Pro Leu Val Leu Pro Gly Pro Asp
                250                 255                 260

ctt tct gcg ccg aca ttg gca aag atc att tcc acc acg ctg cct cgc    931
Leu Ser Ala Pro Thr Leu Ala Lys Ile Ile Ser Thr Thr Leu Pro Arg
            265                 270                 275

gtg gcg cat ggc gtg cct act ctc tgg att cag ctg atg gtt cac tac    979
Val Ala His Gly Val Pro Thr Leu Trp Ile Gln Leu Met Val His Tyr
        280                 285                 290

ctg aaa aat ccc cca gag cgt atg tct ctg cgt gag cta tac gtg ggc    1027
Leu Lys Asn Pro Pro Glu Arg Met Ser Leu Arg Glu Leu Tyr Val Gly
    295                 300                 305

ggt tct gcg gtg cct cca atc gtg atc acc atg tgg gag cag cgc tat    1075
Gly Ser Ala Val Pro Pro Ile Val Ile Thr Met Trp Glu Gln Arg Tyr
310                 315                 320                 325

ggc gtg gat gtt gtc cac gtg tgg ggt atg acg gaa acc tcc acc gtg    1123
Gly Val Asp Val Val His Val Trp Gly Met Thr Glu Thr Ser Thr Val
                330                 335                 340

ggt act gtg tct cgc cca cca tca ggt gtt tct ggt gaa agc cgg tgg    1171
Gly Thr Val Ser Arg Pro Pro Ser Gly Val Ser Gly Glu Ser Arg Trp
            345                 350                 355

aat tat cga gtc tcc cag ggc cga ttc ccc gcc tcc ctg cag tac cgc    1219
Asn Tyr Arg Val Ser Gln Gly Arg Phe Pro Ala Ser Leu Gln Tyr Arg
        360                 365                 370

att gtc aac gac ggc cag gtc atg gcg tcc acc gac cgc aac gag ggc    1267
Ile Val Asn Asp Gly Gln Val Met Ala Ser Thr Asp Arg Asn Glu Gly
    375                 380                 385

gag att cag gtc cgc ggt ccg tgg gtg act gca agt tac ttc cac ccc    1315
Glu Ile Gln Val Arg Gly Pro Trp Val Thr Ala Ser Tyr Phe His Pro
390                 395                 400                 405

gat gtg gaa aaa gaa ggt ggc acc gcc tca aca ttc cgc gac cat gac    1363
Asp Val Glu Lys Glu Gly Gly Thr Ala Ser Thr Phe Arg Asp His Asp
                410                 415                 420

gtt gaa gag gaa aac gat gag ctc ttc acc gcc gac ggc tgg ctg cgc    1411
Val Glu Glu Glu Asn Asp Glu Leu Phe Thr Ala Asp Gly Trp Leu Arg
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            425                 430                 435

acc ggg gac gtt gga tct gtc acc agc gat gga ttc ctc acc atc caa     1459
Thr Gly Asp Val Gly Ser Val Thr Ser Asp Gly Phe Leu Thr Ile Gln
        440                 445                 450

gac cgc gcc cgc gat gtc atc cgt tct ggc ggc gag tgg att tac tcc     1507
Asp Arg Ala Arg Asp Val Ile Arg Ser Gly Gly Glu Trp Ile Tyr Ser
    455                 460                 465

gct cag ctg gaa aac ctc atc gtg gct acg gaa gag gtt gtc gaa tgc     1555
Ala Gln Leu Glu Asn Leu Ile Val Ala Thr Glu Glu Val Val Glu Cys
470                 475                 480                 485

gcc gtc att ggc ttc ccc gat gac aag tgg gtg gaa cgt ccc ctc gca     1603
Ala Val Ile Gly Phe Pro Asp Asp Lys Trp Val Glu Arg Pro Leu Ala
                490                 495                 500

gtc acc atg ctc tac ccc ggc att gaa cgc acc cgg gaa acc gcc gag     1651
Val Thr Met Leu Tyr Pro Gly Ile Glu Arg Thr Arg Glu Thr Ala Glu
            505                 510                 515

cgc ctc cgc gat caa ctt cgc gac cgc cta ccc aac tgg atg ctg cca     1699
Arg Leu Arg Asp Gln Leu Arg Asp Arg Leu Pro Asn Trp Met Leu Pro
        520                 525                 530

gaa tat tgg aca ttt gtt gat gag gtg gat aaa acc tcc gtc ggt aaa     1747
Glu Tyr Trp Thr Phe Val Asp Glu Val Asp Lys Thr Ser Val Gly Lys
    535                 540                 545

tat gac aag aag gac ctc cgc aac cac ctg cgc aac ggc gat ttc gaa     1795
Tyr Asp Lys Lys Asp Leu Arg Asn His Leu Arg Asn Gly Asp Phe Glu
550                 555                 560                 565

gta att aag ctt aaa ggg cca ggt gaa aaa taacttccct atttattccg       1845
Val Ile Lys Leu Lys Gly Pro Gly Glu Lys
                570                 575

gct                                                                 1848


<210> 64
<211> 575
<212> PRT
<213> Corynebacterium glutamicum

<400> 64
Met Leu Ser Thr Met Gln Asp Val Pro Leu Ser Leu Thr Arg Ile Leu
  1               5                  10                  15

Glu Tyr Gly Ser Thr Val His Gly Asp Thr Leu Ile Thr Thr Trp Gly
            20                  25                  30

Gly Ala Asp Gly Ile Glu Gln Ala Gln Gln Thr Phe Ser Ala Val Gly
        35                  40                  45

Ala Arg Ala Ala Ala Leu Ala His Ala Leu His Asp Ser Leu Gly Ile
    50                  55                  60

Thr Gly Asp Gln Arg Val Ala Ser Met Leu Tyr Asn Cys Ala Glu His
 65                  70                  75                  80
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Met Glu Thr Met Phe Ala Val Ala Cys Met Gly Ala Val Phe Asn Pro
85 90 95

Leu Asn Lys Gln Leu Met Asn Asp Gln Ile Val Phe Ile Leu Asn His
100 105 110

Ser Glu Ala Glu Val Val Ile Ala Asp Pro Arg Met Ala Glu Gln Leu
115 120 125

Gly Glu Ile Leu Lys Glu Thr Pro Lys Val Arg Ala Val Val Phe Ile
130 135 140

Gly Pro Asn Asp Phe Ser Ser Ala Ala Ala His Met Pro Glu Gly Met
145 150 155 160

Lys Leu Tyr Ser Tyr Glu Ala Leu Leu Asp Gly Arg Ser Thr Val Tyr
165 170 175

Asn Trp Pro Glu Gln Asp Glu Arg Thr Ala Ala Ala Ile Cys Tyr Ser
180 185 190

Thr Gly Thr Ser Gly Pro Pro Lys Gly Val Val Tyr Ser His Arg Ser
195 200 205

Leu Tyr Leu Gln Ser Leu Ser Leu Arg Thr Thr Asp Ser Leu Ala Val
210 215 220

Glu His Gly Glu Thr Phe Leu Cys Cys Val Pro Ile Tyr His Val Leu
225 230 235 240

Ser Trp Gly Val Pro Ile Ala Ala Phe Met Ser Gly Thr Pro Leu Val
245 250 255

Leu Pro Gly Pro Asp Leu Ser Ala Pro Thr Leu Ala Lys Ile Ile Ser
260 265 270

Thr Thr Leu Pro Arg Val Ala His Gly Val Pro Thr Leu Trp Ile Gln
275 280 285

Leu Met Val His Tyr Leu Lys Asn Pro Pro Glu Arg Met Ser Leu Arg
290 295 300

Glu Leu Tyr Val Gly Gly Ser Ala Val Pro Pro Ile Val Ile Thr Met
305 310 315 320

Trp Glu Gln Arg Tyr Gly Val Asp Val Val His Val Trp Gly Met Thr
325 330 335

Glu Thr Ser Thr Val Gly Thr Val Ser Arg Pro Pro Ser Gly Val Ser
340 345 350

Gly Glu Ser Arg Trp Asn Tyr Arg Val Ser Gln Gly Arg Phe Pro Ala
355 360 365

Ser Leu Gln Tyr Arg Ile Val Asn Asp Gly Gln Val Met Ala Ser Thr
370 375 380

Asp Arg Asn Glu Gly Glu Ile Gln Val Arg Gly Pro Trp Val Thr Ala
385 390 395 400

Ser Tyr Phe His Pro Asp Val Glu Lys Glu Gly Gly Thr Ala Ser Thr
405 410 415

Phe Arg Asp His Asp Val Glu Glu Glu Asn Asp Glu Leu Phe Thr Ala
420 425 430

Asp Gly Trp Leu Arg Thr Gly Asp Val Gly Ser Val Thr Ser Asp Gly
435 440 445

Phe Leu Thr Ile Gln Asp Arg Ala Arg Asp Val Ile Arg Ser Gly Gly
450 455 460

Glu Trp Ile Tyr Ser Ala Gln Leu Glu Asn Leu Ile Val Ala Thr Glu
465 470 475 480

Glu Val Val Glu Cys Ala Val Ile Gly Phe Pro Asp Asp Lys Trp Val
485 490 495

Glu Arg Pro Leu Ala Val Thr Met Leu Tyr Pro Gly Ile Glu Arg Thr
500 505 510

Arg Glu Thr Ala Glu Arg Leu Arg Asp Gln Leu Arg Asp Arg Leu Pro
515 520 525

Asn Trp Met Leu Pro Glu Tyr Trp Thr Phe Val Asp Glu Val Asp Lys
530 535 540

Thr Ser Val Gly Lys Tyr Asp Lys Lys Asp Leu Arg Asn His Leu Arg
545 550 555 560

Asn Gly Asp Phe Glu Val Ile Lys Leu Lys Gly Pro Gly Glu Lys
565 570 575

<210> 65
<211> 1848
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1825)
<223> FRXA01722

<400> 65
ctcattcccc tcgctaaaag ctgcataaag tttcgacgtt ttcaaagttg attgcttgca 60

ctgtcgttgc gtgtcgcatg ccccggctat tgttgattgc atg ctc agc acg atg 115
Met Leu Ser Thr Met
1 5

cag gac gtc cca ctg tca tta acc aga atc ctc gag tac ggg tcc act 163
Gln Asp Val Pro Leu Ser Leu Thr Arg Ile Leu Glu Tyr Gly Ser Thr
10 15 20

gtt cac ggt gat act ttg atc acc acg tgg ggc ggt gcc gat ggc att 211
Val His Gly Asp Thr Leu Ile Thr Thr Trp Gly Gly Ala Asp Gly Ile
25 30 35

gaa caa gca cag caa act ttt agt gct gtg ggg gct aga gct gcg gct 259
Glu Gln Ala Gln Gln Thr Phe Ser Ala Val Gly Ala Arg Ala Ala Ala

```
        40                   45                   50

ttg gct cat gcg ctg cat gat tct tta ggt att act ggg gat cag cga    307
Leu Ala His Ala Leu His Asp Ser Leu Gly Ile Thr Gly Asp Gln Arg
     55                  60                  65

gtg gcg tcg atg ctc tat aac tgc gcg gaa cac atg gaa act atg ttt    355
Val Ala Ser Met Leu Tyr Asn Cys Ala Glu His Met Glu Thr Met Phe
 70                  75                  80                  85

gca gtc gca tgc atg ggt gcc gtg ttt aat ccg ctg aac aag cag ttg    403
Ala Val Ala Cys Met Gly Ala Val Phe Asn Pro Leu Asn Lys Gln Leu
                 90                  95                 100

atg aat gat cag att gtg ttc att ctc aat cac tct gaa gct gaa gtg    451
Met Asn Asp Gln Ile Val Phe Ile Leu Asn His Ser Glu Ala Glu Val
            105                 110                 115

gtt atc gct gat ccg cgc atg gct gaa caa ttg ggt gag atc tta aaa    499
Val Ile Ala Asp Pro Arg Met Ala Glu Gln Leu Gly Glu Ile Leu Lys
        120                 125                 130

gaa aca cca aaa gtt cgt gcc gtg gtg ttt att gga ccg aat gat ttc    547
Glu Thr Pro Lys Val Arg Ala Val Val Phe Ile Gly Pro Asn Asp Phe
    135                 140                 145

tct agc gcg gcg gcc cac atg ccg gag gga atg aag ctg tat tcc tat    595
Ser Ser Ala Ala Ala His Met Pro Glu Gly Met Lys Leu Tyr Ser Tyr
150                 155                 160                 165

gaa gcg ctc ctt gac ggc cgt tcc act gtt tac aac tgg ccc gag cag    643
Glu Ala Leu Leu Asp Gly Arg Ser Thr Val Tyr Asn Trp Pro Glu Gln
                170                 175                 180

gat gaa cgc act gct gct gca att tgc tat tcc acc ggt aca tcg gga    691
Asp Glu Arg Thr Ala Ala Ala Ile Cys Tyr Ser Thr Gly Thr Ser Gly
            185                 190                 195

ccg ccg aag ggt gtg gtg tat tcc cac cgc tcg ctt tat tta cag tcg    739
Pro Pro Lys Gly Val Val Tyr Ser His Arg Ser Leu Tyr Leu Gln Ser
        200                 205                 210

ttg agc ttg cgc acc acg gat tcc ctc gca gtg gaa cac ggc gaa acg    787
Leu Ser Leu Arg Thr Thr Asp Ser Leu Ala Val Glu His Gly Glu Thr
    215                 220                 225

ttc ctg tgc tgt gtg ccg att tac cac gtc ctc agc tgg ggc gtg ccg    835
Phe Leu Cys Cys Val Pro Ile Tyr His Val Leu Ser Trp Gly Val Pro
230                 235                 240                 245

atc gca gcg ttt atg tcc ggc act ccc ctg gtg ctt cct gga ccg gat    883
Ile Ala Ala Phe Met Ser Gly Thr Pro Leu Val Leu Pro Gly Pro Asp
                250                 255                 260

ctt tct gcg ccg aca ttg gca aag atc att tcc acc acg ctg cct cgc    931
Leu Ser Ala Pro Thr Leu Ala Lys Ile Ile Ser Thr Thr Leu Pro Arg
            265                 270                 275

gtg gcg cat ggc gtg cct act ctc tgg att cag ctg atg gtt cac tac    979
Val Ala His Gly Val Pro Thr Leu Trp Ile Gln Leu Met Val His Tyr
        280                 285                 290
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ctg aaa aat ccc cca gag cgt atg tct ctg cgt gag cta tac gtg ggc 1027
Leu Lys Asn Pro Pro Glu Arg Met Ser Leu Arg Glu Leu Tyr Val Gly
295 300 305

ggt tct gcg gtg cct cca atc gtg atc acc atg tgg gag cag cgc tat 1075
Gly Ser Ala Val Pro Pro Ile Val Ile Thr Met Trp Glu Gln Arg Tyr
310 315 320 325

ggc gtg gat gtt gtc cac gtg tgg ggt atg acg gaa acc tcc acc gtg 1123
Gly Val Asp Val Val His Val Trp Gly Met Thr Glu Thr Ser Thr Val
330 335 340

ggt act gtg tct cgc cca cca tca ggt gtt tct ggt gaa agc cgg tgg 1171
Gly Thr Val Ser Arg Pro Pro Ser Gly Val Ser Gly Glu Ser Arg Trp
345 350 355

aat tat cga gtc tcc cag ggc cga ttc ccc gcc tcc ctg cag tac cgc 1219
Asn Tyr Arg Val Ser Gln Gly Arg Phe Pro Ala Ser Leu Gln Tyr Arg
360 365 370

att gtc aac gac ggc cag gtc atg gcg tcc acc gac cgc aac gag ggc 1267
Ile Val Asn Asp Gly Gln Val Met Ala Ser Thr Asp Arg Asn Glu Gly
375 380 385

gag att cag gtc cgc ggt ccg tgg gtg act gca agt tac ttc cac ccc 1315
Glu Ile Gln Val Arg Gly Pro Trp Val Thr Ala Ser Tyr Phe His Pro
390 395 400 405

gat gtg gaa aaa gaa ggt ggc acc gcc tca aca ttc cgc gac cat gac 1363
Asp Val Glu Lys Glu Gly Gly Thr Ala Ser Thr Phe Arg Asp His Asp
410 415 420

gtt gaa gag gaa aac gat gag ctc ttc acc gcc gac ggc tgg ctg cgc 1411
Val Glu Glu Glu Asn Asp Glu Leu Phe Thr Ala Asp Gly Trp Leu Arg
425 430 435

acc ggg gac gtt gga tct gtc acc agc gat gga ttc ctc acc atc caa 1459
Thr Gly Asp Val Gly Ser Val Thr Ser Asp Gly Phe Leu Thr Ile Gln
440 445 450

gac cgc gcc cgc gat gtc atc cgt tct ggc ggc gag tgg att tac tcc 1507
Asp Arg Ala Arg Asp Val Ile Arg Ser Gly Gly Glu Trp Ile Tyr Ser
455 460 465

gct cag ctg gaa aac ctc atc gtg gct acs gaa gag gtt gtc gaa tgc 1555
Ala Gln Leu Glu Asn Leu Ile Val Ala Xaa Glu Glu Val Val Glu Cys
470 475 480 485

gcc gtc att ggc ttc ccc gat gac aag tgg gtg gaa cgt ccc ctc gca 1603
Ala Val Ile Gly Phe Pro Asp Asp Lys Trp Val Glu Arg Pro Leu Ala
490 495 500

gtc acc atg ctc tac ccc ggc att gaa cgc acc cgg gaa acc gcc gag 1651
Val Thr Met Leu Tyr Pro Gly Ile Glu Arg Thr Arg Glu Thr Ala Glu
505 510 515

cgc ctc cgc gat caa ctt cgc gac cgc cta ccc aac tgg atg ctg cca 1699
Arg Leu Arg Asp Gln Leu Arg Asp Arg Leu Pro Asn Trp Met Leu Pro
520 525 530

gaa tat tgg aca ttt gtt gat gag gtg gat aaa acc tcc gtc ggt aaa 1747
Glu Tyr Trp Thr Phe Val Asp Glu Val Asp Lys Thr Ser Val Gly Lys
535 540 545

tat gac aag aag gac ctc cgc aac cac ctg cgc aac ggc gat ttc gaa 1795
Tyr Asp Lys Lys Asp Leu Arg Asn His Leu Arg Asn Gly Asp Phe Glu
550 555 560 565

gta att aag ctt aaa ggg cca ggt gar aaa taacttccct atttattccg 1845
Val Ile Lys Leu Lys Gly Pro Gly Xaa Lys
570 575

gct 1848

<210> 66
<211> 575
<212> PRT
<213> Corynebacterium glutamicum

<400> 66
Met Leu Ser Thr Met Gln Asp Val Pro Leu Ser Leu Thr Arg Ile Leu
1 5 10 15

Glu Tyr Gly Ser Thr Val His Gly Asp Thr Leu Ile Thr Thr Trp Gly
20 25 30

Gly Ala Asp Gly Ile Glu Gln Ala Gln Gln Thr Phe Ser Ala Val Gly
35 40 45

Ala Arg Ala Ala Ala Leu Ala His Ala Leu His Asp Ser Leu Gly Ile
50 55 60

Thr Gly Asp Gln Arg Val Ala Ser Met Leu Tyr Asn Cys Ala Glu His
65 70 75 80

Met Glu Thr Met Phe Ala Val Ala Cys Met Gly Ala Val Phe Asn Pro
85 90 95

Leu Asn Lys Gln Leu Met Asn Asp Gln Ile Val Phe Ile Leu Asn His
100 105 110

Ser Glu Ala Glu Val Val Ile Ala Asp Pro Arg Met Ala Glu Gln Leu
115 120 125

Gly Glu Ile Leu Lys Glu Thr Pro Lys Val Arg Ala Val Val Phe Ile
130 135 140

Gly Pro Asn Asp Phe Ser Ser Ala Ala Ala His Met Pro Glu Gly Met
145 150 155 160

Lys Leu Tyr Ser Tyr Glu Ala Leu Leu Asp Gly Arg Ser Thr Val Tyr
165 170 175

Asn Trp Pro Glu Gln Asp Glu Arg Thr Ala Ala Ala Ile Cys Tyr Ser
180 185 190

Thr Gly Thr Ser Gly Pro Pro Lys Gly Val Val Tyr Ser His Arg Ser
195 200 205

Leu Tyr Leu Gln Ser Leu Ser Leu Arg Thr Thr Asp Ser Leu Ala Val

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    210                 215                 220

Glu His Gly Glu Thr Phe Leu Cys Cys Val Pro Ile Tyr His Val Leu
225                 230                 235                 240

Ser Trp Gly Val Pro Ile Ala Ala Phe Met Ser Gly Thr Pro Leu Val
                245                 250                 255

Leu Pro Gly Pro Asp Leu Ser Ala Pro Thr Leu Ala Lys Ile Ile Ser
            260                 265                 270

Thr Thr Leu Pro Arg Val Ala His Gly Val Pro Thr Leu Trp Ile Gln
        275                 280                 285

Leu Met Val His Tyr Leu Lys Asn Pro Pro Glu Arg Met Ser Leu Arg
    290                 295                 300

Glu Leu Tyr Val Gly Gly Ser Ala Val Pro Pro Ile Val Ile Thr Met
305                 310                 315                 320

Trp Glu Gln Arg Tyr Gly Val Asp Val Val His Val Trp Gly Met Thr
                325                 330                 335

Glu Thr Ser Thr Val Gly Thr Val Ser Arg Pro Pro Ser Gly Val Ser
            340                 345                 350

Gly Glu Ser Arg Trp Asn Tyr Arg Val Ser Gln Gly Arg Phe Pro Ala
        355                 360                 365

Ser Leu Gln Tyr Arg Ile Val Asn Asp Gly Gln Val Met Ala Ser Thr
    370                 375                 380

Asp Arg Asn Glu Gly Glu Ile Gln Val Arg Gly Pro Trp Val Thr Ala
385                 390                 395                 400

Ser Tyr Phe His Pro Asp Val Glu Lys Glu Gly Gly Thr Ala Ser Thr
                405                 410                 415

Phe Arg Asp His Asp Val Glu Glu Glu Asn Asp Glu Leu Phe Thr Ala
            420                 425                 430

Asp Gly Trp Leu Arg Thr Gly Asp Val Gly Ser Val Thr Ser Asp Gly
        435                 440                 445

Phe Leu Thr Ile Gln Asp Arg Ala Arg Asp Val Ile Arg Ser Gly Gly
    450                 455                 460

Glu Trp Ile Tyr Ser Ala Gln Leu Glu Asn Leu Ile Val Ala Xaa Glu
465                 470                 475                 480

Glu Val Val Glu Cys Ala Val Ile Gly Phe Pro Asp Asp Lys Trp Val
                485                 490                 495

Glu Arg Pro Leu Ala Val Thr Met Leu Tyr Pro Gly Ile Glu Arg Thr
            500                 505                 510

Arg Glu Thr Ala Glu Arg Leu Arg Asp Gln Leu Arg Asp Arg Leu Pro
        515                 520                 525

Asn Trp Met Leu Pro Glu Tyr Trp Thr Phe Val Asp Glu Val Asp Lys
    530                 535                 540
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Thr Ser Val Gly Lys Tyr Asp Lys Lys Asp Leu Arg Asn His Leu Arg
545                 550                 555                 560

Asn Gly Asp Phe Glu Val Ile Lys Leu Lys Gly Pro Gly Xaa Lys
                565                 570                 575


<210> 67
<211> 1401
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1378)
<223> RXA01644

<400> 67
gtaggtagag gcttgtggtc actacttgtg gccacatttt aaaaaaatgc acaagaagag 60

aaagcaaagc attatgagta acgccgtagc gcaggacctc atg acc atc gcc gac    115
                                          Met Thr Ile Ala Asp
                                           1               5

atc gtc gag gcc acg acc act gca ccc atc cca ttc cac atc act gcc    163
Ile Val Glu Ala Thr Thr Thr Ala Pro Ile Pro Phe His Ile Thr Ala
                10                  15                  20

ttc gat gga agc ttc act ggc cct gaa gat gct ccc tac cag ctg ttt    211
Phe Asp Gly Ser Phe Thr Gly Pro Glu Asp Ala Pro Tyr Gln Leu Phe
            25                  30                  35

gtt gcc aac acg gat gca gta tcc tac atc gca aca gcg cca gga gat    259
Val Ala Asn Thr Asp Ala Val Ser Tyr Ile Ala Thr Ala Pro Gly Asp
        40                  45                  50

ttg ggt ttg gca cgt gcc tac ctc atg gga gac ctc atc gtg gaa ggt    307
Leu Gly Leu Ala Arg Ala Tyr Leu Met Gly Asp Leu Ile Val Glu Gly
    55                  60                  65

gag cat ccc ggc cat cct tat ggg atc ttt gat gcg ttg aag gag ttc    355
Glu His Pro Gly His Pro Tyr Gly Ile Phe Asp Ala Leu Lys Glu Phe
70                  75                  80                  85

tac cgc tgc ttc aaa cgc cca gat gca tcc acc acc ttg cag atc atg    403
Tyr Arg Cys Phe Lys Arg Pro Asp Ala Ser Thr Thr Leu Gln Ile Met
                90                  95                  100

tgg act ctg cgg aaa atg aat gcc tta aaa ttc cag gaa att cca cca    451
Trp Thr Leu Arg Lys Met Asn Ala Leu Lys Phe Gln Glu Ile Pro Pro
            105                 110                 115

atg gaa caa gcc cct gca tgg cgt aaa gca ctg atc aac ggg cta gca    499
Met Glu Gln Ala Pro Ala Trp Arg Lys Ala Leu Ile Asn Gly Leu Ala
        120                 125                 130

tcc agg cac tcg aaa tcc cgc gac aag aaa gcc att agc tac cac tac    547
Ser Arg His Ser Lys Ser Arg Asp Lys Lys Ala Ile Ser Tyr His Tyr
    135                 140                 145
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gac gtg ggc aat gag ttc tac tcc ctg ttt tta gat gat tcc atg acc 595
Asp Val Gly Asn Glu Phe Tyr Ser Leu Phe Leu Asp Asp Ser Met Thr
150 155 160 165

tat acc tgc gcg tat tat cca acg cca gaa tca agt ttg gaa gaa gcc 643
Tyr Thr Cys Ala Tyr Tyr Pro Thr Pro Glu Ser Ser Leu Glu Glu Ala
170 175 180

caa gaa aac aaa tac cgc ctc atc ttt gaa aaa ctg cgt ctg aaa gaa 691
Gln Glu Asn Lys Tyr Arg Leu Ile Phe Glu Lys Leu Arg Leu Lys Glu
185 190 195

ggc gat cgc ctc cta gac gtg gga tgc ggt tgg gga ggc atg gtc cgc 739
Gly Asp Arg Leu Leu Asp Val Gly Cys Gly Trp Gly Gly Met Val Arg
200 205 210

tac gcc gcc aaa cac ggt gtg aaa gcc atc gga gtt acg ctg tct gaa 787
Tyr Ala Ala Lys His Gly Val Lys Ala Ile Gly Val Thr Leu Ser Glu
215 220 225

cag caa tat gag tgg ggt caa gca gag atc aaa cgc caa ggt ttg gaa 835
Gln Gln Tyr Glu Trp Gly Gln Ala Glu Ile Lys Arg Gln Gly Leu Glu
230 235 240 245

gac ctc gcg gaa att cgc ttc atg gat tac cgc gat gtt cca gaa act 883
Asp Leu Ala Glu Ile Arg Phe Met Asp Tyr Arg Asp Val Pro Glu Thr
250 255 260

gga ttc gat gcg atc tca gca atc ggc atc att gaa cac atc ggt gtg 931
Gly Phe Asp Ala Ile Ser Ala Ile Gly Ile Ile Glu His Ile Gly Val
265 270 275

aac aac tat ccc gac tac ttt gaa ttg ctc agc agc aaa ctc aaa aca 979
Asn Asn Tyr Pro Asp Tyr Phe Glu Leu Leu Ser Ser Lys Leu Lys Thr
280 285 290

ggc gga ctg atg ctc aac cac agc atc acc tac cca gac aac cgc ccc 1027
Gly Gly Leu Met Leu Asn His Ser Ile Thr Tyr Pro Asp Asn Arg Pro
295 300 305

cgc cac gca ggt gca ttt att gat cgc tac att ttc ccc gac ggt gaa 1075
Arg His Ala Gly Ala Phe Ile Asp Arg Tyr Ile Phe Pro Asp Gly Glu
310 315 320 325

ctc act ggc tct ggc acc ctg atc aag cac atg cag gac aac ggt ttc 1123
Leu Thr Gly Ser Gly Thr Leu Ile Lys His Met Gln Asp Asn Gly Phe
330 335 340

gaa gtg ctg cac gaa gaa aac ctc cgc ttt gat tac caa cgc acc ctg 1171
Glu Val Leu His Glu Glu Asn Leu Arg Phe Asp Tyr Gln Arg Thr Leu
345 350 355

cac gcg tgg tgc gaa aac ctc aaa gaa aat tgg gag gaa gca gtt gaa 1219
His Ala Trp Cys Glu Asn Leu Lys Glu Asn Trp Glu Glu Ala Val Glu
360 365 370

ctc gcc ggt gaa ccc act gca cga ctc ttt ggc ctg tac atg gca ggt 1267
Leu Ala Gly Glu Pro Thr Ala Arg Leu Phe Gly Leu Tyr Met Ala Gly
375 380 385

tcg gaa tgg gga ttt gcc cac aac atc gtc cag ctg cac caa gta ctg 1315

Ser Glu Trp Gly Phe Ala His Asn Ile Val Gln Leu His Gln Val Leu
390 395 400 405

ggt gtg aaa ctc gat gag cag gga agt cgc gga gaa gtt cct gaa aga 1363
Gly Val Lys Leu Asp Glu Gln Gly Ser Arg Gly Glu Val Pro Glu Arg
410 415 420

atg tgg tgg act atc taaagaaaca atgtttcttt tta 1401
Met Trp Trp Thr Ile
425

<210> 68
<211> 426
<212> PRT
<213> Corynebacterium glutamicum

<400> 68
Met Thr Ile Ala Asp Ile Val Glu Ala Thr Thr Thr Ala Pro Ile Pro
1 5 10 15

Phe His Ile Thr Ala Phe Asp Gly Ser Phe Thr Gly Pro Glu Asp Ala
20 25 30

Pro Tyr Gln Leu Phe Val Ala Asn Thr Asp Ala Val Ser Tyr Ile Ala
35 40 45

Thr Ala Pro Gly Asp Leu Gly Leu Ala Arg Ala Tyr Leu Met Gly Asp
50 55 60

Leu Ile Val Glu Gly Glu His Pro Gly His Pro Tyr Gly Ile Phe Asp
65 70 75 80

Ala Leu Lys Glu Phe Tyr Arg Cys Phe Lys Arg Pro Asp Ala Ser Thr
85 90 95

Thr Leu Gln Ile Met Trp Thr Leu Arg Lys Met Asn Ala Leu Lys Phe
100 105 110

Gln Glu Ile Pro Pro Met Glu Gln Ala Pro Ala Trp Arg Lys Ala Leu
115 120 125

Ile Asn Gly Leu Ala Ser Arg His Ser Lys Ser Arg Asp Lys Lys Ala
130 135 140

Ile Ser Tyr His Tyr Asp Val Gly Asn Glu Phe Tyr Ser Leu Phe Leu
145 150 155 160

Asp Asp Ser Met Thr Tyr Thr Cys Ala Tyr Tyr Pro Thr Pro Glu Ser
165 170 175

Ser Leu Glu Glu Ala Gln Glu Asn Lys Tyr Arg Leu Ile Phe Glu Lys
180 185 190

Leu Arg Leu Lys Glu Gly Asp Arg Leu Leu Asp Val Gly Cys Gly Trp
195 200 205

Gly Gly Met Val Arg Tyr Ala Ala Lys His Gly Val Lys Ala Ile Gly
210 215 220

Val Thr Leu Ser Glu Gln Gln Tyr Glu Trp Gly Gln Ala Glu Ile Lys

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225                 230                 235                 240

Arg Gln Gly Leu Glu Asp Leu Ala Glu Ile Arg Phe Met Asp Tyr Arg
                245                 250                 255

Asp Val Pro Glu Thr Gly Phe Asp Ala Ile Ser Ala Ile Gly Ile Ile
            260                 265                 270

Glu His Ile Gly Val Asn Asn Tyr Pro Asp Tyr Phe Glu Leu Leu Ser
        275                 280                 285

Ser Lys Leu Lys Thr Gly Gly Leu Met Leu Asn His Ser Ile Thr Tyr
    290                 295                 300

Pro Asp Asn Arg Pro Arg His Ala Gly Ala Phe Ile Asp Arg Tyr Ile
305                 310                 315                 320

Phe Pro Asp Gly Glu Leu Thr Gly Ser Gly Thr Leu Ile Lys His Met
                325                 330                 335

Gln Asp Asn Gly Phe Glu Val Leu His Glu Glu Asn Leu Arg Phe Asp
            340                 345                 350

Tyr Gln Arg Thr Leu His Ala Trp Cys Glu Asn Leu Lys Glu Asn Trp
        355                 360                 365

Glu Glu Ala Val Glu Leu Ala Gly Glu Pro Thr Ala Arg Leu Phe Gly
    370                 375                 380

Leu Tyr Met Ala Gly Ser Glu Trp Gly Phe Ala His Asn Ile Val Gln
385                 390                 395                 400

Leu His Gln Val Leu Gly Val Lys Leu Asp Glu Gln Gly Ser Arg Gly
                405                 410                 415

Glu Val Pro Glu Arg Met Trp Trp Thr Ile
            420                 425


<210> 69
<211> 1437
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1414)
<223> RXA02029

<400> 69
cgcacgtaca ctacttttag cagttaaccc gccgaacttt cttgattaag tattcattga 60

gcgttcttgg cataaatccc actggaggtg catcaaacgt atg gca gag gca cgt   115
                                          Met Ala Glu Ala Arg
                                          1               5

ttg cgc cat ctt gaa ccc att gat gtg gaa gag tgg cct ggg gtg gcg   163
Leu Arg His Leu Glu Pro Ile Asp Val Glu Glu Trp Pro Gly Val Ala
                10                  15                  20

tca gtg ccc aac cta gcg ttt gct ggt gca cgc gca cgg caa gca gaa   211
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Ser Val Pro Asn Leu Ala Phe Ala Gly Ala Arg Ala Arg Gln Ala Glu
            25                  30                  35

tat cga ttt gcc aag gcc tgc agc aac gca ggt tta gtt ctg cta gga    259
Tyr Arg Phe Ala Lys Ala Cys Ser Asn Ala Gly Leu Val Leu Leu Gly
        40                  45                  50

aat gac ccg gat ctc att att gat cat gag gaa tta ttc tca cgt ttg    307
Asn Asp Pro Asp Leu Ile Ile Asp His Glu Glu Leu Phe Ser Arg Leu
    55                  60                  65

gcc gca tcg ggc tgg ctg ggg ctc gct gag agc tac atg gca ggc gag    355
Ala Ala Ser Gly Trp Leu Gly Leu Ala Glu Ser Tyr Met Ala Gly Glu
70                  75                  80                  85

tgg cgc agc gag agg ctt gcc gac gtc ttg acc gct ttg ttg gga act    403
Trp Arg Ser Glu Arg Leu Ala Asp Val Leu Thr Ala Leu Leu Gly Thr
                90                  95                  100

ggg ttt aaa ccc cgc ggc aaa cta tct gga tcg ttc acc ctg cca ggg    451
Gly Phe Lys Pro Arg Gly Lys Leu Ser Gly Ser Phe Thr Leu Pro Gly
            105                 110                 115

caa gct gtg gat gcc gga ggc gca cta ccc aat gaa ctc att cgt tta    499
Gln Ala Val Asp Ala Gly Gly Ala Leu Pro Asn Glu Leu Ile Arg Leu
        120                 125                 130

agt tca ggt gat ggc atg agc gca ttt ggt gga gtt ttt gcc tcc ggt    547
Ser Ser Gly Asp Gly Met Ser Ala Phe Gly Gly Val Phe Ala Ser Gly
    135                 140                 145

gtt cca acc act tta cgt acc gca gtg aaa agc cat gtg ccg gga gct    595
Val Pro Thr Thr Leu Arg Thr Ala Val Lys Ser His Val Pro Gly Ala
150                 155                 160                 165

ggt cgc aat agg gag ccc gca tct cac ttt gtg gat atc acc aag atc    643
Gly Arg Asn Arg Glu Pro Ala Ser His Phe Val Asp Ile Thr Lys Ile
                170                 175                 180

tcg gag cct gtg gcc gtg gag cgt gaa gac ctc ggc gag gct cag cgc    691
Ser Glu Pro Val Ala Val Glu Arg Glu Asp Leu Gly Glu Ala Gln Arg
            185                 190                 195

cga gca gcg tcc ttt ttg ctt gac ggc gcc aaa gtt aaa gcc gga agc    739
Arg Ala Ala Ser Phe Leu Leu Asp Gly Ala Lys Val Lys Ala Gly Ser
        200                 205                 210

cat gtg ttg gag ttt ccc agc agt ggt gga gct tta gct att ttg gct    787
His Val Leu Glu Phe Pro Ser Ser Gly Gly Ala Leu Ala Ile Leu Ala
    215                 220                 225

gct cga cgc cag gga act gtt gac gct tta acg gct gat ccc gcg caa    835
Ala Arg Arg Gln Gly Thr Val Asp Ala Leu Thr Ala Asp Pro Ala Gln
230                 235                 240                 245

gtt tca agc ctg gag gag acg ttt gtg ctc gcc ggt gtg gag gag gat    883
Val Ser Ser Leu Glu Glu Thr Phe Val Leu Ala Gly Val Glu Glu Asp
                250                 255                 260

att cac atc gag gtc att ccc cag gcg att ccc tcg cca cgc gaa tgg    931
Ile His Ile Glu Val Ile Pro Gln Ala Ile Pro Ser Pro Arg Glu Trp
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265 270 275

ggt ggc gcc tac gat tcg ata gtc gcc atg gag aag cta gaa gtg gtg 979
Gly Gly Ala Tyr Asp Ser Ile Val Ala Met Glu Lys Leu Glu Val Val
280 285 290

ggc aag cac ggt tcc aag cgg ttt att aaa gct atc gac aga atg ctc 1027
Gly Lys His Gly Ser Lys Arg Phe Ile Lys Ala Ile Asp Arg Met Leu
295 300 305

acc acc ggc ggc aac gta gcc atg caa tcc ttg gta gct act gac caa 1075
Thr Thr Gly Gly Asn Val Ala Met Gln Ser Leu Val Ala Thr Asp Gln
310 315 320 325

tgg agt cct gtg tgt tct gaa gcg att tct ttg ctc aag gcc tat att 1123
Trp Ser Pro Val Cys Ser Glu Ala Ile Ser Leu Leu Lys Ala Tyr Ile
330 335 340

tgg cct gcg ctg cat tac cca act gtt gat gaa gtt cat cag ctt gtt 1171
Trp Pro Ala Leu His Tyr Pro Thr Val Asp Glu Val His Gln Leu Val
345 350 355

gat agg gat tct tct ctg cgc gtg gtg aag gaa aca cac ttt gcg ggc 1219
Asp Arg Asp Ser Ser Leu Arg Val Val Lys Glu Thr His Phe Ala Gly
360 365 370

cat tac cta aaa agc gtg cag ttg caa cgt gaa gtg ttt gaa ggc cag 1267
His Tyr Leu Lys Ser Val Gln Leu Gln Arg Glu Val Phe Glu Gly Gln
375 380 385

ata cgc gaa gcg gcg gca gat ggc ttt gat gcc gtc tac cgc cgc atg 1315
Ile Arg Glu Ala Ala Ala Asp Gly Phe Asp Ala Val Tyr Arg Arg Met
390 395 400 405

tgg gtg tat cac tac gcg ctt att gaa gcc ctg tta cgc ctg gga tgt 1363
Trp Val Tyr His Tyr Ala Leu Ile Glu Ala Leu Leu Arg Leu Gly Cys
410 415 420

ctc aat gca gtg caa ttt gcg ttg acg aca aga aac aga agg ggg cgt 1411
Leu Asn Ala Val Gln Phe Ala Leu Thr Thr Arg Asn Arg Arg Gly Arg
425 430 435

cga taagcaaaaa tcttttagac ctc 1437
Arg

<210> 70
<211> 438
<212> PRT
<213> Corynebacterium glutamicum

<400> 70
Met Ala Glu Ala Arg Leu Arg His Leu Glu Pro Ile Asp Val Glu Glu
1 5 10 15

Trp Pro Gly Val Ala Ser Val Pro Asn Leu Ala Phe Ala Gly Ala Arg
20 25 30

Ala Arg Gln Ala Glu Tyr Arg Phe Ala Lys Ala Cys Ser Asn Ala Gly
35 40 45

Leu Val Leu Leu Gly Asn Asp Pro Asp Leu Ile Ile Asp His Glu Glu
50 55 60

Leu Phe Ser Arg Leu Ala Ala Ser Gly Trp Leu Gly Leu Ala Glu Ser
65 70 75 80

Tyr Met Ala Gly Glu Trp Arg Ser Glu Arg Leu Ala Asp Val Leu Thr
85 90 95

Ala Leu Leu Gly Thr Gly Phe Lys Pro Arg Gly Lys Leu Ser Gly Ser
100 105 110

Phe Thr Leu Pro Gly Gln Ala Val Asp Ala Gly Gly Ala Leu Pro Asn
115 120 125

Glu Leu Ile Arg Leu Ser Ser Gly Asp Gly Met Ser Ala Phe Gly Gly
130 135 140

Val Phe Ala Ser Gly Val Pro Thr Thr Leu Arg Thr Ala Val Lys Ser
145 150 155 160

His Val Pro Gly Ala Gly Arg Asn Arg Glu Pro Ala Ser His Phe Val
165 170 175

Asp Ile Thr Lys Ile Ser Glu Pro Val Ala Val Glu Arg Glu Asp Leu
180 185 190

Gly Glu Ala Gln Arg Arg Ala Ala Ser Phe Leu Leu Asp Gly Ala Lys
195 200 205

Val Lys Ala Gly Ser His Val Leu Glu Phe Pro Ser Ser Gly Gly Ala
210 215 220

Leu Ala Ile Leu Ala Ala Arg Arg Gln Gly Thr Val Asp Ala Leu Thr
225 230 235 240

Ala Asp Pro Ala Gln Val Ser Ser Leu Glu Glu Thr Phe Val Leu Ala
245 250 255

Gly Val Glu Glu Asp Ile His Ile Glu Val Ile Pro Gln Ala Ile Pro
260 265 270

Ser Pro Arg Glu Trp Gly Gly Ala Tyr Asp Ser Ile Val Ala Met Glu
275 280 285

Lys Leu Glu Val Val Gly Lys His Gly Ser Lys Arg Phe Ile Lys Ala
290 295 300

Ile Asp Arg Met Leu Thr Thr Gly Gly Asn Val Ala Met Gln Ser Leu
305 310 315 320

Val Ala Thr Asp Gln Trp Ser Pro Val Cys Ser Glu Ala Ile Ser Leu
325 330 335

Leu Lys Ala Tyr Ile Trp Pro Ala Leu His Tyr Pro Thr Val Asp Glu
340 345 350

Val His Gln Leu Val Asp Arg Asp Ser Ser Leu Arg Val Val Lys Glu
355 360 365

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Thr His Phe Ala Gly His Tyr Leu Lys Ser Val Gln Leu Gln Arg Glu
    370                 375                 380

Val Phe Glu Gly Gln Ile Arg Glu Ala Ala Ala Asp Gly Phe Asp Ala
385                 390                 395                 400

Val Tyr Arg Arg Met Trp Val Tyr His Tyr Ala Leu Ile Glu Ala Leu
                405                 410                 415

Leu Arg Leu Gly Cys Leu Asn Ala Val Gln Phe Ala Leu Thr Thr Arg
            420                 425                 430

Asn Arg Arg Gly Arg Arg
        435


<210> 71
<211> 1140
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1117)
<223> RXA01801

<400> 71
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cacccgcgaa gatttcctgt gatgtgccac actggttctc atg tct aac gta gtg   115
                                           Met Ser Asn Val Val
                                           1               5

aac act ttt gtc cag aat tcc acc ggt atg gtg gag ctt aat cgt ccc   163
Asn Thr Phe Val Gln Asn Ser Thr Gly Met Val Glu Leu Asn Arg Pro
                10                  15                  20

aaa gcg ctc aat tct ctt aat cag gaa atg atc gat ctc gtt cag gaa   211
Lys Ala Leu Asn Ser Leu Asn Gln Glu Met Ile Asp Leu Val Gln Glu
            25                  30                  35

gct cta acc act tgg gct gat gat gat cag gtg cag cag gtt ctc att   259
Ala Leu Thr Thr Trp Ala Asp Asp Asp Gln Val Gln Gln Val Leu Ile
        40                  45                  50

tac tca tcc tcg gag cgt gca ttt tgt gcc ggc ggt gat gtg cgc gcg   307
Tyr Ser Ser Ser Glu Arg Ala Phe Cys Ala Gly Gly Asp Val Arg Ala
    55                  60                  65

gtc cgt gag agc gtg ttg gag ggc gat gtt gcg gcc ggc gat aag tat   355
Val Arg Glu Ser Val Leu Glu Gly Asp Val Ala Ala Gly Asp Lys Tyr
70                  75                  80                  85

ttc atc gat gag ttc gcg atg aac aac acg ttg gga acc tat ccg aag   403
Phe Ile Asp Glu Phe Ala Met Asn Asn Thr Leu Gly Thr Tyr Pro Lys
                90                  95                  100

ccg gtc att tct gtg atc aac ggc gtc gcg atg ggt ggc gga atg gga   451
Pro Val Ile Ser Val Ile Asn Gly Val Ala Met Gly Gly Gly Met Gly
            105                 110                 115
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att tcc atg cat gga tcg cac cgg atc gtc acg gaa aaa gcg ttc gcg 499
Ile Ser Met His Gly Ser His Arg Ile Val Thr Glu Lys Ala Phe Ala
120 125 130

tcg atg cct gag atg gcg atc ggc tat gtt ccc gat gtg ggc ttt act 547
Ser Met Pro Glu Met Ala Ile Gly Tyr Val Pro Asp Val Gly Phe Thr
135 140 145

tat ttc ggt cag cgt gca tcg tcg ctg gcc atc gcc aca ttt ttg gcg 595
Tyr Phe Gly Gln Arg Ala Ser Ser Leu Ala Ile Ala Thr Phe Leu Ala
150 155 160 165

gtg acc ggg tgg cgc atg agc cct gcc gat atg ctg tgg gct ggc gtc 643
Val Thr Gly Trp Arg Met Ser Pro Ala Asp Met Leu Trp Ala Gly Val
170 175 180

gca acg cat ttt gtt gag gat gcg cag ggg ttc att gat gcg gtc ttg 691
Ala Thr His Phe Val Glu Asp Ala Gln Gly Phe Ile Asp Ala Val Leu
185 190 195

aac gag tcg ctt gat ggc gcg ctg gag aaa ttc tcc acg caa cct acg 739
Asn Glu Ser Leu Asp Gly Ala Leu Glu Lys Phe Ser Thr Gln Pro Thr
200 205 210

ggc agc agc gag ctg gcc ggc gtc gcc agc cag att gag gag acc ttt 787
Gly Ser Ser Glu Leu Ala Gly Val Ala Ser Gln Ile Glu Glu Thr Phe
215 220 225

ggg cac agc tct tgg gcg ctt atc gac gcc tcc ctc cgg tct cac ccc 835
Gly His Ser Ser Trp Ala Leu Ile Asp Ala Ser Leu Arg Ser His Pro
230 235 240 245

gat gct gaa ttt gtt gcc aag gtg gat ggg ctg atg gcg tcg gca gca 883
Asp Ala Glu Phe Val Ala Lys Val Asp Gly Leu Met Ala Ser Ala Ala
250 255 260

ccg gca tcg gtg gtg gct acc gtg aag ctg atg cat caa aac agt gag 931
Pro Ala Ser Val Val Ala Thr Val Lys Leu Met His Gln Asn Ser Glu
265 270 275

gcg acc act ctg cgt gaa ggc ttg gac aat gaa ttg gcg atg tct ctt 979
Ala Thr Thr Leu Arg Glu Gly Leu Asp Asn Glu Leu Ala Met Ser Leu
280 285 290

tat atg atc cgc cag cct gat ttt gct gaa ggt gtg cgt gca gtg ttg 1027
Tyr Met Ile Arg Gln Pro Asp Phe Ala Glu Gly Val Arg Ala Val Leu
295 300 305

gtt gat aaa gac cgc aat gca gcc ttc tcc cca gcc aac tac gaa gat 1075
Val Asp Lys Asp Arg Asn Ala Ala Phe Ser Pro Ala Asn Tyr Glu Asp
310 315 320 325

gtt gat gag tca cat ttt gtg acc ttg ttc cag cgc agt tca 1117
Val Asp Glu Ser His Phe Val Thr Leu Phe Gln Arg Ser Ser
330 335

taaaaccgcc aaacttttga tag 1140

<210> 72
<211> 339

<212> PRT
<213> Corynebacterium glutamicum

<400> 72
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Met Ser Asn Val Val Asn Thr Phe Val Gln Asn Ser Thr Gly Met Val
 1               5                  10                  15

Glu Leu Asn Arg Pro Lys Ala Leu Asn Ser Leu Asn Gln Glu Met Ile
            20                  25                  30

Asp Leu Val Gln Glu Ala Leu Thr Thr Trp Ala Asp Asp Asp Gln Val
        35                  40                  45

Gln Gln Val Leu Ile Tyr Ser Ser Ser Glu Arg Ala Phe Cys Ala Gly
    50                  55                  60

Gly Asp Val Arg Ala Val Arg Glu Ser Val Leu Glu Gly Asp Val Ala
65                  70                  75                  80

Ala Gly Asp Lys Tyr Phe Ile Asp Glu Phe Ala Met Asn Asn Thr Leu
                85                  90                  95

Gly Thr Tyr Pro Lys Pro Val Ile Ser Val Ile Asn Gly Val Ala Met
            100                 105                 110

Gly Gly Gly Met Gly Ile Ser Met His Gly Ser His Arg Ile Val Thr
        115                 120                 125

Glu Lys Ala Phe Ala Ser Met Pro Glu Met Ala Ile Gly Tyr Val Pro
    130                 135                 140

Asp Val Gly Phe Thr Tyr Phe Gly Gln Arg Ala Ser Ser Leu Ala Ile
145                 150                 155                 160

Ala Thr Phe Leu Ala Val Thr Gly Trp Arg Met Ser Pro Ala Asp Met
                165                 170                 175

Leu Trp Ala Gly Val Ala Thr His Phe Val Glu Asp Ala Gln Gly Phe
            180                 185                 190

Ile Asp Ala Val Leu Asn Glu Ser Leu Asp Gly Ala Leu Glu Lys Phe
        195                 200                 205

Ser Thr Gln Pro Thr Gly Ser Ser Glu Leu Ala Gly Val Ala Ser Gln
    210                 215                 220

Ile Glu Glu Thr Phe Gly His Ser Ser Trp Ala Leu Ile Asp Ala Ser
225                 230                 235                 240

Leu Arg Ser His Pro Asp Ala Glu Phe Val Ala Lys Val Asp Gly Leu
                245                 250                 255

Met Ala Ser Ala Ala Pro Ala Ser Val Val Ala Thr Val Lys Leu Met
            260                 265                 270

His Gln Asn Ser Glu Ala Thr Thr Leu Arg Glu Gly Leu Asp Asn Glu
        275                 280                 285

Leu Ala Met Ser Leu Tyr Met Ile Arg Gln Pro Asp Phe Ala Glu Gly
    290                 295                 300
```

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Val Arg Ala Val Leu Val Asp Lys Asp Arg Asn Ala Ala Phe Ser Pro
305                 310                 315                 320

Ala Asn Tyr Glu Asp Val Asp Glu Ser His Phe Val Thr Leu Phe Gln
                325                 330                 335

Arg Ser Ser



<210> 73
<211> 1086
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1063)
<223> RXN02512

<400> 73
gctggaaagt ccccattggc taaggaattt accaaggcac cagcaggtgc gaaggcagat 60

tacagcaaca ccaaataaaa attagccgag ggagcatcgc atg aag ccg aag gat   115
                                            Met Lys Pro Lys Asp
                                             1               5

ttc tgc aca gcg gaa aat tgg gcg gag aat tta agc gca ctg ggc tat   163
Phe Cys Thr Ala Glu Asn Trp Ala Glu Asn Leu Ser Ala Leu Gly Tyr
                10                  15                  20

cta gct ggt tgg cgt ttt gtc cgg atg ctc cct ttg cct att gct cgc   211
Leu Ala Gly Trp Arg Phe Val Arg Met Leu Pro Leu Pro Ile Ala Arg
            25                  30                  35

cgg gtg ttt gac ctt ggg gcg gat ctg gcg tcg aaa agc gga aaa ggc   259
Arg Val Phe Asp Leu Gly Ala Asp Leu Ala Ser Lys Ser Gly Lys Gly
        40                  45                  50

atg ggg cag cta cgc gct aat ctg gcg cgg gtg gtc ggt gcg gaa aac   307
Met Gly Gln Leu Arg Ala Asn Leu Ala Arg Val Val Gly Ala Glu Asn
    55                  60                  65

gtt acg cag gcg ctg gtg aag caa gca acg cgc agc tat gcg cgg tat   355
Val Thr Gln Ala Leu Val Lys Gln Ala Thr Arg Ser Tyr Ala Arg Tyr
70                  75                  80                  85

tgg ctg gaa gcg ttc cgg cta ccg gcg atc gcg cga gat cct gag ctg   403
Trp Leu Glu Ala Phe Arg Leu Pro Ala Ile Ala Arg Asp Pro Glu Leu
                90                  95                  100

ctt gcg cgg ttg cgt aag gga act gtt ggc cta gat ttg ttg gat gaa   451
Leu Ala Arg Leu Arg Lys Gly Thr Val Gly Leu Asp Leu Leu Asp Glu
            105                 110                 115

tct ttg gct gcc ggc aag ggc gta gtt ttg acg ctc cca cac agc ggc   499
Ser Leu Ala Ala Gly Lys Gly Val Val Leu Thr Leu Pro His Ser Gly
        120                 125                 130

aac tgg gat atg gct ggc gct ttt ctg att agc cat cat ggg caa ttc   547
Asn Trp Asp Met Ala Gly Ala Phe Leu Ile Ser His His Gly Gln Phe
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    135                 140                 145

acc acc gtt gca gaa agg gtc aag ccg gaa cgc ttg ttt gaa gcg ttc    595
Thr Thr Val Ala Glu Arg Val Lys Pro Glu Arg Leu Phe Glu Ala Phe
150                 155                 160                 165

gtg gag ttt cga gaa agc ctt gga ttt gag gtg ctg cct ctc acc ggt    643
Val Glu Phe Arg Glu Ser Leu Gly Phe Glu Val Leu Pro Leu Thr Gly
                170                 175                 180

ggc gag cgt ccg ccg ttt gaa aag ctg aaa gag cgc ctg aca tct gga    691
Gly Glu Arg Pro Pro Phe Glu Lys Leu Lys Glu Arg Leu Thr Ser Gly
            185                 190                 195

ggt atc gtg tgc ctt ctt ggg gag cgt gac ctg cgg cat tcc ggc gtg    739
Gly Ile Val Cys Leu Leu Gly Glu Arg Asp Leu Arg His Ser Gly Val
        200                 205                 210

gag acc act ttt ttt ggt gag aag acc tcc atg cca gca gga cct gcg    787
Glu Thr Thr Phe Phe Gly Glu Lys Thr Ser Met Pro Ala Gly Pro Ala
    215                 220                 225

cag ctg gcc att gaa aca ggt gcg gcg ctg cac gtg gtg cat cca tgg    835
Gln Leu Ala Ile Glu Thr Gly Ala Ala Leu His Val Val His Pro Trp
230                 235                 240                 245

ttc gat gac gac ggc tgg ggt ctc agc gta tcc gat gcc gtg acc gtg    883
Phe Asp Asp Asp Gly Trp Gly Leu Ser Val Ser Asp Ala Val Thr Val
                250                 255                 260

gat aat tta tcc gac acg gtg cag cgg atc gca cat ctt ttt atg gca    931
Asp Asn Leu Ser Asp Thr Val Gln Arg Ile Ala His Leu Phe Met Ala
            265                 270                 275

aat att acg gcg cac ccc gct gat tgg cat atg ctc caa ccc ctg tgg    979
Asn Ile Thr Ala His Pro Ala Asp Trp His Met Leu Gln Pro Leu Trp
        280                 285                 290

ttt ggt gat ttg gat ccg gag cgt ctc aag cgc tct agg gag cag aca    1027
Phe Gly Asp Leu Asp Pro Glu Arg Leu Lys Arg Ser Arg Glu Gln Thr
    295                 300                 305

aat gtt cac aaa ccg gtg gca tta cag gag gac aat taggtgcgaa         1073
Asn Val His Lys Pro Val Ala Leu Gln Glu Asp Asn
310                 315                 320

ttggaatggt ctg                                                     1086


<210> 74
<211> 321
<212> PRT
<213> Corynebacterium glutamicum

<400> 74
Met Lys Pro Lys Asp Phe Cys Thr Ala Glu Asn Trp Ala Glu Asn Leu
  1               5                  10                  15

Ser Ala Leu Gly Tyr Leu Ala Gly Trp Arg Phe Val Arg Met Leu Pro
            20                  25                  30
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```
Leu Pro Ile Ala Arg Arg Val Phe Asp Leu Gly Ala Asp Leu Ala Ser
        35                  40                  45

Lys Ser Gly Lys Gly Met Gly Gln Leu Arg Ala Asn Leu Ala Arg Val
    50                  55                  60

Val Gly Ala Glu Asn Val Thr Gln Ala Leu Val Lys Gln Ala Thr Arg
65                  70                  75                  80

Ser Tyr Ala Arg Tyr Trp Leu Glu Ala Phe Arg Leu Pro Ala Ile Ala
                85                  90                  95

Arg Asp Pro Glu Leu Leu Ala Arg Leu Arg Lys Gly Thr Val Gly Leu
            100                 105                 110

Asp Leu Leu Asp Glu Ser Leu Ala Ala Gly Lys Gly Val Val Leu Thr
        115                 120                 125

Leu Pro His Ser Gly Asn Trp Asp Met Ala Gly Ala Phe Leu Ile Ser
    130                 135                 140

His His Gly Gln Phe Thr Thr Val Ala Glu Arg Val Lys Pro Glu Arg
145                 150                 155                 160

Leu Phe Glu Ala Phe Val Glu Phe Arg Glu Ser Leu Gly Phe Glu Val
                165                 170                 175

Leu Pro Leu Thr Gly Gly Glu Arg Pro Pro Phe Glu Lys Leu Lys Glu
            180                 185                 190

Arg Leu Thr Ser Gly Gly Ile Val Cys Leu Leu Gly Glu Arg Asp Leu
        195                 200                 205

Arg His Ser Gly Val Glu Thr Thr Phe Phe Gly Glu Lys Thr Ser Met
    210                 215                 220

Pro Ala Gly Pro Ala Gln Leu Ala Ile Glu Thr Gly Ala Ala Leu His
225                 230                 235                 240

Val Val His Pro Trp Phe Asp Asp Asp Gly Trp Gly Leu Ser Val Ser
                245                 250                 255

Asp Ala Val Thr Val Asp Asn Leu Ser Asp Thr Val Gln Arg Ile Ala
            260                 265                 270

His Leu Phe Met Ala Asn Ile Thr Ala His Pro Ala Asp Trp His Met
        275                 280                 285

Leu Gln Pro Leu Trp Phe Gly Asp Leu Asp Pro Glu Arg Leu Lys Arg
    290                 295                 300

Ser Arg Glu Gln Thr Asn Val His Lys Pro Val Ala Leu Gln Glu Asp
305                 310                 315                 320

Asn
```

<210> 75
<211> 1057
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1057)
<223> FRXA02512

<400> 75
gctggaaagt ccccattggc taaggaattt accaaggcac cagcaggtgc gaaggcagat 60

tacagcaaca ccaaataaaa attagccgag ggagcatcgc atg aag ccg aag gat 115
Met Lys Pro Lys Asp
1 5

ttc tgc aca gcg gaa aat tgg gcg gag aat tta agc gca ctg ggc tat 163
Phe Cys Thr Ala Glu Asn Trp Ala Glu Asn Leu Ser Ala Leu Gly Tyr
10 15 20

cta gct ggt tgg cgt ttt gtc cgg atg ctc cct ttg cct att gct cgc 211
Leu Ala Gly Trp Arg Phe Val Arg Met Leu Pro Leu Pro Ile Ala Arg
25 30 35

cgg gtg ttt gac ctt ggg gcg gat ctg gcg tcg aaa agc gga aaa ggc 259
Arg Val Phe Asp Leu Gly Ala Asp Leu Ala Ser Lys Ser Gly Lys Gly
40 45 50

atg ggg cag cta cgc gct aat ctg gcg cgg gtg gtc ggt gcg gaa aac 307
Met Gly Gln Leu Arg Ala Asn Leu Ala Arg Val Val Gly Ala Glu Asn
55 60 65

gtt acg cag gcg ctg gtg aag caa gca acg cgc agc tat gcg cgg tat 355
Val Thr Gln Ala Leu Val Lys Gln Ala Thr Arg Ser Tyr Ala Arg Tyr
70 75 80 85

tgg ctg gaa gcg ttc cgg cta ccg gcg atc gcg cga gat cct gag ctg 403
Trp Leu Glu Ala Phe Arg Leu Pro Ala Ile Ala Arg Asp Pro Glu Leu
90 95 100

ctt gcg cgg ttg cgt aag gga act gtt ggc cta gat ttg ttg gat gaa 451
Leu Ala Arg Leu Arg Lys Gly Thr Val Gly Leu Asp Leu Leu Asp Glu
105 110 115

tct ttg gct gcc ggc aag ggc gta gtt ttg acg ctc cca cac agc ggc 499
Ser Leu Ala Ala Gly Lys Gly Val Val Leu Thr Leu Pro His Ser Gly
120 125 130

aac tgg gat atg gct ggc gct ttt ctg att agc cat cat ggg caa ttc 547
Asn Trp Asp Met Ala Gly Ala Phe Leu Ile Ser His His Gly Gln Phe
135 140 145

acc acc gtt gca gaa agg gtc aag ccg gaa cgc ttg ttt gaa gcg ttc 595
Thr Thr Val Ala Glu Arg Val Lys Pro Glu Arg Leu Phe Glu Ala Phe
150 155 160 165

gtg gag ttt cga gaa agc ctt gga ttt gag gtg ctg cct ctc acc ggt 643
Val Glu Phe Arg Glu Ser Leu Gly Phe Glu Val Leu Pro Leu Thr Gly
170 175 180

ggc gag cgt ccg ccg ttt gaa aag ctg aaa gag cgc ctg aca tct gga 691
Gly Glu Arg Pro Pro Phe Glu Lys Leu Lys Glu Arg Leu Thr Ser Gly
185 190 195

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ggt atc gtg tgc ctt ctt ggg gag cgt gac ctg cgg cat tcc ggc gtg    739
Gly Ile Val Cys Leu Leu Gly Glu Arg Asp Leu Arg His Ser Gly Val
        200                 205                 210

gag acc act ttt ttt ggt gag aag acc tcc atg cca gca gga cct gcg    787
Glu Thr Thr Phe Phe Gly Glu Lys Thr Ser Met Pro Ala Gly Pro Ala
    215                 220                 225

cag ctg gcc att gaa aca ggt gcg gcg ctg cac gtg gtg cat cca tgg    835
Gln Leu Ala Ile Glu Thr Gly Ala Ala Leu His Val Val His Pro Trp
230                 235                 240                 245

ttc gat gac gac ggc tgg ggt ctc agc gta tcc gat gcc gtg acc gtg    883
Phe Asp Asp Asp Gly Trp Gly Leu Ser Val Ser Asp Ala Val Thr Val
                250                 255                 260

gat aat tta tcc gac acg gtg cag cgg atc gca cat ctt ttt atg gca    931
Asp Asn Leu Ser Asp Thr Val Gln Arg Ile Ala His Leu Phe Met Ala
            265                 270                 275

aat att acg gcg cac ccc gct gat tgg cat atg ctc caa ccc ctg tgg    979
Asn Ile Thr Ala His Pro Ala Asp Trp His Met Leu Gln Pro Leu Trp
        280                 285                 290

ttt ggt gat ttg gat ccg gag cgt ctc aag cgc tct agg gag cag aca    1027
Phe Gly Asp Leu Asp Pro Glu Arg Leu Lys Arg Ser Arg Glu Gln Thr
    295                 300                 305

aat gtt cac aaa ccg gtg gca tta cag gag                            1057
Asn Val His Lys Pro Val Ala Leu Gln Glu
310                 315


<210> 76
<211> 319
<212> PRT
<213> Corynebacterium glutamicum

<400> 76
Met Lys Pro Lys Asp Phe Cys Thr Ala Glu Asn Trp Ala Glu Asn Leu
  1               5                  10                  15

Ser Ala Leu Gly Tyr Leu Ala Gly Trp Arg Phe Val Arg Met Leu Pro
             20                  25                  30

Leu Pro Ile Ala Arg Arg Val Phe Asp Leu Gly Ala Asp Leu Ala Ser
         35                  40                  45

Lys Ser Gly Lys Gly Met Gly Gln Leu Arg Ala Asn Leu Ala Arg Val
     50                  55                  60

Val Gly Ala Glu Asn Val Thr Gln Ala Leu Val Lys Gln Ala Thr Arg
 65                  70                  75                  80

Ser Tyr Ala Arg Tyr Trp Leu Glu Ala Phe Arg Leu Pro Ala Ile Ala
                 85                  90                  95

Arg Asp Pro Glu Leu Leu Ala Arg Leu Arg Lys Gly Thr Val Gly Leu
            100                 105                 110
```

Asp Leu Leu Asp Glu Ser Leu Ala Ala Gly Lys Gly Val Val Leu Thr
115 120 125

Leu Pro His Ser Gly Asn Trp Asp Met Ala Gly Ala Phe Leu Ile Ser
130 135 140

His His Gly Gln Phe Thr Thr Val Ala Glu Arg Val Lys Pro Glu Arg
145 150 155 160

Leu Phe Glu Ala Phe Val Glu Phe Arg Glu Ser Leu Gly Phe Glu Val
165 170 175

Leu Pro Leu Thr Gly Gly Glu Arg Pro Pro Phe Glu Lys Leu Lys Glu
180 185 190

Arg Leu Thr Ser Gly Gly Ile Val Cys Leu Leu Gly Glu Arg Asp Leu
195 200 205

Arg His Ser Gly Val Glu Thr Thr Phe Phe Gly Glu Lys Thr Ser Met
210 215 220

Pro Ala Gly Pro Ala Gln Leu Ala Ile Glu Thr Gly Ala Ala Leu His
225 230 235 240

Val Val His Pro Trp Phe Asp Asp Asp Gly Trp Gly Leu Ser Val Ser
245 250 255

Asp Ala Val Thr Val Asp Asn Leu Ser Asp Thr Val Gln Arg Ile Ala
260 265 270

His Leu Phe Met Ala Asn Ile Thr Ala His Pro Ala Asp Trp His Met
275 280 285

Leu Gln Pro Leu Trp Phe Gly Asp Leu Asp Pro Glu Arg Leu Lys Arg
290 295 300

Ser Arg Glu Gln Thr Asn Val His Lys Pro Val Ala Leu Gln Glu
305 310 315

<210> 77
<211> 1389
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1366)
<223> RXA00899

<400> 77
tttgctgctc ccctacgtcg gactcccact gttcctgctt atgggatcgc catacatcaa 60

ccggtgacgc caccgcatcc aacaagaaat caacgacctc atg gaa gac gtc cac 115
Met Glu Asp Val His
1 5

gac gac gtc ccc gac atc ccc acc gga atg gat gtc tcc gcg gaa gtt 163
Asp Asp Val Pro Asp Ile Pro Thr Gly Met Asp Val Ser Ala Glu Val
10 15 20

```
gaa tct gtc atc aaa ctc aac cgc cgc ctc acc cgc atg cca gca gtg     211
Glu Ser Val Ile Lys Leu Asn Arg Arg Leu Thr Arg Met Pro Ala Val
            25                  30                  35

acc ggc gga aac aac ggc ttc tac tcc gac tac cgt gaa tcc ctc aaa     259
Thr Gly Gly Asn Asn Gly Phe Tyr Ser Asp Tyr Arg Glu Ser Leu Lys
        40                  45                  50

cgg atg acc gcc gca atc gac gaa gcc gaa gaa tac atc tac gtc gag     307
Arg Met Thr Ala Ala Ile Asp Glu Ala Glu Glu Tyr Ile Tyr Val Glu
    55                  60                  65

atc tac atc atg gcc tgg gat tcc tac acc caa cca ttc ttc gca gca     355
Ile Tyr Ile Met Ala Trp Asp Ser Tyr Thr Gln Pro Phe Phe Ala Ala
70                  75                  80                  85

ctc gaa cga gcc cac aac cgc ggc gtc aaa gtc cga ctc ctt ttc gac     403
Leu Glu Arg Ala His Asn Arg Gly Val Lys Val Arg Leu Leu Phe Asp
                90                  95                  100

cac gtc ggc agc tgg aaa tac ccc ggc tac cac cgc ctc aaa aaa gaa     451
His Val Gly Ser Trp Lys Tyr Pro Gly Tyr His Arg Leu Lys Lys Glu
            105                 110                 115

ctc aac cgc atg ggc ttc gcc tgg tac ctc atg ctc ccc ctc caa ccc     499
Leu Asn Arg Met Gly Phe Ala Trp Tyr Leu Met Leu Pro Leu Gln Pro
        120                 125                 130

tgg cga cgc cgc ttc cgc cga ccc gac ctg cgc aac cac cgc aaa atg     547
Trp Arg Arg Arg Phe Arg Arg Pro Asp Leu Arg Asn His Arg Lys Met
    135                 140                 145

ctc atc atc gac ggc cac acc gca ttc atg ggc tcc caa aat ctc atc     595
Leu Ile Ile Asp Gly His Thr Ala Phe Met Gly Ser Gln Asn Leu Ile
150                 155                 160                 165

gcc ccg agt tac cta caa aag aaa aac atc aaa ctc ggc cgc gaa tgg     643
Ala Pro Ser Tyr Leu Gln Lys Lys Asn Ile Lys Leu Gly Arg Glu Trp
                170                 175                 180

aaa gac ctc atg gtc gaa ctc acc ggc ccc atc gtc tcc tcc atg gaa     691
Lys Asp Leu Met Val Glu Leu Thr Gly Pro Ile Val Ser Ser Met Glu
            185                 190                 195

atg atc ttc gcc ggc gac tgg tac gtc gaa tcc aac gaa gcc ctc gac     739
Met Ile Phe Ala Gly Asp Trp Tyr Val Glu Ser Asn Glu Ala Leu Asp
        200                 205                 210

atc cgc gac cac gca gaa gcc cac ggc tac atc ggc aac act caa aaa     787
Ile Arg Asp His Ala Glu Ala His Gly Tyr Ile Gly Asn Thr Gln Lys
    215                 220                 225

gac tcc gcc acc aac ctc gtg cag ctc atc ccc tcc ggc cct ggt tac     835
Asp Ser Ala Thr Asn Leu Val Gln Leu Ile Pro Ser Gly Pro Gly Tyr
230                 235                 240                 245

acc aca gaa ccc aac ctg cgc atg ttc aac tcc atc gtt cac cac gcc     883
Thr Thr Glu Pro Asn Leu Arg Met Phe Asn Ser Ile Val His His Ala
                250                 255                 260

aaa gaa cga ctc atc ttg tgc agc ccc tac ttc atc ccc gac gaa tcc     931
```

```
Lys Glu Arg Leu Ile Leu Cys Ser Pro Tyr Phe Ile Pro Asp Glu Ser
            265                 270                 275

ctc ctc gaa gcc gtc acc tca gcc tgc tac cgc gga gta acc gtc gaa      979
Leu Leu Glu Ala Val Thr Ser Ala Cys Tyr Arg Gly Val Thr Val Glu
        280                 285                 290

cta ttc gtc tct gaa caa gcc gac caa ttc gcc atc gac cac gcc caa     1027
Leu Phe Val Ser Glu Gln Ala Asp Gln Phe Ala Ile Asp His Ala Gln
    295                 300                 305

tcc tcc tac tac cag gca ctc ctt gaa gcc ggc gtg aaa atc tac caa     1075
Ser Ser Tyr Tyr Gln Ala Leu Leu Glu Ala Gly Val Lys Ile Tyr Gln
310                 315                 320                 325

ttc ccc aaa ccc gac gtc ctc cac acc aag tac atg atc gcc gac ccc     1123
Phe Pro Lys Pro Asp Val Leu His Thr Lys Tyr Met Ile Ala Asp Pro
                330                 335                 340

gac gac acc acc ggc aac gaa gcc ctc gga gtc ctc gga tcc tcc aac     1171
Asp Asp Thr Thr Gly Asn Glu Ala Leu Gly Val Leu Gly Ser Ser Asn
            345                 350                 355

ctc gac atc cgc agc ttt ggc ctc aac tac gaa atc tcc ctg atg atc     1219
Leu Asp Ile Arg Ser Phe Gly Leu Asn Tyr Glu Ile Ser Leu Met Ile
        360                 365                 370

gcc aaa ggc aac ctc atc cac gaa ctc aac gcc ctc acc gac cgt tac     1267
Ala Lys Gly Asn Leu Ile His Glu Leu Asn Ala Leu Thr Asp Arg Tyr
    375                 380                 385

cgc aca gta agt ttc aag ctc acc ttg gat aag tgg aac cag cgc agt     1315
Arg Thr Val Ser Phe Lys Leu Thr Leu Asp Lys Trp Asn Gln Arg Ser
390                 395                 400                 405

tgg cgg cgc cgc tac gtg gac aat gtc atg cgt ttg acc tcg gcg ctg     1363
Trp Arg Arg Arg Tyr Val Asp Asn Val Met Arg Leu Thr Ser Ala Leu
                410                 415                 420

cag tagtttggcg cgtttggagt gcg                                       1389
Gln


&lt;210&gt; 78
&lt;211&gt; 422
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 78
Met Glu Asp Val His Asp Asp Val Pro Asp Ile Pro Thr Gly Met Asp
  1               5                  10                  15

Val Ser Ala Glu Val Glu Ser Val Ile Lys Leu Asn Arg Arg Leu Thr
             20                  25                  30

Arg Met Pro Ala Val Thr Gly Gly Asn Asn Gly Phe Tyr Ser Asp Tyr
        35                  40                  45

Arg Glu Ser Leu Lys Arg Met Thr Ala Ala Ile Asp Glu Ala Glu Glu
    50                  55                  60
```

```
Tyr Ile Tyr Val Glu Ile Tyr Ile Met Ala Trp Asp Ser Tyr Thr Gln
 65                  70                  75                  80

Pro Phe Phe Ala Ala Leu Glu Arg Ala His Asn Arg Gly Val Lys Val
                 85                  90                  95

Arg Leu Leu Phe Asp His Val Gly Ser Trp Lys Tyr Pro Gly Tyr His
            100                 105                 110

Arg Leu Lys Lys Glu Leu Asn Arg Met Gly Phe Ala Trp Tyr Leu Met
        115                 120                 125

Leu Pro Leu Gln Pro Trp Arg Arg Arg Phe Arg Arg Pro Asp Leu Arg
    130                 135                 140

Asn His Arg Lys Met Leu Ile Ile Asp Gly His Thr Ala Phe Met Gly
145                 150                 155                 160

Ser Gln Asn Leu Ile Ala Pro Ser Tyr Leu Gln Lys Lys Asn Ile Lys
                165                 170                 175

Leu Gly Arg Glu Trp Lys Asp Leu Met Val Glu Leu Thr Gly Pro Ile
            180                 185                 190

Val Ser Ser Met Glu Met Ile Phe Ala Gly Asp Trp Tyr Val Glu Ser
        195                 200                 205

Asn Glu Ala Leu Asp Ile Arg Asp His Ala Glu Ala His Gly Tyr Ile
    210                 215                 220

Gly Asn Thr Gln Lys Asp Ser Ala Thr Asn Leu Val Gln Leu Ile Pro
225                 230                 235                 240

Ser Gly Pro Gly Tyr Thr Thr Glu Pro Asn Leu Arg Met Phe Asn Ser
                245                 250                 255

Ile Val His His Ala Lys Glu Arg Leu Ile Leu Cys Ser Pro Tyr Phe
            260                 265                 270

Ile Pro Asp Glu Ser Leu Leu Glu Ala Val Thr Ser Ala Cys Tyr Arg
        275                 280                 285

Gly Val Thr Val Glu Leu Phe Val Ser Glu Gln Ala Asp Gln Phe Ala
    290                 295                 300

Ile Asp His Ala Gln Ser Ser Tyr Tyr Gln Ala Leu Leu Glu Ala Gly
305                 310                 315                 320

Val Lys Ile Tyr Gln Phe Pro Lys Pro Asp Val Leu His Thr Lys Tyr
                325                 330                 335

Met Ile Ala Asp Pro Asp Asp Thr Thr Gly Asn Glu Ala Leu Gly Val
            340                 345                 350

Leu Gly Ser Ser Asn Leu Asp Ile Arg Ser Phe Gly Leu Asn Tyr Glu
        355                 360                 365

Ile Ser Leu Met Ile Ala Lys Gly Asn Leu Ile His Glu Leu Asn Ala
    370                 375                 380
```

```
Leu Thr Asp Arg Tyr Arg Thr Val Ser Phe Lys Leu Thr Leu Asp Lys
385                 390                 395                 400

Trp Asn Gln Arg Ser Trp Arg Arg Arg Tyr Val Asp Asn Val Met Arg
                405                 410                 415

Leu Thr Ser Ala Leu Gln
            420


<210> 79
<211> 1452
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1429)
<223> RXN00819

<400> 79
gatgaggttc gtccgggaat cctcaaagac aatgcggtga aggtacttgg cctagccgct 60

agcactgagc gcggatctca agcagaaaag gtcgtgcaac atg cgt gat ccc att   115
                                           Met Arg Asp Pro Ile
                                           1               5

caa ggt gct gtt att cct tct gat ctt ttt ggt ttc gca gaa gtt ctc   163
Gln Gly Ala Val Ile Pro Ser Asp Leu Phe Gly Phe Ala Glu Val Leu
                10                  15                  20

acc gaa gcc gaa cgc gca gtt ctt ctg gaa acc cgc agg gtg ctt gag   211
Thr Glu Ala Glu Arg Ala Val Leu Leu Glu Thr Arg Arg Val Leu Glu
            25                  30                  35

gaa gag gtg aag cct tat att aat gag gcc tgg gat aag gca gtc ttc   259
Glu Glu Val Lys Pro Tyr Ile Asn Glu Ala Trp Asp Lys Ala Val Phe
        40                  45                  50

ccc gat gag atc gtg cag ccc ctc caa gat ctg caa ttg ctt gat ccg   307
Pro Asp Glu Ile Val Gln Pro Leu Gln Asp Leu Gln Leu Leu Asp Pro
    55                  60                  65

cct gca ctt cgg gaa gca ggg gag tcg gtt cga gac att ttc act ggt   355
Pro Ala Leu Arg Glu Ala Gly Glu Ser Val Arg Asp Ile Phe Thr Gly
70                  75                  80                  85

ttc cgc aat ttt gaa ctc gcg cgc tgt gac atc aat gtt ggt acc tat   403
Phe Arg Asn Phe Glu Leu Ala Arg Cys Asp Ile Asn Val Gly Thr Tyr
                90                  95                  100

tac aac gca tct gct ggt ctc ttc cga acg gcc tgc atg gtt ggt ggc   451
Tyr Asn Ala Ser Ala Gly Leu Phe Arg Thr Ala Cys Met Val Gly Gly
            105                 110                 115

tcc ccg gag cag gcg cag cga ttg gat gcg cag atc aaa tct ggt gag   499
Ser Pro Glu Gln Ala Gln Arg Leu Asp Ala Gln Ile Lys Ser Gly Glu
        120                 125                 130

gtc aag ggc gtt ttt gca ctg acg gaa cct gat cat ggc tct gat atc   547
Val Lys Gly Val Phe Ala Leu Thr Glu Pro Asp His Gly Ser Asp Ile
```

135 140 145

gca ggt ggt ctg gca acc acg gcc act aag gac gca gac acc ggc gag 595
Ala Gly Gly Leu Ala Thr Thr Ala Thr Lys Asp Ala Asp Thr Gly Glu
150 155 160 165

tgg att atc aat ggt gaa aaa cgg tgg atc ggt ggt gct tcc act gct 643
Trp Ile Ile Asn Gly Glu Lys Arg Trp Ile Gly Gly Ala Ser Thr Ala
170 175 180

gat ttg atc gct acc ttc gcc agg gat aca gcc gat aac cag gtg aaa 691
Asp Leu Ile Ala Thr Phe Ala Arg Asp Thr Ala Asp Asn Gln Val Lys
185 190 195

tgc ttc ctc gtg gca cct cag gca gag ggc gtg tcc atg gag att att 739
Cys Phe Leu Val Ala Pro Gln Ala Glu Gly Val Ser Met Glu Ile Ile
200 205 210

gat cgc aaa gcc tca ctg cgc atc atg caa aat gca cac att acc tat 787
Asp Arg Lys Ala Ser Leu Arg Ile Met Gln Asn Ala His Ile Thr Tyr
215 220 225

aac aat gtc cgg gtg tct ggg gat gcg cgg ctg cac aac atc aat tct 835
Asn Asn Val Arg Val Ser Gly Asp Ala Arg Leu His Asn Ile Asn Ser
230 235 240 245

ttc aag gat gtt tcg gaa tgc ctg cgc cgt atg cgt tcc gat gtg gcg 883
Phe Lys Asp Val Ser Glu Cys Leu Arg Arg Met Arg Ser Asp Val Ala
250 255 260

tgg atg gcg gtc ggt gcg cag gca ggt gcc tat gaa gca gcc gtg aag 931
Trp Met Ala Val Gly Ala Gln Ala Gly Ala Tyr Glu Ala Ala Val Lys
265 270 275

tat gtg cgc agc agg gaa cag ttt ggc cgt ccg atc gcg ggg ttc cag 979
Tyr Val Arg Ser Arg Glu Gln Phe Gly Arg Pro Ile Ala Gly Phe Gln
280 285 290

ttg att cag gaa aag ctc gcg ctc atg ctg ggc aat ctc acg gcg tcg 1027
Leu Ile Gln Glu Lys Leu Ala Leu Met Leu Gly Asn Leu Thr Ala Ser
295 300 305

ctg ggc atg atg gtc aaa ctc acc gat cag cag cag gcg gga att ttc 1075
Leu Gly Met Met Val Lys Leu Thr Asp Gln Gln Gln Ala Gly Ile Phe
310 315 320 325

aaa gag gaa aac tcc gcg ctg gcg aaa atg ttt acc tcg ctc aaa ctt 1123
Lys Glu Glu Asn Ser Ala Leu Ala Lys Met Phe Thr Ser Leu Lys Leu
330 335 340

cgg gag acc gct agt tgg gcg cgg gaa atc tgc gga ggc aac ggc atc 1171
Arg Glu Thr Ala Ser Trp Ala Arg Glu Ile Cys Gly Gly Asn Gly Ile
345 350 355

att ttg gac aac gat gtt gcc cgg ttc cat gcc gat gca gaa gcc gtc 1219
Ile Leu Asp Asn Asp Val Ala Arg Phe His Ala Asp Ala Glu Ala Val
360 365 370

tat tca tat gaa ggc acc cac gaa atc aat gca ctc atc gtt ggn cgn 1267
Tyr Ser Tyr Glu Gly Thr His Glu Ile Asn Ala Leu Ile Val Gly Arg
375 380 385

ncc att ctg ggn cnt ctn ttc ttt tta tat tat nac nct ttt gag gag 1315
Xaa Ile Leu Gly Xaa Leu Phe Phe Leu Tyr Tyr Xaa Xaa Phe Glu Glu
390 395 400 405

gat ctt cat gac tac ttc cac cac ccc aaa cca tcg ttt ctt tcg aag 1363
Asp Leu His Asp Tyr Phe His His Pro Lys Pro Ser Phe Leu Ser Lys
410 415 420

acg cac caa ccc tca ccg gcc agg acc tgg gct ttt cgc agt ggc gca 1411
Thr His Gln Pro Ser Pro Ala Arg Thr Trp Ala Phe Arg Ser Gly Ala
425 430 435

ctg tca ccc agg aga tgg tgaacacctt ggcggacgca act 1452
Leu Ser Pro Arg Arg Trp
440

<210> 80
<211> 443
<212> PRT
<213> Corynebacterium glutamicum

<400> 80
Met Arg Asp Pro Ile Gln Gly Ala Val Ile Pro Ser Asp Leu Phe Gly
1 5 10 15

Phe Ala Glu Val Leu Thr Glu Ala Glu Arg Ala Val Leu Leu Glu Thr
20 25 30

Arg Arg Val Leu Glu Glu Glu Val Lys Pro Tyr Ile Asn Glu Ala Trp
35 40 45

Asp Lys Ala Val Phe Pro Asp Glu Ile Val Gln Pro Leu Gln Asp Leu
50 55 60

Gln Leu Leu Asp Pro Pro Ala Leu Arg Glu Ala Gly Glu Ser Val Arg
65 70 75 80

Asp Ile Phe Thr Gly Phe Arg Asn Phe Glu Leu Ala Arg Cys Asp Ile
85 90 95

Asn Val Gly Thr Tyr Tyr Asn Ala Ser Ala Gly Leu Phe Arg Thr Ala
100 105 110

Cys Met Val Gly Gly Ser Pro Glu Gln Ala Gln Arg Leu Asp Ala Gln
115 120 125

Ile Lys Ser Gly Glu Val Lys Gly Val Phe Ala Leu Thr Glu Pro Asp
130 135 140

His Gly Ser Asp Ile Ala Gly Gly Leu Ala Thr Thr Ala Thr Lys Asp
145 150 155 160

Ala Asp Thr Gly Glu Trp Ile Ile Asn Gly Glu Lys Arg Trp Ile Gly
165 170 175

Gly Ala Ser Thr Ala Asp Leu Ile Ala Thr Phe Ala Arg Asp Thr Ala
180 185 190

Asp Asn Gln Val Lys Cys Phe Leu Val Ala Pro Gln Ala Glu Gly Val

```
        195                 200                 205

Ser Met Glu Ile Ile Asp Arg Lys Ala Ser Leu Arg Ile Met Gln Asn
    210                 215                 220

Ala His Ile Thr Tyr Asn Asn Val Arg Val Ser Gly Asp Ala Arg Leu
225                 230                 235                 240

His Asn Ile Asn Ser Phe Lys Asp Val Ser Glu Cys Leu Arg Arg Met
                245                 250                 255

Arg Ser Asp Val Ala Trp Met Ala Val Gly Ala Gln Ala Gly Ala Tyr
            260                 265                 270

Glu Ala Ala Val Lys Tyr Val Arg Ser Arg Glu Gln Phe Gly Arg Pro
        275                 280                 285

Ile Ala Gly Phe Gln Leu Ile Gln Glu Lys Leu Ala Leu Met Leu Gly
    290                 295                 300

Asn Leu Thr Ala Ser Leu Gly Met Met Val Lys Leu Thr Asp Gln Gln
305                 310                 315                 320

Gln Ala Gly Ile Phe Lys Glu Glu Asn Ser Ala Leu Ala Lys Met Phe
                325                 330                 335

Thr Ser Leu Lys Leu Arg Glu Thr Ala Ser Trp Ala Arg Glu Ile Cys
            340                 345                 350

Gly Gly Asn Gly Ile Ile Leu Asp Asn Asp Val Ala Arg Phe His Ala
        355                 360                 365

Asp Ala Glu Ala Val Tyr Ser Tyr Glu Gly Thr His Glu Ile Asn Ala
    370                 375                 380

Leu Ile Val Gly Arg Xaa Ile Leu Gly Xaa Leu Phe Phe Leu Tyr Tyr
385                 390                 395                 400

Xaa Xaa Phe Glu Glu Asp Leu His Asp Tyr Phe His His Pro Lys Pro
                405                 410                 415

Ser Phe Leu Ser Lys Thr His Gln Pro Ser Pro Ala Arg Thr Trp Ala
            420                 425                 430

Phe Arg Ser Gly Ala Leu Ser Pro Arg Arg Trp
        435                 440


<210> 81
<211> 1030
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (18)..(1007)
<223> FRXA00819

<400> 81
tcttccgaac ggcctgcatg gtt ggt ggc tcc ccg gag cag gcg cag cga ttg 53
                  Met Val Gly Gly Ser Pro Glu Gln Ala Gln Arg Leu
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1 5 10

gat gcg cag atc aaa tct ggt gag gtc aag ggc gtt ttt gca ctg acg 101
Asp Ala Gln Ile Lys Ser Gly Glu Val Lys Gly Val Phe Ala Leu Thr
15 20 25

gaa cct gat cat ggc tct gat atc gca ggt ggt ctg gca acc acg gcc 149
Glu Pro Asp His Gly Ser Asp Ile Ala Gly Gly Leu Ala Thr Thr Ala
30 35 40

act aag gac gca gac acc ggc gag tgg att atc aat ggt gaa aaa cgg 197
Thr Lys Asp Ala Asp Thr Gly Glu Trp Ile Ile Asn Gly Glu Lys Arg
45 50 55 60

tgg atc ggt ggt gct tcc act gct gat ttg atc gct acc ttc gcc agg 245
Trp Ile Gly Gly Ala Ser Thr Ala Asp Leu Ile Ala Thr Phe Ala Arg
65 70 75

gat aca gcc gat aac cag gtg aaa tgc ttc ctc gtg gca cct cag gca 293
Asp Thr Ala Asp Asn Gln Val Lys Cys Phe Leu Val Ala Pro Gln Ala
80 85 90

gag ggc gtg tcc atg gag att att gat cgc aaa gcc tca ctg cgc atc 341
Glu Gly Val Ser Met Glu Ile Ile Asp Arg Lys Ala Ser Leu Arg Ile
95 100 105

atg caa aat gca cac att acc tat aac aat gtc cgg gtg tct ggg gat 389
Met Gln Asn Ala His Ile Thr Tyr Asn Asn Val Arg Val Ser Gly Asp
110 115 120

gcg cgg ctg cac aac atc aat tct ttc aag gat gtt tcg gaa tgc ctg 437
Ala Arg Leu His Asn Ile Asn Ser Phe Lys Asp Val Ser Glu Cys Leu
125 130 135 140

cgc cgt atg cgt tcc gat gtg gcg tgg atg gcg gtc ggt gcg cag gca 485
Arg Arg Met Arg Ser Asp Val Ala Trp Met Ala Val Gly Ala Gln Ala
145 150 155

ggt gcc tat gaa gca gcc gtg aag tat gtg cgc agc agg gaa cag ttt 533
Gly Ala Tyr Glu Ala Ala Val Lys Tyr Val Arg Ser Arg Glu Gln Phe
160 165 170

ggc cgt ccg atc gcg ggg ttc cag ttg att cag gaa aag ctc gcg ctc 581
Gly Arg Pro Ile Ala Gly Phe Gln Leu Ile Gln Glu Lys Leu Ala Leu
175 180 185

atg ctg ggc aat ctc acg gcg tcg ctg ggc atg atg gtc aaa ctc acc 629
Met Leu Gly Asn Leu Thr Ala Ser Leu Gly Met Met Val Lys Leu Thr
190 195 200

gat cag cag cag gcg gga att ttc aaa gag gaa aac tcc gcg ctg gcg 677
Asp Gln Gln Gln Ala Gly Ile Phe Lys Glu Glu Asn Ser Ala Leu Ala
205 210 215 220

aaa atg ttt acc tcg ctc aaa ctt cgg gag acc gct agt tgg gcg cgg 725
Lys Met Phe Thr Ser Leu Lys Leu Arg Glu Thr Ala Ser Trp Ala Arg
225 230 235

gaa atc tgc gga ggc aac ggc atc att ttg gac aac gat gtt gcc cgg 773
Glu Ile Cys Gly Gly Asn Gly Ile Ile Leu Asp Asn Asp Val Ala Arg
240 245 250

```
ttc cat gcc gat gca gaa gcc gtc tat tca tat gaa ggc acc cac gaa      821
Phe His Ala Asp Ala Glu Ala Val Tyr Ser Tyr Glu Gly Thr His Glu
        255                     260                     265

atc aat gca ctc atc gtt ggn cgn ncc att ctg ggn cnt ctn ttc ttt      869
Ile Asn Ala Leu Ile Val Gly Arg Xaa Ile Leu Gly Xaa Leu Phe Phe
    270                     275                     280

tta tat tat nac nct ttt gag gag gat ctt cat gac tac ttc cac cac      917
Leu Tyr Tyr Xaa Xaa Phe Glu Glu Asp Leu His Asp Tyr Phe His His
285                     290                     295                 300

ccc aaa cca tcg ttt ctt tcg aag acg cac caa ccc tca ccg gcc agg      965
Pro Lys Pro Ser Phe Leu Ser Lys Thr His Gln Pro Ser Pro Ala Arg
                305                     310                     315

acc tgg gct ttt cgc agt ggc gca ctg tca ccc agg aga tgg              1007
Thr Trp Ala Phe Arg Ser Gly Ala Leu Ser Pro Arg Arg Trp
            320                     325                     330

tgaacacctt cgcggacgca act                                            1030


&lt;210&gt; 82
&lt;211&gt; 330
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 82
Met Val Gly Gly Ser Pro Glu Gln Ala Gln Arg Leu Asp Ala Gln Ile
  1               5                  10                  15

Lys Ser Gly Glu Val Lys Gly Val Phe Ala Leu Thr Glu Pro Asp His
             20                  25                  30

Gly Ser Asp Ile Ala Gly Gly Leu Ala Thr Thr Ala Thr Lys Asp Ala
         35                  40                  45

Asp Thr Gly Glu Trp Ile Ile Asn Gly Glu Lys Arg Trp Ile Gly Gly
     50                  55                  60

Ala Ser Thr Ala Asp Leu Ile Ala Thr Phe Ala Arg Asp Thr Ala Asp
 65                  70                  75                  80

Asn Gln Val Lys Cys Phe Leu Val Ala Pro Gln Ala Glu Gly Val Ser
                 85                  90                  95

Met Glu Ile Ile Asp Arg Lys Ala Ser Leu Arg Ile Met Gln Asn Ala
            100                 105                 110

His Ile Thr Tyr Asn Asn Val Arg Val Ser Gly Asp Ala Arg Leu His
        115                 120                 125

Asn Ile Asn Ser Phe Lys Asp Val Ser Glu Cys Leu Arg Arg Met Arg
    130                 135                 140

Ser Asp Val Ala Trp Met Ala Val Gly Ala Gln Ala Gly Ala Tyr Glu
145                 150                 155                 160

Ala Ala Val Lys Tyr Val Arg Ser Arg Glu Gln Phe Gly Arg Pro Ile
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                165                 170                 175

Ala Gly Phe Gln Leu Ile Gln Glu Lys Leu Ala Leu Met Leu Gly Asn
            180                 185                 190

Leu Thr Ala Ser Leu Gly Met Met Val Lys Leu Thr Asp Gln Gln Gln
        195                 200                 205

Ala Gly Ile Phe Lys Glu Glu Asn Ser Ala Leu Ala Lys Met Phe Thr
    210                 215                 220

Ser Leu Lys Leu Arg Glu Thr Ala Ser Trp Ala Arg Glu Ile Cys Gly
225                 230                 235                 240

Gly Asn Gly Ile Ile Leu Asp Asn Asp Val Ala Arg Phe His Ala Asp
                245                 250                 255

Ala Glu Ala Val Tyr Ser Tyr Glu Gly Thr His Glu Ile Asn Ala Leu
            260                 265                 270

Ile Val Gly Arg Xaa Ile Leu Gly Xaa Leu Phe Phe Leu Tyr Tyr Xaa
        275                 280                 285

Xaa Phe Glu Glu Asp Leu His Asp Tyr Phe His His Pro Lys Pro Ser
    290                 295                 300

Phe Leu Ser Lys Thr His Gln Pro Ser Pro Ala Arg Thr Trp Ala Phe
305                 310                 315                 320

Arg Ser Gly Ala Leu Ser Pro Arg Arg Trp
                325                 330


<210> 83
<211> 391
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(391)
<223> FRXA01766

<400> 83
gatgaggttc gtccgggaat cctcaaagac aatgcggtga aggtacttgg cctagccgct 60

agcactgagc gcggatctca agcagaaaag gtcgtgcaac atg cgt gat ccc att   115
                                           Met Arg Asp Pro Ile
                                           1               5

caa ggt gct gtt att cct tct gat ctt ttt ggt ttc gca gaa gtt ctc   163
Gln Gly Ala Val Ile Pro Ser Asp Leu Phe Gly Phe Ala Glu Val Leu
                10                  15                  20

acc gaa gcc gaa cgc gca gtt ctt ctg gaa acc cgc agg gtg ctt gag   211
Thr Glu Ala Glu Arg Ala Val Leu Leu Glu Thr Arg Arg Val Leu Glu
            25                  30                  35

gaa gag gtg aag cct tat att aat gag gcc tgg gat aag gca gtc ttc   259
Glu Glu Val Lys Pro Tyr Ile Asn Glu Ala Trp Asp Lys Ala Val Phe
        40                  45                  50
```

```
ccc gat gag atc gtg cag ccc ctc caa gat ctg caa ttg ctt gat ccg    307
Pro Asp Glu Ile Val Gln Pro Leu Gln Asp Leu Gln Leu Leu Asp Pro
    55                  60                  65

cct gca ctt cgg gaa gca ggg gag tcg gtt cga gac att ttc act ggt    355
Pro Ala Leu Arg Glu Ala Gly Glu Ser Val Arg Asp Ile Phe Thr Gly
70                  75                  80                  85

ttc cgc aat ttt gaa ctc gcg cgc tgt gac atc aat                    391
Phe Arg Asn Phe Glu Leu Ala Arg Cys Asp Ile Asn
                90                  95
```

<210> 84
<211> 97
<212> PRT
<213> Corynebacterium glutamicum

<400> 84

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Met Arg Asp Pro Ile Gln Gly Ala Val Ile Pro Ser Asp Leu Phe Gly
1               5                   10                  15

Phe Ala Glu Val Leu Thr Glu Ala Glu Arg Ala Val Leu Leu Glu Thr
            20                  25                  30

Arg Arg Val Leu Glu Glu Glu Val Lys Pro Tyr Ile Asn Glu Ala Trp
        35                  40                  45

Asp Lys Ala Val Phe Pro Asp Glu Ile Val Gln Pro Leu Gln Asp Leu
    50                  55                  60

Gln Leu Leu Asp Pro Pro Ala Leu Arg Glu Ala Gly Glu Ser Val Arg
65                  70                  75                  80

Asp Ile Phe Thr Gly Phe Arg Asn Phe Glu Leu Ala Arg Cys Asp Ile
                85                  90                  95

Asn
```

<210> 85
<211> 1659
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1636)
<223> RXN01762

<400> 85

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tggagtgatg aattttccta tagaacgttt tttaaacgat tgacttttta aacgtttacg 60

cttttaatga cttcaaacgt gatctaaagc acaaaggaga atg aaa gtg aac ctc    115
                                           Met Lys Val Asn Leu
                                           1               5

gga ata gga agc tac cca cga cgc agg gca act gtt cga cca gag tcc    163
Gly Ile Gly Ser Tyr Pro Arg Arg Arg Ala Thr Val Arg Pro Glu Ser
```

10 15 20

act gca atc gaa ttc gaa ggc acc agc atc acc tac gga gaa ttc agc 211
Thr Ala Ile Glu Phe Glu Gly Thr Ser Ile Thr Tyr Gly Glu Phe Ser
25 30 35

aaa cga gtc aat cgg ctt gga cat gct ctt cta gac ctc ggc gtt gcg 259
Lys Arg Val Asn Arg Leu Gly His Ala Leu Leu Asp Leu Gly Val Ala
40 45 50

cac caa gat cga gta gct tat gtc gga ttc aac cac cct gcc ctg cta 307
His Gln Asp Arg Val Ala Tyr Val Gly Phe Asn His Pro Ala Leu Leu
55 60 65

gaa gtg ttc ttt tca acg aac ctc att ggg gca aca ccc gtg ctt gtt 355
Glu Val Phe Phe Ser Thr Asn Leu Ile Gly Ala Thr Pro Val Leu Val
70 75 80 85

aac cct cgc cta tcg gca aac gaa atc gat tac atc atc caa gac agc 403
Asn Pro Arg Leu Ser Ala Asn Glu Ile Asp Tyr Ile Ile Gln Asp Ser
90 95 100

ggt gcg agc atc gtg ttt tac gga atc gac ctc atc gag cac gcc act 451
Gly Ala Ser Ile Val Phe Tyr Gly Ile Asp Leu Ile Glu His Ala Thr
105 110 115

tac ctc caa gaa ctc cat cca gag atc atc atg gtg gcc gtt gaa ggc 499
Tyr Leu Gln Glu Leu His Pro Glu Ile Ile Met Val Ala Val Glu Gly
120 125 130

gat gag ggt cca ggt ttg cgt cga aaa gcg ctt att gaa gcg gcg agc 547
Asp Glu Gly Pro Gly Leu Arg Arg Lys Ala Leu Ile Glu Ala Ala Ser
135 140 145

gac gcc gac atc gac cta gaa gtc agc gat gat gac ctg gtg ctg ctc 595
Asp Ala Asp Ile Asp Leu Glu Val Ser Asp Asp Asp Leu Val Leu Leu
150 155 160 165

atg tac acc tcc gga acc act ggc cgc cca aag ggc gcc atg tta tcc 643
Met Tyr Thr Ser Gly Thr Thr Gly Arg Pro Lys Gly Ala Met Leu Ser
170 175 180

cac cga aac ctc ttc ttt aac tac ttc aat gcc ctg ctc agc cag gaa 691
His Arg Asn Leu Phe Phe Asn Tyr Phe Asn Ala Leu Leu Ser Gln Glu
185 190 195

att gaa caa ggc gcg gta ctt tta tcc act gcg ccg tta ttc cac atc 739
Ile Glu Gln Gly Ala Val Leu Leu Ser Thr Ala Pro Leu Phe His Ile
200 205 210

gcg ggc ctc aac atg acc acc atc ccg gtg atg atg aag ggc gga aag 787
Ala Gly Leu Asn Met Thr Thr Ile Pro Val Met Met Lys Gly Gly Lys
215 220 225

gtg atc atc cac cgc gaa ttc cgg gca gag cac gtc ctc gac gaa atc 835
Val Ile Ile His Arg Glu Phe Arg Ala Glu His Val Leu Asp Glu Ile
230 235 240 245

gaa cgc tcc aag gta tcc gaa tcc ttc atg gtg cca gcg atg atc gac 883
Glu Arg Ser Lys Val Ser Glu Ser Phe Met Val Pro Ala Met Ile Asp
250 255 260

```
atg ttg tcc aac cac cca tca ttt gcc gaa cgc gac ctt tct tcc ctt    931
Met Leu Ser Asn His Pro Ser Phe Ala Glu Arg Asp Leu Ser Ser Leu
            265                 270                 275

cgc gcc atc atg gtg ggc ggc tct ccc ctt agc gaa cgt gcg ctg cga    979
Arg Ala Ile Met Val Gly Gly Ser Pro Leu Ser Glu Arg Ala Leu Arg
        280                 285                 290

atc tgg caa gga cgc gac gta aaa att gtc caa ggc ttc ggc atg aca    1027
Ile Trp Gln Gly Arg Asp Val Lys Ile Val Gln Gly Phe Gly Met Thr
    295                 300                 305

gaa acc gca ccg ggc gcc tgt atc ctc gag gca aca gac aca agc aca    1075
Glu Thr Ala Pro Gly Ala Cys Ile Leu Glu Ala Thr Asp Thr Ser Thr
310                 315                 320                 325

cac ctt gga acc gca ggt cga gcc cac ttc ttc acc gac atc aaa cta    1123
His Leu Gly Thr Ala Gly Arg Ala His Phe Phe Thr Asp Ile Lys Leu
                330                 335                 340

gtg gac ccg aaa acc ggc gaa gaa gtc ccc acc gga gag gcc ggc gaa    1171
Val Asp Pro Lys Thr Gly Glu Glu Val Pro Thr Gly Glu Ala Gly Glu
            345                 350                 355

gtt ctc atc cgc gga cca cat gtg atg acc gga tac tgg aac cga cca    1219
Val Leu Ile Arg Gly Pro His Val Met Thr Gly Tyr Trp Asn Arg Pro
        360                 365                 370

gaa gac acc gcc agc gca cta caa aat ggc tgg tac cac tcc gga gat    1267
Glu Asp Thr Ala Ser Ala Leu Gln Asn Gly Trp Tyr His Ser Gly Asp
    375                 380                 385

atc gcc atc aaa gat gaa gac ggc tac tac acc atc aaa gac cgc atc    1315
Ile Ala Ile Lys Asp Glu Asp Gly Tyr Tyr Thr Ile Lys Asp Arg Ile
390                 395                 400                 405

aaa gac atg tac atc tcc ggc ggc gaa aac att tac ccc gca gaa gtc    1363
Lys Asp Met Tyr Ile Ser Gly Gly Glu Asn Ile Tyr Pro Ala Glu Val
                410                 415                 420

gaa caa gca ctc cag gaa ctg gaa gca gtc ctt gat gcc gca gtc atc    1411
Glu Gln Ala Leu Gln Glu Leu Glu Ala Val Leu Asp Ala Ala Val Ile
            425                 430                 435

gga gtc ccc gat gaa cga tgg ggc gaa act ggc atc gcc ttt gtc tcc    1459
Gly Val Pro Asp Glu Arg Trp Gly Glu Thr Gly Ile Ala Phe Val Ser
        440                 445                 450

atc cga gaa agc tac ctg acc aac cca cca acc gga ccg gaa cta cga    1507
Ile Arg Glu Ser Tyr Leu Thr Asn Pro Pro Thr Gly Pro Glu Leu Arg
    455                 460                 465

gaa cta cta ggc agt gtc cta gcc aga tac aaa ctt cca cga gaa atc    1555
Glu Leu Leu Gly Ser Val Leu Ala Arg Tyr Lys Leu Pro Arg Glu Ile
470                 475                 480                 485

cac atc atc gaa gaa ctc ccc cgc aac gcc aca ggc aaa atc caa aag    1603
His Ile Ile Glu Glu Leu Pro Arg Asn Ala Thr Gly Lys Ile Gln Lys
                490                 495                 500
```

```
aac atc ctg cga gac ttc acc atc ccc gtt tca taaaccccc aacgtcactt 1656
Asn Ile Leu Arg Asp Phe Thr Ile Pro Val Ser
            505                 510

tga                                                              1659


<210> 86
<211> 512
<212> PRT
<213> Corynebacterium glutamicum

<400> 86
Met Lys Val Asn Leu Gly Ile Gly Ser Tyr Pro Arg Arg Arg Ala Thr
  1               5                  10                  15

Val Arg Pro Glu Ser Thr Ala Ile Glu Phe Glu Gly Thr Ser Ile Thr
             20                  25                  30

Tyr Gly Glu Phe Ser Lys Arg Val Asn Arg Leu Gly His Ala Leu Leu
         35                  40                  45

Asp Leu Gly Val Ala His Gln Asp Arg Val Ala Tyr Val Gly Phe Asn
     50                  55                  60

His Pro Ala Leu Leu Glu Val Phe Phe Ser Thr Asn Leu Ile Gly Ala
 65                  70                  75                  80

Thr Pro Val Leu Val Asn Pro Arg Leu Ser Ala Asn Glu Ile Asp Tyr
                 85                  90                  95

Ile Ile Gln Asp Ser Gly Ala Ser Ile Val Phe Tyr Gly Ile Asp Leu
            100                 105                 110

Ile Glu His Ala Thr Tyr Leu Gln Glu Leu His Pro Glu Ile Ile Met
        115                 120                 125

Val Ala Val Glu Gly Asp Glu Gly Pro Gly Leu Arg Arg Lys Ala Leu
    130                 135                 140

Ile Glu Ala Ala Ser Asp Ala Asp Ile Asp Leu Glu Val Ser Asp Asp
145                 150                 155                 160

Asp Leu Val Leu Leu Met Tyr Thr Ser Gly Thr Thr Gly Arg Pro Lys
                165                 170                 175

Gly Ala Met Leu Ser His Arg Asn Leu Phe Phe Asn Tyr Phe Asn Ala
            180                 185                 190

Leu Leu Ser Gln Glu Ile Glu Gln Gly Ala Val Leu Leu Ser Thr Ala
        195                 200                 205

Pro Leu Phe His Ile Ala Gly Leu Asn Met Thr Thr Ile Pro Val Met
    210                 215                 220

Met Lys Gly Gly Lys Val Ile Ile His Arg Glu Phe Arg Ala Glu His
225                 230                 235                 240

Val Leu Asp Glu Ile Glu Arg Ser Lys Val Ser Glu Ser Phe Met Val
                245                 250                 255
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Pro Ala Met Ile Asp Met Leu Ser Asn His Pro Ser Phe Ala Glu Arg
            260                 265                 270

Asp Leu Ser Ser Leu Arg Ala Ile Met Val Gly Gly Ser Pro Leu Ser
        275                 280                 285

Glu Arg Ala Leu Arg Ile Trp Gln Gly Arg Asp Val Lys Ile Val Gln
    290                 295                 300

Gly Phe Gly Met Thr Glu Thr Ala Pro Gly Ala Cys Ile Leu Glu Ala
305                 310                 315                 320

Thr Asp Thr Ser Thr His Leu Gly Thr Ala Gly Arg Ala His Phe Phe
                325                 330                 335

Thr Asp Ile Lys Leu Val Asp Pro Lys Thr Gly Glu Glu Val Pro Thr
            340                 345                 350

Gly Glu Ala Gly Glu Val Leu Ile Arg Gly Pro His Val Met Thr Gly
        355                 360                 365

Tyr Trp Asn Arg Pro Glu Asp Thr Ala Ser Ala Leu Gln Asn Gly Trp
    370                 375                 380

Tyr His Ser Gly Asp Ile Ala Ile Lys Asp Glu Asp Gly Tyr Tyr Thr
385                 390                 395                 400

Ile Lys Asp Arg Ile Lys Asp Met Tyr Ile Ser Gly Gly Glu Asn Ile
                405                 410                 415

Tyr Pro Ala Glu Val Glu Gln Ala Leu Gln Glu Leu Glu Ala Val Leu
            420                 425                 430

Asp Ala Ala Val Ile Gly Val Pro Asp Glu Arg Trp Gly Glu Thr Gly
        435                 440                 445

Ile Ala Phe Val Ser Ile Arg Glu Ser Tyr Leu Thr Asn Pro Pro Thr
    450                 455                 460

Gly Pro Glu Leu Arg Glu Leu Leu Gly Ser Val Leu Ala Arg Tyr Lys
465                 470                 475                 480

Leu Pro Arg Glu Ile His Ile Ile Glu Glu Leu Pro Arg Asn Ala Thr
                485                 490                 495

Gly Lys Ile Gln Lys Asn Ile Leu Arg Asp Phe Thr Ile Pro Val Ser
            500                 505                 510
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<210> 87
<211> 1372
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1363)
<223> FRXA01762

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<400> 87
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cttttaatga cttcaaacgt gatctaaagc acaaaggaga atg aaa gtg aac ctc    115
                                           Met Lys Val Asn Leu
                                            1               5

gga ata gga agc tac cca cga cgc agg gca act gtt cga cca gag tcc    163
Gly Ile Gly Ser Tyr Pro Arg Arg Arg Ala Thr Val Arg Pro Glu Ser
                10                  15                  20

act gca atc gaa ttc gaa ggc acc agc atc acc tac gga gaa ttc agc    211
Thr Ala Ile Glu Phe Glu Gly Thr Ser Ile Thr Tyr Gly Glu Phe Ser
            25                  30                  35

aaa cga gtc aat cgg ctt gga cat gct ctt cta gac ctc ggc gtt gcg    259
Lys Arg Val Asn Arg Leu Gly His Ala Leu Leu Asp Leu Gly Val Ala
        40                  45                  50

cac caa gat cga gta gct tat gtc gga ttc aac cac cct gcc ctg cta    307
His Gln Asp Arg Val Ala Tyr Val Gly Phe Asn His Pro Ala Leu Leu
    55                  60                  65

gaa gtg ttc ttt tca acg aac ctc att ggg gca aca ccc gtg ctt gtt    355
Glu Val Phe Phe Ser Thr Asn Leu Ile Gly Ala Thr Pro Val Leu Val
70                  75                  80                  85

aac cct cgc cta tcg gca aac gaa atc gat tac atc atc caa gac agc    403
Asn Pro Arg Leu Ser Ala Asn Glu Ile Asp Tyr Ile Ile Gln Asp Ser
                90                  95                  100

ggt gcg agc atc gtg ttt tac gga atc gac ctc atc gag cac gcc act    451
Gly Ala Ser Ile Val Phe Tyr Gly Ile Asp Leu Ile Glu His Ala Thr
            105                 110                 115

tac ctc caa gaa ctc cat cca gag atc atc atg gtg gcc gtt gaa ggc    499
Tyr Leu Gln Glu Leu His Pro Glu Ile Ile Met Val Ala Val Glu Gly
        120                 125                 130

gat gag ggt cca ggt ttg cgt cga aaa gcg ctt att gaa gcg gcg agc    547
Asp Glu Gly Pro Gly Leu Arg Arg Lys Ala Leu Ile Glu Ala Ala Ser
    135                 140                 145

gac gcc gac atc gac cta gaa gtc agc gat gat gac ctg gtg ctg ctc    595
Asp Ala Asp Ile Asp Leu Glu Val Ser Asp Asp Asp Leu Val Leu Leu
150                 155                 160                 165

atg tac acc tcc gga acc act ggc cgc cca aag ggc gcc atg tta tcc    643
Met Tyr Thr Ser Gly Thr Thr Gly Arg Pro Lys Gly Ala Met Leu Ser
                170                 175                 180

cac cga aac ctc ttc ttt aac tac ttc aat gcc ctg ctc agc cag gaa    691
His Arg Asn Leu Phe Phe Asn Tyr Phe Asn Ala Leu Leu Ser Gln Glu
            185                 190                 195

att gaa caa ggc gcg gta ctt tta tcc act gcg ccg tta ttc cac atc    739
Ile Glu Gln Gly Ala Val Leu Leu Ser Thr Ala Pro Leu Phe His Ile
        200                 205                 210

gcg ggc ctc aac atg acc acc atc ccg gtg atg atg aag ggc gga aag    787
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Ala Gly Leu Asn Met Thr Thr Ile Pro Val Met Met Lys Gly Gly Lys
215 220 225

gtg atc atc cac cgc gaa ttc cgg gca gag cac gtc ctc gac gaa atc 835
Val Ile Ile His Arg Glu Phe Arg Ala Glu His Val Leu Asp Glu Ile
230 235 240 245

gaa cgc tcc aag gta tcc gaa tcc ttc atg gtg cca gcg atg atc gac 883
Glu Arg Ser Lys Val Ser Glu Ser Phe Met Val Pro Ala Met Ile Asp
250 255 260

atg ttg tcc aac cac cca tca ttt gcc gaa cgc gac ctt tct tcc ctt 931
Met Leu Ser Asn His Pro Ser Phe Ala Glu Arg Asp Leu Ser Ser Leu
265 270 275

cgc gcc atc atg gtg ggc ggc tct ccc ctt agc gaa cgt gcg ctg cga 979
Arg Ala Ile Met Val Gly Gly Ser Pro Leu Ser Glu Arg Ala Leu Arg
280 285 290

atc tgg caa gga cgc gac gta aaa att gtc caa ggc ttc ggc atg aca 1027
Ile Trp Gln Gly Arg Asp Val Lys Ile Val Gln Gly Phe Gly Met Thr
295 300 305

gaa acc gca ccg ggc gcc tgt atc ctc gag gca aca gac aca agc aca 1075
Glu Thr Ala Pro Gly Ala Cys Ile Leu Glu Ala Thr Asp Thr Ser Thr
310 315 320 325

cac ctt gga acc gca ggt cga gcc cac ttc ttc acc gac atc aaa cta 1123
His Leu Gly Thr Ala Gly Arg Ala His Phe Phe Thr Asp Ile Lys Leu
330 335 340

gtg gac ccg aaa acc ggc gaa gaa gtc ccc acc gga gag gcc ggc gaa 1171
Val Asp Pro Lys Thr Gly Glu Glu Val Pro Thr Gly Glu Ala Gly Glu
345 350 355

gtt ctc atc cgc gga cca cat gtg atg acc gga tac tgg aac cga cca 1219
Val Leu Ile Arg Gly Pro His Val Met Thr Gly Tyr Trp Asn Arg Pro
360 365 370

gaa gac acc gcc agc gca cta caa aat ggc tgg tac cac tcc gga gat 1267
Glu Asp Thr Ala Ser Ala Leu Gln Asn Gly Trp Tyr His Ser Gly Asp
375 380 385

atc gcc atc aaa gat gaa gac ggc tac tac acc atc aaa gac cgc atc 1315
Ile Ala Ile Lys Asp Glu Asp Gly Tyr Tyr Thr Ile Lys Asp Arg Ile
390 395 400 405

aaa gac atg tac atc tcc ggc ggc gaa aac att tac ccc gca gaa gtc 1363
Lys Asp Met Tyr Ile Ser Gly Gly Glu Asn Ile Tyr Pro Ala Glu Val
410 415 420

taagtaccc 1372

<210> 88
<211> 421
<212> PRT
<213> Corynebacterium glutamicum

<400> 88
Met Lys Val Asn Leu Gly Ile Gly Ser Tyr Pro Arg Arg Arg Ala Thr

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Val Arg Pro Glu Ser Thr Ala Ile Glu Phe Glu Gly Thr Ser Ile Thr
20 25 30

Tyr Gly Glu Phe Ser Lys Arg Val Asn Arg Leu Gly His Ala Leu Leu
35 40 45

Asp Leu Gly Val Ala His Gln Asp Arg Val Ala Tyr Val Gly Phe Asn
50 55 60

His Pro Ala Leu Leu Glu Val Phe Phe Ser Thr Asn Leu Ile Gly Ala
65 70 75 80

Thr Pro Val Leu Val Asn Pro Arg Leu Ser Ala Asn Glu Ile Asp Tyr
85 90 95

Ile Ile Gln Asp Ser Gly Ala Ser Ile Val Phe Tyr Gly Ile Asp Leu
100 105 110

Ile Glu His Ala Thr Tyr Leu Gln Glu Leu His Pro Glu Ile Ile Met
115 120 125

Val Ala Val Glu Gly Asp Glu Gly Pro Gly Leu Arg Arg Lys Ala Leu
130 135 140

Ile Glu Ala Ala Ser Asp Ala Asp Ile Asp Leu Glu Val Ser Asp Asp
145 150 155 160

Asp Leu Val Leu Leu Met Tyr Thr Ser Gly Thr Thr Gly Arg Pro Lys
165 170 175

Gly Ala Met Leu Ser His Arg Asn Leu Phe Phe Asn Tyr Phe Asn Ala
180 185 190

Leu Leu Ser Gln Glu Ile Glu Gln Gly Ala Val Leu Leu Ser Thr Ala
195 200 205

Pro Leu Phe His Ile Ala Gly Leu Asn Met Thr Thr Ile Pro Val Met
210 215 220

Met Lys Gly Gly Lys Val Ile Ile His Arg Glu Phe Arg Ala Glu His
225 230 235 240

Val Leu Asp Glu Ile Glu Arg Ser Lys Val Ser Glu Ser Phe Met Val
245 250 255

Pro Ala Met Ile Asp Met Leu Ser Asn His Pro Ser Phe Ala Glu Arg
260 265 270

Asp Leu Ser Ser Leu Arg Ala Ile Met Val Gly Gly Ser Pro Leu Ser
275 280 285

Glu Arg Ala Leu Arg Ile Trp Gln Gly Arg Asp Val Lys Ile Val Gln
290 295 300

Gly Phe Gly Met Thr Glu Thr Ala Pro Gly Ala Cys Ile Leu Glu Ala
305 310 315 320

Thr Asp Thr Ser Thr His Leu Gly Thr Ala Gly Arg Ala His Phe Phe
325 330 335

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Thr Asp Ile Lys Leu Val Asp Pro Lys Thr Gly Glu Glu Val Pro Thr
            340                 345                 350

Gly Glu Ala Gly Glu Val Leu Ile Arg Gly Pro His Val Met Thr Gly
        355                 360                 365

Tyr Trp Asn Arg Pro Glu Asp Thr Ala Ser Ala Leu Gln Asn Gly Trp
    370                 375                 380

Tyr His Ser Gly Asp Ile Ala Ile Lys Asp Glu Asp Gly Tyr Tyr Thr
385                 390                 395                 400

Ile Lys Asp Arg Ile Lys Asp Met Tyr Ile Ser Gly Gly Glu Asn Ile
                405                 410                 415

Tyr Pro Ala Glu Val
            420


<210> 89
<211> 867
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(844)
<223> RXA00681

<400> 89
aagggcaagg ttgtcattgt tgatccagat gcgccacgca tcgaaggacc cggcgcgcac 60

agccatgcgc actcagtagc agcacatggg gtggatacac atg cct agt cca cgc    115
                                           Met Pro Ser Pro Arg
                                           1               5

act gtt ctt atc act ggt gcc gct ggc ggt ttg ggt cgg gca ttc gct    163
Thr Val Leu Ile Thr Gly Ala Ala Gly Gly Leu Gly Arg Ala Phe Ala
                10                  15                  20

gaa ggt ttc gca gcc caa gga gac cgt atc gcg gtg gcg gat atc aat    211
Glu Gly Phe Ala Ala Gln Gly Asp Arg Ile Ala Val Ala Asp Ile Asn
            25                  30                  35

ctg gat ggg gcg caa gag acc gtt gac aag ctg aaa gca ttg ggc gca    259
Leu Asp Gly Ala Gln Glu Thr Val Asp Lys Leu Lys Ala Leu Gly Ala
        40                  45                  50

gat gcc gca gcc ttt gaa gtt gat gtc acg tct ttg gag tcc acc gag    307
Asp Ala Ala Ala Phe Glu Val Asp Val Thr Ser Leu Glu Ser Thr Glu
    55                  60                  65

gcc cta gcc gcc ggt gcc gct gag ttt ggc ggt ggc cga att gat gtc    355
Ala Leu Ala Ala Gly Ala Ala Glu Phe Gly Gly Gly Arg Ile Asp Val
70                  75                  80                  85

ctt att aat aac gca gcg ata tat gcg aca gtg act cgt tca ccg ttt    403
Leu Ile Asn Asn Ala Ala Ile Tyr Ala Thr Val Thr Arg Ser Pro Phe
                90                  95                  100
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gag gat att gac cct gcg gag tgg gat ttg gtc atg gga gtc aat ctc      451
Glu Asp Ile Asp Pro Ala Glu Trp Asp Leu Val Met Gly Val Asn Leu
            105                 110                 115

aaa ggc ccg tgg ttg gtg acg cgt tct gtg agt ccg ttt ttg tcc gat      499
Lys Gly Pro Trp Leu Val Thr Arg Ser Val Ser Pro Phe Leu Ser Asp
        120                 125                 130

aat gcc cgt gtg gtc aat ctt tcc agc gcg act gtg ttt tca gga tct      547
Asn Ala Arg Val Val Asn Leu Ser Ser Ala Thr Val Phe Ser Gly Ser
    135                 140                 145

gca cac tgg gcg cac tac gtg gca tcc aaa ggt ggg gtc att gct tta      595
Ala His Trp Ala His Tyr Val Ala Ser Lys Gly Gly Val Ile Ala Leu
150                 155                 160                 165

acc agg gtg ctt gct aaa gag ctg ggt ggt cgt ggg atc acg gtc aat      643
Thr Arg Val Leu Ala Lys Glu Leu Gly Gly Arg Gly Ile Thr Val Asn
                170                 175                 180

gcg gtt gcg cct ggg ttt acg ctg act gaa gcc agc ttg gga ctc atg      691
Ala Val Ala Pro Gly Phe Thr Leu Thr Glu Ala Ser Leu Gly Leu Met
            185                 190                 195

gat agc gcg gaa acg tac ggt gtc gat cgc gga tcc atc aag cgc gca      739
Asp Ser Ala Glu Thr Tyr Gly Val Asp Arg Gly Ser Ile Lys Arg Ala
        200                 205                 210

agc caa ccg aaa gac atc gtc ggc acc acc atg ttt ctt gca tcc cca      787
Ser Gln Pro Lys Asp Ile Val Gly Thr Thr Met Phe Leu Ala Ser Pro
    215                 220                 225

gaa gcc gaa tac atc act ggg caa aca ctc atc gtt gat ggt ggc cga      835
Glu Ala Glu Tyr Ile Thr Gly Gln Thr Leu Ile Val Asp Gly Gly Arg
230                 235                 240                 245

cag ttc atc taagtactaa aagttctaag gag                                867
Gln Phe Ile
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<210> 90
<211> 248
<212> PRT
<213> Corynebacterium glutamicum

<400> 90

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Met Pro Ser Pro Arg Thr Val Leu Ile Thr Gly Ala Ala Gly Gly Leu
  1               5                  10                  15

Gly Arg Ala Phe Ala Glu Gly Phe Ala Ala Gln Gly Asp Arg Ile Ala
             20                  25                  30

Val Ala Asp Ile Asn Leu Asp Gly Ala Gln Glu Thr Val Asp Lys Leu
         35                  40                  45

Lys Ala Leu Gly Ala Asp Ala Ala Ala Phe Glu Val Asp Val Thr Ser
     50                  55                  60

Leu Glu Ser Thr Glu Ala Leu Ala Ala Gly Ala Ala Glu Phe Gly Gly
 65                  70                  75                  80
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Gly Arg Ile Asp Val Leu Ile Asn Asn Ala Ala Ile Tyr Ala Thr Val
85 90 95

Thr Arg Ser Pro Phe Glu Asp Ile Asp Pro Ala Glu Trp Asp Leu Val
100 105 110

Met Gly Val Asn Leu Lys Gly Pro Trp Leu Val Thr Arg Ser Val Ser
115 120 125

Pro Phe Leu Ser Asp Asn Ala Arg Val Val Asn Leu Ser Ser Ala Thr
130 135 140

Val Phe Ser Gly Ser Ala His Trp Ala His Tyr Val Ala Ser Lys Gly
145 150 155 160

Gly Val Ile Ala Leu Thr Arg Val Leu Ala Lys Glu Leu Gly Gly Arg
165 170 175

Gly Ile Thr Val Asn Ala Val Ala Pro Gly Phe Thr Leu Thr Glu Ala
180 185 190

Ser Leu Gly Leu Met Asp Ser Ala Glu Thr Tyr Gly Val Asp Arg Gly
195 200 205

Ser Ile Lys Arg Ala Ser Gln Pro Lys Asp Ile Val Gly Thr Thr Met
210 215 220

Phe Leu Ala Ser Pro Glu Ala Glu Tyr Ile Thr Gly Gln Thr Leu Ile
225 230 235 240

Val Asp Gly Gly Arg Gln Phe Ile
245

<210> 91
<211> 837
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(814)
<223> RXA00802

<400> 91
gccatggtga tcacaccagt gtgggggctg aggctccaca cttggaggaa tggattaaac 60

gcgggcacta agccccgaac gattagtagg cttgggcacc atg gat ctt aaa ctt 115
Met Asp Leu Lys Leu
1 5

ggt ggc caa gtc ata ctt gtt gtt ggc ggt gca gga act att ggt tct 163
Gly Gly Gln Val Ile Leu Val Val Gly Gly Ala Gly Thr Ile Gly Ser
10 15 20

gaa gtt gta aaa ctc tta act gaa gaa ggc gca acc gcg gta gcg gcg 211
Glu Val Val Lys Leu Leu Thr Glu Glu Gly Ala Thr Ala Val Ala Ala
25 30 35

tcg aga agc acg ccc tta tct att gac gct tcg gat gaa gcg tcc gtc 259

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Ser Arg Ser Thr Pro Leu Ser Ile Asp Ala Ser Asp Glu Ala Ser Val
        40                  45                  50

cgt gcg ggc att gat cag gtg atc gca gaa cat ggt cgc ctg gat ggg    307
Arg Ala Gly Ile Asp Gln Val Ile Ala Glu His Gly Arg Leu Asp Gly
    55                  60                  65

ctg gtt gtt tct tct gca ccc gct gcg caa acg ctc agc gcg gag aca    355
Leu Val Val Ser Ser Ala Pro Ala Ala Gln Thr Leu Ser Ala Glu Thr
70                  75                  80                  85

gca gat gat ccg gac act gtg ttg gct gct att gaa ggc aaa gcc atc    403
Ala Asp Asp Pro Asp Thr Val Leu Ala Ala Ile Glu Gly Lys Ala Ile
                90                  95                  100

acg ttt atg aag gct gca acc gtg gcg ctc gag aag atg cgt gag gct    451
Thr Phe Met Lys Ala Ala Thr Val Ala Leu Glu Lys Met Arg Glu Ala
            105                 110                 115

gga cat ggg cgc atc gtt gca ctt tcc ggc atg aac tca tac aaa aca    499
Gly His Gly Arg Ile Val Ala Leu Ser Gly Met Asn Ser Tyr Lys Thr
        120                 125                 130

ttg agt act act gcg tcg gcg cga aat gct gcg ctg aat gtc gtg gtg    547
Leu Ser Thr Thr Ala Ser Ala Arg Asn Ala Ala Leu Asn Val Val Val
    135                 140                 145

aaa aat ttg gcg gat cgt cac gcg ggc acc gga att aca gta aat gcg    595
Lys Asn Leu Ala Asp Arg His Ala Gly Thr Gly Ile Thr Val Asn Ala
150                 155                 160                 165

att agc ccg gga ttc gtg gta gct gag cca gac gct gag gta aac cgc    643
Ile Ser Pro Gly Phe Val Val Ala Glu Pro Asp Ala Glu Val Asn Arg
                170                 175                 180

gca aat ggt gac acc acg tgg agg agg tcg cgg agg cga tcg cgt ttt    691
Ala Asn Gly Asp Thr Thr Trp Arg Arg Ser Arg Arg Arg Ser Arg Phe
            185                 190                 195

tgt tgt cgc cgc gca ccg cat caa ttt ctg gag aga tta ttt cgg tgg    739
Cys Cys Arg Arg Ala Pro His Gln Phe Leu Glu Arg Leu Phe Arg Trp
        200                 205                 210

gac ata agg cga agg gca tca tcc ttc ctt agc tcg cgt gag ctt ccc    787
Asp Ile Arg Arg Arg Ala Ser Ser Phe Leu Ser Ser Arg Glu Leu Pro
    215                 220                 225

aag cgt aag cac ccc cgt gtg agg gca taacggccgt tctgttaaag          834
Lys Arg Lys His Pro Arg Val Arg Ala
230                 235

att                                                                837


<210> 92
<211> 238
<212> PRT
<213> Corynebacterium glutamicum

<400> 92
Met Asp Leu Lys Leu Gly Gly Gln Val Ile Leu Val Val Gly Gly Ala
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1 5 10 15

Gly Thr Ile Gly Ser Glu Val Val Lys Leu Leu Thr Glu Glu Gly Ala
20 25 30

Thr Ala Val Ala Ala Ser Arg Ser Thr Pro Leu Ser Ile Asp Ala Ser
35 40 45

Asp Glu Ala Ser Val Arg Ala Gly Ile Asp Gln Val Ile Ala Glu His
50 55 60

Gly Arg Leu Asp Gly Leu Val Val Ser Ser Ala Pro Ala Ala Gln Thr
65 70 75 80

Leu Ser Ala Glu Thr Ala Asp Asp Pro Asp Thr Val Leu Ala Ala Ile
85 90 95

Glu Gly Lys Ala Ile Thr Phe Met Lys Ala Ala Thr Val Ala Leu Glu
100 105 110

Lys Met Arg Glu Ala Gly His Gly Arg Ile Val Ala Leu Ser Gly Met
115 120 125

Asn Ser Tyr Lys Thr Leu Ser Thr Thr Ala Ser Ala Arg Asn Ala Ala
130 135 140

Leu Asn Val Val Val Lys Asn Leu Ala Asp Arg His Ala Gly Thr Gly
145 150 155 160

Ile Thr Val Asn Ala Ile Ser Pro Gly Phe Val Val Ala Glu Pro Asp
165 170 175

Ala Glu Val Asn Arg Ala Asn Gly Asp Thr Thr Trp Arg Arg Ser Arg
180 185 190

Arg Arg Ser Arg Phe Cys Cys Arg Arg Ala Pro His Gln Phe Leu Glu
195 200 205

Arg Leu Phe Arg Trp Asp Ile Arg Arg Arg Ala Ser Ser Phe Leu Ser
210 215 220

Ser Arg Glu Leu Pro Lys Arg Lys His Pro Arg Val Arg Ala
225 230 235

<210> 93
<211> 329
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(306)
<223> RXA02133

<400> 93
gaa aac ccc tac att ggc gga gct gga tac aac gca gca aaa ttc ggt 48
Glu Asn Pro Tyr Ile Gly Gly Ala Gly Tyr Asn Ala Ala Lys Phe Gly
1 5 10 15

gta gca gca ttc aac cgt gtg ctt cgc ttg gaa acc cac cag cag acc 96

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Val Ala Ala Phe Asn Arg Val Leu Arg Leu Glu Thr His Gln Gln Thr
            20                  25                  30

ctt cgc gta tct gag atc gat cca ggt cga gtt gcc acg gaa gaa ttc    144
Leu Arg Val Ser Glu Ile Asp Pro Gly Arg Val Ala Thr Glu Glu Phe
        35                  40                  45

tcc ctc gtt cgt ttc ggc gga gat aaa gaa cgc gca gaa gca gtc tat    192
Ser Leu Val Arg Phe Gly Gly Asp Lys Glu Arg Ala Glu Ala Val Tyr
    50                  55                  60

gac gac gtc ctc aac ctc acc gct gaa gac atc gca gag tct gtg cgt    240
Asp Asp Val Leu Asn Leu Thr Ala Glu Asp Ile Ala Glu Ser Val Arg
65                  70                  75                  80

tgg gtc gcg agc ctt cca aag cac atg aac att gac cgc atg cgt att    288
Trp Val Ala Ser Leu Pro Lys His Met Asn Ile Asp Arg Met Arg Ile
                85                  90                  95

aca cct cgc gat cag gtc taaaacccgc actcttttga aat                  329
Thr Pro Arg Asp Gln Val
            100


<210> 94
<211> 102
<212> PRT
<213> Corynebacterium glutamicum

<400> 94
Glu Asn Pro Tyr Ile Gly Gly Ala Gly Tyr Asn Ala Ala Lys Phe Gly
1               5                   10                  15

Val Ala Ala Phe Asn Arg Val Leu Arg Leu Glu Thr His Gln Gln Thr
            20                  25                  30

Leu Arg Val Ser Glu Ile Asp Pro Gly Arg Val Ala Thr Glu Glu Phe
        35                  40                  45

Ser Leu Val Arg Phe Gly Gly Asp Lys Glu Arg Ala Glu Ala Val Tyr
    50                  55                  60

Asp Asp Val Leu Asn Leu Thr Ala Glu Asp Ile Ala Glu Ser Val Arg
65                  70                  75                  80

Trp Val Ala Ser Leu Pro Lys His Met Asn Ile Asp Arg Met Arg Ile
                85                  90                  95

Thr Pro Arg Asp Gln Val
            100


<210> 95
<211> 1347
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1324)
<223> RXN01114
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ttcgacagat ctctctgcac tctaaattaa ggatcaaaaa atg aac cct caa gat   115
                                            Met Asn Pro Gln Asp
                                             1               5

att gtc atc tgt tcc cca ttg cgc acc cca gtt ggt gct tac ggc gga   163
Ile Val Ile Cys Ser Pro Leu Arg Thr Pro Val Gly Ala Tyr Gly Gly
                10                  15                  20

tcc ttc acc ggc gtc cct gtt gaa gaa ttg gcc acc acc gtg atc aac   211
Ser Phe Thr Gly Val Pro Val Glu Glu Leu Ala Thr Thr Val Ile Asn
            25                  30                  35

gcg atc gtt gag gca acc ggc atc acc ggc gac gat gtg gac gat ctg   259
Ala Ile Val Glu Ala Thr Gly Ile Thr Gly Asp Asp Val Asp Asp Leu
        40                  45                  50

atc ctc ggc cag gca tcc ccc aac ggt gcg gct cca gca ctg ggc cgt   307
Ile Leu Gly Gln Ala Ser Pro Asn Gly Ala Ala Pro Ala Leu Gly Arg
    55                  60                  65

gtt gtt gct cta gat tcc aag ctt ggc caa aac gtt cca ggc atg cag   355
Val Val Ala Leu Asp Ser Lys Leu Gly Gln Asn Val Pro Gly Met Gln
70                  75                  80                  85

ctt gat cgc cgc tgt ggt tcc ggc ctg cag gca atc gtc acc gct gct   403
Leu Asp Arg Arg Cys Gly Ser Gly Leu Gln Ala Ile Val Thr Ala Ala
                90                  95                  100

gca cac gtt gca tcc ggc gct gct gat ctg atc atc gca ggt ggc gca   451
Ala His Val Ala Ser Gly Ala Ala Asp Leu Ile Ile Ala Gly Gly Ala
            105                 110                 115

gaa tcc atg agc cgc gtt gag tac acc gtg tcc ggc gat atc cgt tgg   499
Glu Ser Met Ser Arg Val Glu Tyr Thr Val Ser Gly Asp Ile Arg Trp
        120                 125                 130

ggt gtc aag ggc ggc gac atg cag ctt cgt gac cgc ctt gca gaa gca   547
Gly Val Lys Gly Gly Asp Met Gln Leu Arg Asp Arg Leu Ala Glu Ala
    135                 140                 145

cgc gaa acc gct ggc gga cgc aac cac ccg atc cct ggt ggc atg atc   595
Arg Glu Thr Ala Gly Gly Arg Asn His Pro Ile Pro Gly Gly Met Ile
150                 155                 160                 165

gag acc gct gag aac ctg cgt cgc gaa tac ggc atc tcc cgc gag gag   643
Glu Thr Ala Glu Asn Leu Arg Arg Glu Tyr Gly Ile Ser Arg Glu Glu
                170                 175                 180

cag gac aag atc tcc gca gcg tcc cag cag cgt tgg ggc aag gct gct   691
Gln Asp Lys Ile Ser Ala Ala Ser Gln Gln Arg Trp Gly Lys Ala Ala
            185                 190                 195

gat gcg ggg ctt ttc gac gac gag atc gtg cca gtc acc gtc cct gcc   739
Asp Ala Gly Leu Phe Asp Asp Glu Ile Val Pro Val Thr Val Pro Ala
        200                 205                 210

aag aag cgc ggc cag gag cca acc atc gtt tct cga gac gag cat ggt   787
```

```
Lys Lys Arg Gly Gln Glu Pro Thr Ile Val Ser Arg Asp Glu His Gly
    215                 220                 225

cga cca gga aca acc gtc gaa aag ctt gct gct ttg cgc ccc atc atg    835
Arg Pro Gly Thr Thr Val Glu Lys Leu Ala Ala Leu Arg Pro Ile Met
230                 235                 240                 245

ggc cgc cag gat gcg gaa gca acc gtc acc gct ggc aac gcg tcc ggc    883
Gly Arg Gln Asp Ala Glu Ala Thr Val Thr Ala Gly Asn Ala Ser Gly
                250                 255                 260

caa aat gat ggc gct gct gcc gtc atc gtg acc act cgc gcc aag gcc    931
Gln Asn Asp Gly Ala Ala Ala Val Ile Val Thr Thr Arg Ala Lys Ala
            265                 270                 275

gag gag aag ggc ctg cgc cca gtc atg cgt ttg gct ggc tgg tct gtg    979
Glu Glu Lys Gly Leu Arg Pro Val Met Arg Leu Ala Gly Trp Ser Val
        280                 285                 290

gct gct gtt ccc cca gag acc atg ggt att gga cct gtt cct gcc acc    1027
Ala Ala Val Pro Pro Glu Thr Met Gly Ile Gly Pro Val Pro Ala Thr
    295                 300                 305

aag aag gtc ctg gat cgt ttg ggc ctt acc ctg gag gac atc ggc gcg    1075
Lys Lys Val Leu Asp Arg Leu Gly Leu Thr Leu Glu Asp Ile Gly Ala
310                 315                 320                 325

atc gaa ctc aac gaa gct ttc gca gct cag gca ctg tct gtg ctg aag    1123
Ile Glu Leu Asn Glu Ala Phe Ala Ala Gln Ala Leu Ser Val Leu Lys
                330                 335                 340

gaa tgg aac att tct tgg gaa gat gag cgc gtc aac cca ctg ggt tcc    1171
Glu Trp Asn Ile Ser Trp Glu Asp Glu Arg Val Asn Pro Leu Gly Ser
            345                 350                 355

ggt att tcc atg gga cac cca gtc ggt gcc acc ggt gct cgc atg gca    1219
Gly Ile Ser Met Gly His Pro Val Gly Ala Thr Gly Ala Arg Met Ala
        360                 365                 370

gta acc ttg gct cac cgc atg cag cgt gaa aac act cag tac gga ctg    1267
Val Thr Leu Ala His Arg Met Gln Arg Glu Asn Thr Gln Tyr Gly Leu
    375                 380                 385

gcc acc atg tgc atc ggt ggc ggc cag ggt ctt gca gct gtc ttt gaa    1315
Ala Thr Met Cys Ile Gly Gly Gly Gln Gly Leu Ala Ala Val Phe Glu
390                 395                 400                 405

aag gag aac taaaaatggc tattttgcac agc                              1347
Lys Glu Asn


<210> 96
<211> 408
<212> PRT
<213> Corynebacterium glutamicum

<400> 96
Met Asn Pro Gln Asp Ile Val Ile Cys Ser Pro Leu Arg Thr Pro Val
  1               5                  10                  15
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Gly Ala Tyr Gly Gly Ser Phe Thr Gly Val Pro Val Glu Glu Leu Ala
            20                  25                  30

Thr Thr Val Ile Asn Ala Ile Val Glu Ala Thr Gly Ile Thr Gly Asp
        35                  40                  45

Asp Val Asp Asp Leu Ile Leu Gly Gln Ala Ser Pro Asn Gly Ala Ala
    50                  55                  60

Pro Ala Leu Gly Arg Val Val Ala Leu Asp Ser Lys Leu Gly Gln Asn
65                  70                  75                  80

Val Pro Gly Met Gln Leu Asp Arg Arg Cys Gly Ser Gly Leu Gln Ala
                85                  90                  95

Ile Val Thr Ala Ala Ala His Val Ala Ser Gly Ala Ala Asp Leu Ile
            100                 105                 110

Ile Ala Gly Gly Ala Glu Ser Met Ser Arg Val Glu Tyr Thr Val Ser
        115                 120                 125

Gly Asp Ile Arg Trp Gly Val Lys Gly Gly Asp Met Gln Leu Arg Asp
    130                 135                 140

Arg Leu Ala Glu Ala Arg Glu Thr Ala Gly Gly Arg Asn His Pro Ile
145                 150                 155                 160

Pro Gly Gly Met Ile Glu Thr Ala Glu Asn Leu Arg Arg Glu Tyr Gly
                165                 170                 175

Ile Ser Arg Glu Glu Gln Asp Lys Ile Ser Ala Ala Ser Gln Gln Arg
            180                 185                 190

Trp Gly Lys Ala Ala Asp Ala Gly Leu Phe Asp Asp Glu Ile Val Pro
        195                 200                 205

Val Thr Val Pro Ala Lys Lys Arg Gly Gln Glu Pro Thr Ile Val Ser
    210                 215                 220

Arg Asp Glu His Gly Arg Pro Gly Thr Thr Val Glu Lys Leu Ala Ala
225                 230                 235                 240

Leu Arg Pro Ile Met Gly Arg Gln Asp Ala Glu Ala Thr Val Thr Ala
                245                 250                 255

Gly Asn Ala Ser Gly Gln Asn Asp Gly Ala Ala Ala Val Ile Val Thr
            260                 265                 270

Thr Arg Ala Lys Ala Glu Glu Lys Gly Leu Arg Pro Val Met Arg Leu
        275                 280                 285

Ala Gly Trp Ser Val Ala Ala Val Pro Pro Glu Thr Met Gly Ile Gly
    290                 295                 300

Pro Val Pro Ala Thr Lys Lys Val Leu Asp Arg Leu Gly Leu Thr Leu
305                 310                 315                 320

Glu Asp Ile Gly Ala Ile Glu Leu Asn Glu Ala Phe Ala Ala Gln Ala
                325                 330                 335

Leu Ser Val Leu Lys Glu Trp Asn Ile Ser Trp Glu Asp Glu Arg Val
```

340 345 350

Asn Pro Leu Gly Ser Gly Ile Ser Met Gly His Pro Val Gly Ala Thr
355 360 365

Gly Ala Arg Met Ala Val Thr Leu Ala His Arg Met Gln Arg Glu Asn
370 375 380

Thr Gln Tyr Gly Leu Ala Thr Met Cys Ile Gly Gly Gly Gln Gly Leu
385 390 395 400

Ala Ala Val Phe Glu Lys Glu Asn
405

<210> 97
<211> 815
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(792)
<223> FRXA01114

<400> 97
cgc ctt gca gaa gca cgc gaa acc gct ggc gga cgc aac cac ccg atc 48
Arg Leu Ala Glu Ala Arg Glu Thr Ala Gly Gly Arg Asn His Pro Ile
1 5 10 15

cct ggt ggc atg atc gag acc gct gag aac ctg cgt cgc gaa tac ggc 96
Pro Gly Gly Met Ile Glu Thr Ala Glu Asn Leu Arg Arg Glu Tyr Gly
20 25 30

atc tcc cgc gag gag cag gac aag atc tcc gca gcg tcc cag cag cgt 144
Ile Ser Arg Glu Glu Gln Asp Lys Ile Ser Ala Ala Ser Gln Gln Arg
35 40 45

tgg ggc aag gct gct gat gcg ggg ctt ttc gac gac gag atc gtg cca 192
Trp Gly Lys Ala Ala Asp Ala Gly Leu Phe Asp Asp Glu Ile Val Pro
50 55 60

gtc acc gtc cct gcc aag aag cgc ggc cag gag cca acc atc gtt tct 240
Val Thr Val Pro Ala Lys Lys Arg Gly Gln Glu Pro Thr Ile Val Ser
65 70 75 80

cga gac gag cat ggt cga cca gga aca acc gtc gaa aag ctt gct gct 288
Arg Asp Glu His Gly Arg Pro Gly Thr Thr Val Glu Lys Leu Ala Ala
85 90 95

ttg cgc ccc atc atg ggc cgc cag gat gcg gaa gca acc gtc acc gct 336
Leu Arg Pro Ile Met Gly Arg Gln Asp Ala Glu Ala Thr Val Thr Ala
100 105 110

ggc aac gcg tcc ggc caa aat gat ggc gct gct gcc gtc atc gtg acc 384
Gly Asn Ala Ser Gly Gln Asn Asp Gly Ala Ala Ala Val Ile Val Thr
115 120 125

act cgc gcc aag gcc gag gag aag ggc ctg cgc cca gtc atg cgt ttg 432
Thr Arg Ala Lys Ala Glu Glu Lys Gly Leu Arg Pro Val Met Arg Leu
130 135 140

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gct ggc tgg tct gtg gct gct gtt ccc cca gag acc atg ggt att gga     480
Ala Gly Trp Ser Val Ala Ala Val Pro Pro Glu Thr Met Gly Ile Gly
145                 150                 155                 160

cct gtt cct gcc acc aag aag gtc ctg gat cgt ttg ggc ctt acc ctg     528
Pro Val Pro Ala Thr Lys Lys Val Leu Asp Arg Leu Gly Leu Thr Leu
                165                 170                 175

gag gac atc ggc gcg atc gaa ctc aac gaa gct ttc gca gct cag gca     576
Glu Asp Ile Gly Ala Ile Glu Leu Asn Glu Ala Phe Ala Ala Gln Ala
            180                 185                 190

ctg tct gtg ctg aag gaa tgg aac att tct tgg gaa gat gag cgc gtc     624
Leu Ser Val Leu Lys Glu Trp Asn Ile Ser Trp Glu Asp Glu Arg Val
        195                 200                 205

aac cca ctg ggt tcc ggt att tcc atg gga cac cca gtc ggt gcc acc     672
Asn Pro Leu Gly Ser Gly Ile Ser Met Gly His Pro Val Gly Ala Thr
    210                 215                 220

ggt gct cgc atg gca gta acc ttg gct cac cgc atg cag cgt gaa aac     720
Gly Ala Arg Met Ala Val Thr Leu Ala His Arg Met Gln Arg Glu Asn
225                 230                 235                 240

act cag tac gga ctg gcc acc atg tgc atc ggt ggc ggc cag ggt ctt     768
Thr Gln Tyr Gly Leu Ala Thr Met Cys Ile Gly Gly Gly Gln Gly Leu
                245                 250                 255

gca gct gtc ttt gaa aag gag aac taaaaatggc tattttgcac agc          815
Ala Ala Val Phe Glu Lys Glu Asn
            260


<210> 98
<211> 264
<212> PRT
<213> Corynebacterium glutamicum

<400> 98
Arg Leu Ala Glu Ala Arg Glu Thr Ala Gly Gly Arg Asn His Pro Ile
  1               5                  10                  15

Pro Gly Gly Met Ile Glu Thr Ala Glu Asn Leu Arg Arg Glu Tyr Gly
            20                  25                  30

Ile Ser Arg Glu Glu Gln Asp Lys Ile Ser Ala Ala Ser Gln Gln Arg
        35                  40                  45

Trp Gly Lys Ala Ala Asp Ala Gly Leu Phe Asp Asp Glu Ile Val Pro
    50                  55                  60

Val Thr Val Pro Ala Lys Lys Arg Gly Gln Glu Pro Thr Ile Val Ser
65                  70                  75                  80

Arg Asp Glu His Gly Arg Pro Gly Thr Thr Val Glu Lys Leu Ala Ala
                85                  90                  95

Leu Arg Pro Ile Met Gly Arg Gln Asp Ala Glu Ala Thr Val Thr Ala
            100                 105                 110
```

```
Gly Asn Ala Ser Gly Gln Asn Asp Gly Ala Ala Ala Val Ile Val Thr
        115                 120                 125

Thr Arg Ala Lys Ala Glu Glu Lys Gly Leu Arg Pro Val Met Arg Leu
    130                 135                 140

Ala Gly Trp Ser Val Ala Ala Val Pro Pro Glu Thr Met Gly Ile Gly
145                 150                 155                 160

Pro Val Pro Ala Thr Lys Lys Val Leu Asp Arg Leu Gly Leu Thr Leu
                165                 170                 175

Glu Asp Ile Gly Ala Ile Glu Leu Asn Glu Ala Phe Ala Ala Gln Ala
            180                 185                 190

Leu Ser Val Leu Lys Glu Trp Asn Ile Ser Trp Glu Asp Glu Arg Val
        195                 200                 205

Asn Pro Leu Gly Ser Gly Ile Ser Met Gly His Pro Val Gly Ala Thr
    210                 215                 220

Gly Ala Arg Met Ala Val Thr Leu Ala His Arg Met Gln Arg Glu Asn
225                 230                 235                 240

Thr Gln Tyr Gly Leu Ala Thr Met Cys Ile Gly Gly Gly Gln Gly Leu
                245                 250                 255

Ala Ala Val Phe Glu Lys Glu Asn
            260


<210> 99
<211> 978
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(955)
<223> RXA01894

<400> 99
agaatttttt cgaaaatgct ggcaccatca acagtgacat tgttagaaac ttcaaggaga 60

acccatgaat gaaccggagc aacatcaccg gtccatgagg atg ccc aaa ccc aaa    115
                                         Met Pro Lys Pro Lys
                                           1               5

aat aat gcg ggt cga gat ctc aaa gct gcc att gct gtg ggg atc gga    163
Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile Ala Val Gly Ile Gly
                10                  15                  20

ctg ggg gtc ctg gtt ctt ttg ggg att gtc cta agc cca tgg ggt tgg    211
Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu Ser Pro Trp Gly Trp
            25                  30                  35

tac atc ctc gtt gca ggt ttt atg gct gca gca aca tgg gaa gtt ggt    259
Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala Thr Trp Glu Val Gly
        40                  45                  50

agc aga ctt aaa gaa ggc ggc tat cat ttg cca ctg ccg att atg atc    307
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Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro Leu Pro Ile Met Ile
55 60 65

atc ggc ggt cag gca atc atc tgg ctg tca tgg cca ttt ggc acg atg 355
Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp Pro Phe Gly Thr Met
70 75 80 85

ggc att ttg gcg tct ttt gtg gcc act gtg ttg gtg ctg atg tat ttc 403
Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu Val Leu Met Tyr Phe
90 95 100

cga att ttc tac aat ggc acg gaa aaa gaa gcc cgc aac tat ttg agg 451
Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala Arg Asn Tyr Leu Arg
105 110 115

gac acc tct gtg ggc atc ttc gtg ctc acc tgg att cca ttg ttc gga 499
Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp Ile Pro Leu Phe Gly
120 125 130

agc ttc gct gcg atg ctg tcg ctg atg caa aac aat tcc atc ccg ggt 547
Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn Asn Ser Ile Pro Gly
135 140 145

aca tat ttc att ttg acg ttc atg ctg tgt gtg atc gca tcg gat gtg 595
Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val Ile Ala Ser Asp Val
150 155 160 165

ggc ggg tat atc gcg ggt gtg ttc ttt gga tcg cac cca atg gcg ccg 643
Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser His Pro Met Ala Pro
170 175 180

ttg gtg agt ccg aag aag tct tgg gaa ggc ttt gcc ggc tcc att gtc 691
Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe Ala Gly Ser Ile Val
185 190 195

tta gga tcg gtc act ggt gca ctc agt gtt cac ttc ctg ctc gat cac 739
Leu Gly Ser Val Thr Gly Ala Leu Ser Val His Phe Leu Leu Asp His
200 205 210

cac tgg tgg atg ggt gtg atc ttg ggt tgt gcc cta gtt gtg tgc gcc 787
His Trp Trp Met Gly Val Ile Leu Gly Cys Ala Leu Val Val Cys Ala
215 220 225

acg ttg ggt gac ttg gtt gag tcg cag ttc aaa cgc gat ttg ggc atc 835
Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys Arg Asp Leu Gly Ile
230 235 240 245

aag gat atg tcg aac ctt ctt cca ggc cac ggc gga ttg atg gac cgt 883
Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly Gly Leu Met Asp Arg
250 255 260

ttg gat ggc atg ctc ccg gcc gcg atg gtg acg tgg ttg atc ctg agt 931
Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr Trp Leu Ile Leu Ser
265 270 275

gtg atc agc agc tcg tat ccg tcg taaagcttgg gccagcttta agt 978
Val Ile Ser Ser Ser Tyr Pro Ser
280 285

<210> 100

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<211> 285
<212> PRT
<213> Corynebacterium glutamicum

<400> 100
Met Pro Lys Pro Lys Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile
 1               5                  10                  15

Ala Val Gly Ile Gly Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu
            20                  25                  30

Ser Pro Trp Gly Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala
        35                  40                  45

Thr Trp Glu Val Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro
    50                  55                  60

Leu Pro Ile Met Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp
65                  70                  75                  80

Pro Phe Gly Thr Met Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu
                85                  90                  95

Val Leu Met Tyr Phe Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala
            100                 105                 110

Arg Asn Tyr Leu Arg Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp
        115                 120                 125

Ile Pro Leu Phe Gly Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn
    130                 135                 140

Asn Ser Ile Pro Gly Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val
145                 150                 155                 160

Ile Ala Ser Asp Val Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser
                165                 170                 175

His Pro Met Ala Pro Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe
            180                 185                 190

Ala Gly Ser Ile Val Leu Gly Ser Val Thr Gly Ala Leu Ser Val His
        195                 200                 205

Phe Leu Leu Asp His His Trp Trp Met Gly Val Ile Leu Gly Cys Ala
    210                 215                 220

Leu Val Val Cys Ala Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys
225                 230                 235                 240

Arg Asp Leu Gly Ile Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly
                245                 250                 255

Gly Leu Met Asp Arg Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr
            260                 265                 270

Trp Leu Ile Leu Ser Val Ile Ser Ser Ser Tyr Pro Ser
        275                 280                 285

<210> 101
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<211> 600
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(577)
<223> RXA02599

<400> 101
gatcaagcat catacgatgt cggagattgt ggcgggcgtt gttacaggag cagttgcaac 60

cggcatttgt tatgcactcc tacttgcgta aaggagaatt atg gat cag cta atc    115
                                          Met Asp Gln Leu Ile
                                          1               5

ctc gac gca ttt atc ggc ttg aga gtg act tgg ctg agt ccg gtg att    163
Leu Asp Ala Phe Ile Gly Leu Arg Val Thr Trp Leu Ser Pro Val Ile
                10                  15                  20

att ttg ttc acc cag ctc acc ggg cca aca ctg atg ttt gtg tat gcg    211
Ile Leu Phe Thr Gln Leu Thr Gly Pro Thr Leu Met Phe Val Tyr Ala
            25                  30                  35

ctt gtg tgg ggc ttg ttg cgc aag agc gcc act gcc ccg atc gcg gtg    259
Leu Val Trp Gly Leu Leu Arg Lys Ser Ala Thr Ala Pro Ile Ala Val
        40                  45                  50

ggg ctg gct aat ctg atc agt cat ttt ctc aag agg gcg ttt gaa cgg    307
Gly Leu Ala Asn Leu Ile Ser His Phe Leu Lys Arg Ala Phe Glu Arg
    55                  60                  65

cct cga cca aat aca gca gag cac ttg gtt gta gaa act aac ttt tca    355
Pro Arg Pro Asn Thr Ala Glu His Leu Val Val Glu Thr Asn Phe Ser
70                  75                  80                  85

ttc cct tct ggt cat gct gtg ggc gct gca gca tgt gcc gtg gca gtg    403
Phe Pro Ser Gly His Ala Val Gly Ala Ala Ala Cys Ala Val Ala Val
                90                  95                  100

ggg tac tcc gtg aac cgg tgg tgg aaa ctc acg ctg tgg gta atc gcg    451
Gly Tyr Ser Val Asn Arg Trp Trp Lys Leu Thr Leu Trp Val Ile Ala
            105                 110                 115

ctg ctt gtg ggg ctg tct cgg ttg tat gtc ggt gtg cat tgg ccc agc    499
Leu Leu Val Gly Leu Ser Arg Leu Tyr Val Gly Val His Trp Pro Ser
        120                 125                 130

gat gtg ctt gcc ggc tgg gcc atc ggt gcg ttg act tca gtg gtg gtg    547
Asp Val Leu Ala Gly Trp Ala Ile Gly Ala Leu Thr Ser Val Val Val
    135                 140                 145

ttt acc agc tgg aac ctc ctc cag cgc cgc tgaaaccact gctgaaagtg      597
Phe Thr Ser Trp Asn Leu Leu Gln Arg Arg
150                 155

gta                                                                600


<210> 102
<211> 159
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<212> PRT
<213> Corynebacterium glutamicum

<400> 102
Met Asp Gln Leu Ile Leu Asp Ala Phe Ile Gly Leu Arg Val Thr Trp
 1               5                  10                  15

Leu Ser Pro Val Ile Ile Leu Phe Thr Gln Leu Thr Gly Pro Thr Leu
            20                  25                  30

Met Phe Val Tyr Ala Leu Val Trp Gly Leu Leu Arg Lys Ser Ala Thr
        35                  40                  45

Ala Pro Ile Ala Val Gly Leu Ala Asn Leu Ile Ser His Phe Leu Lys
    50                  55                  60

Arg Ala Phe Glu Arg Pro Arg Pro Asn Thr Ala Glu His Leu Val Val
65                  70                  75                  80

Glu Thr Asn Phe Ser Phe Pro Ser Gly His Ala Val Gly Ala Ala Ala
                85                  90                  95

Cys Ala Val Ala Val Gly Tyr Ser Val Asn Arg Trp Trp Lys Leu Thr
            100                 105                 110

Leu Trp Val Ile Ala Leu Leu Val Gly Leu Ser Arg Leu Tyr Val Gly
        115                 120                 125

Val His Trp Pro Ser Asp Val Leu Ala Gly Trp Ala Ile Gly Ala Leu
    130                 135                 140

Thr Ser Val Val Val Phe Thr Ser Trp Asn Leu Leu Gln Arg Arg
145                 150                 155


<210> 103
<211> 999
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(976)
<223> RXN02638

<400> 103
ctctgttgtt gttcctgagg cgcttcgtcc attcgtgggc aaagacgtgc tcaagccagt 60

gaaacaagcc ggttaattaa gcggaaagct cgtggtcgac atg gtc aaa agg ttt   115
                                           Met Val Lys Arg Phe
                                            1               5

ggc ttt ttc gta gag gat tcc ctg cct aag gtt ccg ctg cat ccc gaa   163
Gly Phe Phe Val Glu Asp Ser Leu Pro Lys Val Pro Leu His Pro Glu
                10                  15                  20

gag tca cgg gag acg ttt tat ggg cgc atc atc att agt gct gtg cgg   211
Glu Ser Arg Glu Thr Phe Tyr Gly Arg Ile Ile Ile Ser Ala Val Arg
            25                  30                  35

acg gtg atg aaa gcc cag gat gtg cag att tcc atc ttc ggt gcg gag   259
```

```
Thr Val Met Lys Ala Gln Asp Val Gln Ile Ser Ile Phe Gly Ala Glu
        40                  45                  50

aac att ccg acc acc ggc ggc gca ctt ttc gca tca acc aca ctg gtt     307
Asn Ile Pro Thr Thr Gly Gly Ala Leu Phe Ala Ser Thr Thr Leu Val
    55                  60                  65

att atg act tca ttc tgg gtg gta tcc ccc gca ttc gtg cgg ggt aag     355
Ile Met Thr Ser Phe Trp Val Val Ser Pro Ala Phe Val Arg Gly Lys
70                  75                  80                  85

cgc ctg gtt cga ttc atg gcg aag aag gaa att ttc gac acc cca gtt     403
Arg Leu Val Arg Phe Met Ala Lys Lys Glu Ile Phe Asp Thr Pro Val
                90                  95                  100

gtc ggc acc ctc atg cgc tgg atg aag cac gtc tct gtg gac cgc tcc     451
Val Gly Thr Leu Met Arg Trp Met Lys His Val Ser Val Asp Arg Ser
            105                 110                 115

gca ggt gcc ggt tcc atg gaa gat gcg cgg aag cgt ctc gac gcc ggc     499
Ala Gly Ala Gly Ser Met Glu Asp Ala Arg Lys Arg Leu Asp Ala Gly
        120                 125                 130

agc ctc gtc ggt atc ttc cct gag gcg acg gtg tca cgg tcc ttt gaa     547
Ser Leu Val Gly Ile Phe Pro Glu Ala Thr Val Ser Arg Ser Phe Glu
    135                 140                 145

atc aag gaa cta aaa act ggc gcc gtc cgc atc gcc gac agc gct aac     595
Ile Lys Glu Leu Lys Thr Gly Ala Val Arg Ile Ala Asp Ser Ala Asn
150                 155                 160                 165

gtt ccg ctg ctg cca ctt att att tgg ggc ggc cag cgc atc atc acc     643
Val Pro Leu Leu Pro Leu Ile Ile Trp Gly Gly Gln Arg Ile Ile Thr
                170                 175                 180

aaa gac atc gag cgc gac ttc ggc cgc tcc cac atc ccc gta ttc atc     691
Lys Asp Ile Glu Arg Asp Phe Gly Arg Ser His Ile Pro Val Phe Ile
            185                 190                 195

agc gtg ggt gaa ccc gtc gac gcc agc ggc gat ccc gac gaa gca acg     739
Ser Val Gly Glu Pro Val Asp Ala Ser Gly Asp Pro Asp Glu Ala Thr
        200                 205                 210

gaa cgc ctc tac gag gct atg aaa aag ctt ctc gac gaa acc cgc acc     787
Glu Arg Leu Tyr Glu Ala Met Lys Lys Leu Leu Asp Glu Thr Arg Thr
    215                 220                 225

gcc tac gaa caa aag tat ggc cca ttc gaa ggt gga gaa ttg tgg cgc     835
Ala Tyr Glu Gln Lys Tyr Gly Pro Phe Glu Gly Gly Glu Leu Trp Arg
230                 235                 240                 245

ccg aaa tcc ctc ggc ggc ggc gcc cca acg ttg gag cag gcg aaa atg     883
Pro Lys Ser Leu Gly Gly Gly Ala Pro Thr Leu Glu Gln Ala Lys Met
                250                 255                 260

ttg gaa atc gcc gaa cgg gaa cgt cga caa gca aaa cgc gcg gca aag     931
Leu Glu Ile Ala Glu Arg Glu Arg Arg Gln Ala Lys Arg Ala Ala Lys
            265                 270                 275

gtc gcc aag aaa cgc acc acc ttt ata agg aaa atc ttt aaa aaa         976
Val Ala Lys Lys Arg Thr Thr Phe Ile Arg Lys Ile Phe Lys Lys
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280 285 290

tgattgcact gggttcagcg ccc 999

<210> 104
<211> 292
<212> PRT
<213> Corynebacterium glutamicum

<400> 104
Met Val Lys Arg Phe Gly Phe Phe Val Glu Asp Ser Leu Pro Lys Val
1 5 10 15

Pro Leu His Pro Glu Glu Ser Arg Glu Thr Phe Tyr Gly Arg Ile Ile
20 25 30

Ile Ser Ala Val Arg Thr Val Met Lys Ala Gln Asp Val Gln Ile Ser
35 40 45

Ile Phe Gly Ala Glu Asn Ile Pro Thr Thr Gly Gly Ala Leu Phe Ala
50 55 60

Ser Thr Thr Leu Val Ile Met Thr Ser Phe Trp Val Val Ser Pro Ala
65 70 75 80

Phe Val Arg Gly Lys Arg Leu Val Arg Phe Met Ala Lys Lys Glu Ile
85 90 95

Phe Asp Thr Pro Val Val Gly Thr Leu Met Arg Trp Met Lys His Val
100 105 110

Ser Val Asp Arg Ser Ala Gly Ala Gly Ser Met Glu Asp Ala Arg Lys
115 120 125

Arg Leu Asp Ala Gly Ser Leu Val Gly Ile Phe Pro Glu Ala Thr Val
130 135 140

Ser Arg Ser Phe Glu Ile Lys Glu Leu Lys Thr Gly Ala Val Arg Ile
145 150 155 160

Ala Asp Ser Ala Asn Val Pro Leu Leu Pro Leu Ile Ile Trp Gly Gly
165 170 175

Gln Arg Ile Ile Thr Lys Asp Ile Glu Arg Asp Phe Gly Arg Ser His
180 185 190

Ile Pro Val Phe Ile Ser Val Gly Glu Pro Val Asp Ala Ser Gly Asp
195 200 205

Pro Asp Glu Ala Thr Glu Arg Leu Tyr Glu Ala Met Lys Lys Leu Leu
210 215 220

Asp Glu Thr Arg Thr Ala Tyr Glu Gln Lys Tyr Gly Pro Phe Glu Gly
225 230 235 240

Gly Glu Leu Trp Arg Pro Lys Ser Leu Gly Gly Gly Ala Pro Thr Leu
245 250 255

Glu Gln Ala Lys Met Leu Glu Ile Ala Glu Arg Glu Arg Arg Gln Ala
260 265 270

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Lys Arg Ala Ala Lys Val Ala Lys Lys Arg Thr Thr Phe Ile Arg Lys
        275                 280                 285

Ile Phe Lys Lys
    290


<210> 105
<211> 534
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (8)..(511)
<223> FRXA02638

<400> 105
atgaagaatg gcg cgg aag cgt ctt aac gcc ggc agc ctc gtc ggt atc      49
           Met Ala Arg Lys Arg Leu Asn Ala Gly Ser Leu Val Gly Ile
             1               5                  10

ttc cct gag gcg acg gtg tca cgg tcc ttt gaa atc aag gaa cta aaa      97
Phe Pro Glu Ala Thr Val Ser Arg Ser Phe Glu Ile Lys Glu Leu Lys
 15                  20                  25                  30

act ggc gcc gtc cgc atc gcc gac agc gct aac gtt ccg ctg ctg cca     145
Thr Gly Ala Val Arg Ile Ala Asp Ser Ala Asn Val Pro Leu Leu Pro
                 35                  40                  45

ctt att att tgg ggc ggc cag cgc atc atc acc aaa gac atc gag cgc     193
Leu Ile Ile Trp Gly Gly Gln Arg Ile Ile Thr Lys Asp Ile Glu Arg
             50                  55                  60

gac ttc ggc cgc tcc cac atc ccc gta ttc atc agc gtg ggt gaa ccc     241
Asp Phe Gly Arg Ser His Ile Pro Val Phe Ile Ser Val Gly Glu Pro
         65                  70                  75

gtc gac gcc agc ggc gat ccc gac gaa gca acg gaa cgc ctc tac gag     289
Val Asp Ala Ser Gly Asp Pro Asp Glu Ala Thr Glu Arg Leu Tyr Glu
     80                  85                  90

gct atg aaa aag ctt ctc gac gaa acc cgc acc gcc tac gaa caa aag     337
Ala Met Lys Lys Leu Leu Asp Glu Thr Arg Thr Ala Tyr Glu Gln Lys
 95                 100                 105                 110

tat ggc cca ttc gaa ggt gga gaa ttg tgg cgc ccg aaa tcc ctc ggc     385
Tyr Gly Pro Phe Glu Gly Gly Glu Leu Trp Arg Pro Lys Ser Leu Gly
                115                 120                 125

ggc ggc gcc cca acg ttg gag cag gcg aaa atg ttg gaa atc gcc gaa     433
Gly Gly Ala Pro Thr Leu Glu Gln Ala Lys Met Leu Glu Ile Ala Glu
            130                 135                 140

cgg gaa cgt cga caa gca aaa cgc gcg gca aag gtc gcc aag aaa cgc     481
Arg Glu Arg Arg Gln Ala Lys Arg Ala Ala Lys Val Ala Lys Lys Arg
        145                 150                 155

acc acc ttt ata agg aaa atc ttt aaa aaa tgattgcact gggttcagcg       531
Thr Thr Phe Ile Arg Lys Ile Phe Lys Lys
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    160                 165

ccc                                                                   534


<210> 106
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 106
Met Ala Arg Lys Arg Leu Asn Ala Gly Ser Leu Val Gly Ile Phe Pro
1               5                   10                  15

Glu Ala Thr Val Ser Arg Ser Phe Glu Ile Lys Glu Leu Lys Thr Gly
            20                  25                  30

Ala Val Arg Ile Ala Asp Ser Ala Asn Val Pro Leu Leu Pro Leu Ile
        35                  40                  45

Ile Trp Gly Gly Gln Arg Ile Ile Thr Lys Asp Ile Glu Arg Asp Phe
    50                  55                  60

Gly Arg Ser His Ile Pro Val Phe Ile Ser Val Gly Glu Pro Val Asp
65                  70                  75                  80

Ala Ser Gly Asp Pro Asp Glu Ala Thr Glu Arg Leu Tyr Glu Ala Met
                85                  90                  95

Lys Lys Leu Leu Asp Glu Thr Arg Thr Ala Tyr Glu Gln Lys Tyr Gly
            100                 105                 110

Pro Phe Glu Gly Gly Glu Leu Trp Arg Pro Lys Ser Leu Gly Gly Gly
        115                 120                 125

Ala Pro Thr Leu Glu Gln Ala Lys Met Leu Glu Ile Ala Glu Arg Glu
    130                 135                 140

Arg Arg Gln Ala Lys Arg Ala Ala Lys Val Ala Lys Lys Arg Thr Thr
145                 150                 155                 160

Phe Ile Arg Lys Ile Phe Lys Lys
                165


<210> 107
<211> 637
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(637)
<223> RXA00856

<400> 107
gtttttagga atagagtggg ctcaagcttt gtgacaagtt ttttggagaa atcattacta 60

gtcgtagtct tcaatttggg tgcaggtagg gtggaacacc gtg agt gat gta tca   115
                                           Val Ser Asp Val Ser
                                           1               5
```

gca ggc gta aat ggc gca caa gat cca agc aat caa gcg gtc aag cct 163
Ala Gly Val Asn Gly Ala Gln Asp Pro Ser Asn Gln Ala Val Lys Pro
10 15 20

tcc aac tgg aac ctt ccg aac ttc ttg acc agc ttg cgt atc att gtc 211
Ser Asn Trp Asn Leu Pro Asn Phe Leu Thr Ser Leu Arg Ile Ile Val
25 30 35

atc cct ttg ttt gcg tgg ctt acg ctt aaa ggt gag acg gaa aac aat 259
Ile Pro Leu Phe Ala Trp Leu Thr Leu Lys Gly Glu Thr Glu Asn Asn
40 45 50

gct ttt gcc tgg tgg gcg ttg gtt gtt ttc att ttg ctc atg atc acc 307
Ala Phe Ala Trp Trp Ala Leu Val Val Phe Ile Leu Leu Met Ile Thr
55 60 65

gac aag ctt gac ggc gat att gcg cga gca cgt ggc ctg gtc act gac 355
Asp Lys Leu Asp Gly Asp Ile Ala Arg Ala Arg Gly Leu Val Thr Asp
70 75 80 85

ttt ggc aag atc gcg gat ccg att gcc gat aag gcg ttg atg acc aca 403
Phe Gly Lys Ile Ala Asp Pro Ile Ala Asp Lys Ala Leu Met Thr Thr
90 95 100

gca ttt gtc tgt ttc aac atc atc ggc att ttg ccc tgg tgg gtc act 451
Ala Phe Val Cys Phe Asn Ile Ile Gly Ile Leu Pro Trp Trp Val Thr
105 110 115

gcg ttg att gtg ctt cga gag ttc ggc att acc atc tgg cgt ttc ttc 499
Ala Leu Ile Val Leu Arg Glu Phe Gly Ile Thr Ile Trp Arg Phe Phe
120 125 130

caa ctg cgc gct gga aat gtt gtg cct gca tca aag ggg ggc aag ctt 547
Gln Leu Arg Ala Gly Asn Val Val Pro Ala Ser Lys Gly Gly Lys Leu
135 140 145

aag act gct ctg cag act gtt gcc gtt gct ctg tat ctg tgc cct ttc 595
Lys Thr Ala Leu Gln Thr Val Ala Val Ala Leu Tyr Leu Cys Pro Phe
150 155 160 165

cca agt tgg atg gat att cca agc cag atc gtc atg tat gca 637
Pro Ser Trp Met Asp Ile Pro Ser Gln Ile Val Met Tyr Ala
170 175

<210> 108
<211> 179
<212> PRT
<213> Corynebacterium glutamicum

<400> 108
Val Ser Asp Val Ser Ala Gly Val Asn Gly Ala Gln Asp Pro Ser Asn
1 5 10 15

Gln Ala Val Lys Pro Ser Asn Trp Asn Leu Pro Asn Phe Leu Thr Ser
20 25 30

Leu Arg Ile Ile Val Ile Pro Leu Phe Ala Trp Leu Thr Leu Lys Gly
35 40 45

Glu Thr Glu Asn Asn Ala Phe Ala Trp Trp Ala Leu Val Val Phe Ile
50 55 60

Leu Leu Met Ile Thr Asp Lys Leu Asp Gly Asp Ile Ala Arg Ala Arg
65 70 75 80

Gly Leu Val Thr Asp Phe Gly Lys Ile Ala Asp Pro Ile Ala Asp Lys
85 90 95

Ala Leu Met Thr Thr Ala Phe Val Cys Phe Asn Ile Ile Gly Ile Leu
100 105 110

Pro Trp Trp Val Thr Ala Leu Ile Val Leu Arg Glu Phe Gly Ile Thr
115 120 125

Ile Trp Arg Phe Phe Gln Leu Arg Ala Gly Asn Val Val Pro Ala Ser
130 135 140

Lys Gly Gly Lys Leu Lys Thr Ala Leu Gln Thr Val Ala Val Ala Leu
145 150 155 160

Tyr Leu Cys Pro Phe Pro Ser Trp Met Asp Ile Pro Ser Gln Ile Val
165 170 175

Met Tyr Ala

<210> 109
<211> 780
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(757)
<223> RXA02511

<400> 109
ccatgcttgc gcaagcatgg ggcaccattg atggggcacc aggcactgtc gacccaacgc 60

tgacttcagc gatccgtacc gcagcaccga aggagcactg atg ctg gga ctt cat 115
Met Leu Gly Leu His
1 5

gga cgt aag cct gcg cag gtt att gtt gag cct gtt gcc aaa ttg atg 163
Gly Arg Lys Pro Ala Gln Val Ile Val Glu Pro Val Ala Lys Leu Met
10 15 20

atc aag ttg aag gtg acg cct aat cag ctc acc tta gtc agc gct ggc 211
Ile Lys Leu Lys Val Thr Pro Asn Gln Leu Thr Leu Val Ser Ala Gly
25 30 35

ctc acc gtt ggg gtg gct ttg ctg ctg att cct acg ggg cat ttg att 259
Leu Thr Val Gly Val Ala Leu Leu Leu Ile Pro Thr Gly His Leu Ile
40 45 50

tgg gcg gca gtt ttg acg ggc ctg ttt gcg gct ttc gac atg att gat 307
Trp Ala Ala Val Leu Thr Gly Leu Phe Ala Ala Phe Asp Met Ile Asp
55 60 65

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ggc acg gtt gct cgc atg caa ggt ggt ggc acc aaa ttt ggt gcc acc    355
Gly Thr Val Ala Arg Met Gln Gly Gly Gly Thr Lys Phe Gly Ala Thr
 70                  75                  80                  85

ttg gat gcc acg tgt gac cgc atc act gat ggt gca cta ttt ggt gcg    403
Leu Asp Ala Thr Cys Asp Arg Ile Thr Asp Gly Ala Leu Phe Gly Ala
                 90                  95                 100

att acc tgg tgg ctg gtg tat tcc tac gat gca cca cag gca ttg gtc    451
Ile Thr Trp Trp Leu Val Tyr Ser Tyr Asp Ala Pro Gln Ala Leu Val
            105                 110                 115

gct gcc tcc ttg gtt tgt ttg gtt gcc tcc cag gtg atc tct tac gtg    499
Ala Ala Ser Leu Val Cys Leu Val Ala Ser Gln Val Ile Ser Tyr Val
        120                 125                 130

aaa gcc agg gga gag gcc tcc gga ttc acc atg gac ggc ggt ctc gtg    547
Lys Ala Arg Gly Glu Ala Ser Gly Phe Thr Met Asp Gly Gly Leu Val
    135                 140                 145

gaa cgc cct gag cgt ctg att gtc agc ctt gtt ggt ttg ggg ctg acc    595
Glu Arg Pro Glu Arg Leu Ile Val Ser Leu Val Gly Leu Gly Leu Thr
150                 155                 160                 165

gga atg ggc gtt cca tat gcc atc gat gtg gca ctg tgg gcc ctt gca    643
Gly Met Gly Val Pro Tyr Ala Ile Asp Val Ala Leu Trp Ala Leu Ala
                170                 175                 180

gct ggc agt att tac act gtt gtg cag cgc ttg gtc atg gct gga aag    691
Ala Gly Ser Ile Tyr Thr Val Val Gln Arg Leu Val Met Ala Gly Lys
            185                 190                 195

tcc cca ttg gct aag gaa ttt acc aag gca cca gca ggt gcg aag gca    739
Ser Pro Leu Ala Lys Glu Phe Thr Lys Ala Pro Ala Gly Ala Lys Ala
        200                 205                 210

gat tac agc aac acc aaa taaaaattag ccgagggagc atc                  780
Asp Tyr Ser Asn Thr Lys
    215


<210> 110
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

<400> 110
Met Leu Gly Leu His Gly Arg Lys Pro Ala Gln Val Ile Val Glu Pro
  1               5                  10                  15

Val Ala Lys Leu Met Ile Lys Leu Lys Val Thr Pro Asn Gln Leu Thr
             20                  25                  30

Leu Val Ser Ala Gly Leu Thr Val Gly Val Ala Leu Leu Leu Ile Pro
         35                  40                  45

Thr Gly His Leu Ile Trp Ala Ala Val Leu Thr Gly Leu Phe Ala Ala
     50                  55                  60

Phe Asp Met Ile Asp Gly Thr Val Ala Arg Met Gln Gly Gly Gly Thr
 65                  70                  75                  80
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Lys Phe Gly Ala Thr Leu Asp Ala Thr Cys Asp Arg Ile Thr Asp Gly
                85                  90                  95

Ala Leu Phe Gly Ala Ile Thr Trp Trp Leu Val Tyr Ser Tyr Asp Ala
            100                 105                 110

Pro Gln Ala Leu Val Ala Ala Ser Leu Val Cys Leu Val Ala Ser Gln
        115                 120                 125

Val Ile Ser Tyr Val Lys Ala Arg Gly Glu Ala Ser Gly Phe Thr Met
    130                 135                 140

Asp Gly Gly Leu Val Glu Arg Pro Glu Arg Leu Ile Val Ser Leu Val
145                 150                 155                 160

Gly Leu Gly Leu Thr Gly Met Gly Val Pro Tyr Ala Ile Asp Val Ala
                165                 170                 175

Leu Trp Ala Leu Ala Ala Gly Ser Ile Tyr Thr Val Val Gln Arg Leu
            180                 185                 190

Val Met Ala Gly Lys Ser Pro Leu Ala Lys Glu Phe Thr Lys Ala Pro
        195                 200                 205

Ala Gly Ala Lys Ala Asp Tyr Ser Asn Thr Lys
    210                 215


<210> 111
<211> 678
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(655)
<223> RXN02836

<400> 111
ccatcactcg gcttcaccgt ctacggtgct gcccgcagga cagagcgccc ccaaaagctc 60

gcttcagacg ggatccaccc cctcgagatg gacgtcaccg atg aca atc gat gaa   115
                                            Met Thr Ile Asp Glu
                                            1               5

ggc cgt cgc cag ttc gag gtc aat gta ttc ggc gcg atg gcc ctc acc   163
Gly Arg Arg Gln Phe Glu Val Asn Val Phe Gly Ala Met Ala Leu Thr
                10                  15                  20

cga ctc gtc ctg ccc cac atg cag aaa caa aag tgg ggg acg atc gtg   211
Arg Leu Val Leu Pro His Met Gln Lys Gln Lys Trp Gly Thr Ile Val
            25                  30                  35

aac atc aca tcg atg ggc ggg aag atc tac acg cct ctc ggc ggc tgg   259
Asn Ile Thr Ser Met Gly Gly Lys Ile Tyr Thr Pro Leu Gly Gly Trp
        40                  45                  50

tat cac ggc acc aag ttc gcc ctc gag gcc ctc tcg gac gcc ctc cgc   307
Tyr His Gly Thr Lys Phe Ala Leu Glu Ala Leu Ser Asp Ala Leu Arg
    55                  60                  65
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ctg gag gtc gcc cca ttc ggc atc gac gtt gtt gtc atc gaa ccg ggc     355
Leu Glu Val Ala Pro Phe Gly Ile Asp Val Val Val Ile Glu Pro Gly
 70                 75                  80                  85

ggc atc gcc acc gag tgg gga gga atc gct gcc gac aat ctc gac gca     403
Gly Ile Ala Thr Glu Trp Gly Gly Ile Ala Ala Asp Asn Leu Asp Ala
                90                  95                 100

gtg tcg aaa gac agc gca tac aag cgc cag gct gac gca gta tcg aag     451
Val Ser Lys Asp Ser Ala Tyr Lys Arg Gln Ala Asp Ala Val Ser Lys
            105                 110                 115

tcg ttg cga tct gag gcg aac agc aac cgc aac tca cca ccg tcg gtt     499
Ser Leu Arg Ser Glu Ala Asn Ser Asn Arg Asn Ser Pro Pro Ser Val
        120                 125                 130

gtc gcc gat gcg att gga aag gcc gtg acg gca cgt cac ccc aag acc     547
Val Ala Asp Ala Ile Gly Lys Ala Val Thr Ala Arg His Pro Lys Thr
    135                 140                 145

cgc tat gcc atc ggc ttc ggt gcc aaa ccg ctg att gcc tcg cgc aac     595
Arg Tyr Ala Ile Gly Phe Gly Ala Lys Pro Leu Ile Ala Ser Arg Asn
150                 155                 160                 165

atc ctc acc gat cgc cag ttc gac cca gtg atc act cga gcg act ggc     643
Ile Leu Thr Asp Arg Gln Phe Asp Pro Val Ile Thr Arg Ala Thr Gly
                170                 175                 180

gtc ccc cgc gac tgaccactct tctgcgcccg tca                           678
Val Pro Arg Asp
            185


&lt;210&gt; 112
&lt;211&gt; 185
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 112
Met Thr Ile Asp Glu Gly Arg Arg Gln Phe Glu Val Asn Val Phe Gly
  1               5                  10                  15

Ala Met Ala Leu Thr Arg Leu Val Leu Pro His Met Gln Lys Gln Lys
            20                  25                  30

Trp Gly Thr Ile Val Asn Ile Thr Ser Met Gly Gly Lys Ile Tyr Thr
        35                  40                  45

Pro Leu Gly Gly Trp Tyr His Gly Thr Lys Phe Ala Leu Glu Ala Leu
    50                  55                  60

Ser Asp Ala Leu Arg Leu Glu Val Ala Pro Phe Gly Ile Asp Val Val
65                  70                  75                  80

Val Ile Glu Pro Gly Gly Ile Ala Thr Glu Trp Gly Gly Ile Ala Ala
                85                  90                  95

Asp Asn Leu Asp Ala Val Ser Lys Asp Ser Ala Tyr Lys Arg Gln Ala
            100                 105                 110
```

```
Asp Ala Val Ser Lys Ser Leu Arg Ser Glu Ala Asn Ser Asn Arg Asn
        115                 120                 125

Ser Pro Pro Ser Val Val Ala Asp Ala Ile Gly Lys Ala Val Thr Ala
    130                 135                 140

Arg His Pro Lys Thr Arg Tyr Ala Ile Gly Phe Gly Ala Lys Pro Leu
145                 150                 155                 160

Ile Ala Ser Arg Asn Ile Leu Thr Asp Arg Gln Phe Asp Pro Val Ile
                165                 170                 175

Thr Arg Ala Thr Gly Val Pro Arg Asp
            180                 185


<210> 113
<211> 406
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(406)
<223> FRXA02836

<400> 113
ccatcactcg gcttcaccgt ctacggtgct gcccgcagga cagagcgccc ccaaaagctc 60

gcttcagacg ggatccaccc cctcgagatg gacgtcaccg atg aca atc gat gaa    115
                                          Met Thr Ile Asp Glu
                                          1               5

ggc cgt cgc cag ttc gag gtc aat gta ttc ggc gcg atg gcc ctc acc    163
Gly Arg Arg Gln Phe Glu Val Asn Val Phe Gly Ala Met Ala Leu Thr
                10                  15                  20

cga ctc gtc ctg ccc cac atg cag aaa caa aag tgg ggg acg atc gtg    211
Arg Leu Val Leu Pro His Met Gln Lys Gln Lys Trp Gly Thr Ile Val
            25                  30                  35

aac atc aca tcg atg ggc ggg aag atc tac acg cct ctc ggc ggc tgg    259
Asn Ile Thr Ser Met Gly Gly Lys Ile Tyr Thr Pro Leu Gly Gly Trp
        40                  45                  50

tat cac ggc acc aag ttc gcc ctc gag gcc ctc tcg gac gcc ctc cgc    307
Tyr His Gly Thr Lys Phe Ala Leu Glu Ala Leu Ser Asp Ala Leu Arg
    55                  60                  65

ctg gag gtc gcc cca ttc ggc atc gac gtt gtt gtc atc gaa ccg ggc    355
Leu Glu Val Ala Pro Phe Gly Ile Asp Val Val Val Ile Glu Pro Gly
70                  75                  80                  85

ggc atc gcc acc gag tgg gga gga atc gct gcc gac aat ctc gac gca    403
Gly Ile Ala Thr Glu Trp Gly Gly Ile Ala Ala Asp Asn Leu Asp Ala
                90                  95                  100

gtg                                                                406
Val
```

```
<210> 114
<211> 102
<212> PRT
<213> Corynebacterium glutamicum

<400> 114
Met Thr Ile Asp Glu Gly Arg Arg Gln Phe Glu Val Asn Val Phe Gly
1               5                   10                  15

Ala Met Ala Leu Thr Arg Leu Val Leu Pro His Met Gln Lys Gln Lys
            20                  25                  30

Trp Gly Thr Ile Val Asn Ile Thr Ser Met Gly Gly Lys Ile Tyr Thr
        35                  40                  45

Pro Leu Gly Gly Trp Tyr His Gly Thr Lys Phe Ala Leu Glu Ala Leu
    50                  55                  60

Ser Asp Ala Leu Arg Leu Glu Val Ala Pro Phe Gly Ile Asp Val Val
65                  70                  75                  80

Val Ile Glu Pro Gly Gly Ile Ala Thr Glu Trp Gly Gly Ile Ala Ala
                85                  90                  95

Asp Asn Leu Asp Ala Val
            100


<210> 115
<211> 1227
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1204)
<223> RXA02578

<400> 115
ggcaaaaatg aggaacagca cgcccgcaat aatgaggacc gttgcagatc gcttcataaa 60

aacagcccac acctttccgc taaactcgca tgttgaaata atg tct acc caa tca    115
                                           Met Ser Thr Gln Ser
                                           1               5

tat gca ccc atc cgc cat cgc gga ttc atc agc tca ctc gag gga cta    163
Tyr Ala Pro Ile Arg His Arg Gly Phe Ile Ser Ser Leu Glu Gly Leu
                10                  15                  20

cgc gca atc gcc tcc ctg gga gtc ttg gcg acc cac gtt gca ttc caa    211
Arg Ala Ile Ala Ser Leu Gly Val Leu Ala Thr His Val Ala Phe Gln
            25                  30                  35

acc tcc gtc gac ccc gcc agc aac atc ggt gca gta ctc gcg cgt ttc    259
Thr Ser Val Asp Pro Ala Ser Asn Ile Gly Ala Val Leu Ala Arg Phe
        40                  45                  50

gac ttt ttc gtc gcc gtc ttc ttc gcc ctc tcc gcc ttc gtt ctt tgg    307
Asp Phe Phe Val Ala Val Phe Phe Ala Leu Ser Ala Phe Val Leu Trp
    55                  60                  65
```

```
cga cgc cgc gcc ggg caa cca gtg gga ctg tac tac ctc aaa cgc cta      355
Arg Arg Arg Ala Gly Gln Pro Val Gly Leu Tyr Tyr Leu Lys Arg Leu
 70                  75                  80                  85

gcc cgc atc atg ccc gca tac tgg gca acg gtc att gca gtc ctg ctg      403
Ala Arg Ile Met Pro Ala Tyr Trp Ala Thr Val Ile Ala Val Leu Leu
                 90                  95                 100

ttt att ccc acc ggc ccc tgg tta gcc aac ctg acg atg acc caa atc      451
Phe Ile Pro Thr Gly Pro Trp Leu Ala Asn Leu Thr Met Thr Gln Ile
            105                 110                 115

tac tgg cca gac ggg ctc atg aca ggc ctc acc cac ctt tgg tcc ctg      499
Tyr Trp Pro Asp Gly Leu Met Thr Gly Leu Thr His Leu Trp Ser Leu
        120                 125                 130

tgc gtg gaa gtg gcg ttt tac ctg gtg atg ccg ctt ctc gcg tgg gtg      547
Cys Val Glu Val Ala Phe Tyr Leu Val Met Pro Leu Leu Ala Trp Val
    135                 140                 145

ttg gat agg ttt ggt cgg ccg gtg cgc atc ctg ttg att gtt ggt ggg      595
Leu Asp Arg Phe Gly Arg Pro Val Arg Ile Leu Leu Ile Val Gly Gly
150                 155                 160                 165

gca gtg ttg agt ctg gcg tgg ccg tgg att ccc ctt gtg gag cat gcg      643
Ala Val Leu Ser Leu Ala Trp Pro Trp Ile Pro Leu Val Glu His Ala
                170                 175                 180

ttg gac gag ggg tgg gcg aac atg cag atc tgg cca ccc gct tac gct      691
Leu Asp Glu Gly Trp Ala Asn Met Gln Ile Trp Pro Pro Ala Tyr Ala
            185                 190                 195

tgc tgg ttt gca gtc ggc atg atc gcc gca gaa att gaa gga gtt cga      739
Cys Trp Phe Ala Val Gly Met Ile Ala Ala Glu Ile Glu Gly Val Arg
        200                 205                 210

ttc cca cgg gtt ccg agc ttt gtg tgg gtg ggt tta gct tta gtg gtc      787
Phe Pro Arg Val Pro Ser Phe Val Trp Val Gly Leu Ala Leu Val Val
    215                 220                 225

gct tgg atc gcg ggc caa gaa tgg ttc gga cca cta ggt tta gtg cac      835
Ala Trp Ile Ala Gly Gln Glu Trp Phe Gly Pro Leu Gly Leu Val His
230                 235                 240                 245

ccc agc ccc tgg gaa ttc aac tta aga gtc ctc gcg ggc aca ctt ttc      883
Pro Ser Pro Trp Glu Phe Asn Leu Arg Val Leu Ala Gly Thr Leu Phe
                250                 255                 260

gct gta ttt ctg gtg gtt ccc tac gcg ctg ggt acg ccc tct cgg ctt      931
Ala Val Phe Leu Val Val Pro Tyr Ala Leu Gly Thr Pro Ser Arg Leu
            265                 270                 275

ctt gat tcc agt tgg atg aaa acg ctc ggc acc tgg tcg tat tcc atc      979
Leu Asp Ser Ser Trp Met Lys Thr Leu Gly Thr Trp Ser Tyr Ser Ile
        280                 285                 290

ttc ctc tgg cac ctt ccc gtg ctg acg att gtg ttc cca ctg ctc ggg     1027
Phe Leu Trp His Leu Pro Val Leu Thr Ile Val Phe Pro Leu Leu Gly
    295                 300                 305
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ttg cct tta ttt agt gga aat ttc ctg ttg gtg ttc atc gtg acg gtc    1075
Leu Pro Leu Phe Ser Gly Asn Phe Leu Leu Val Phe Ile Val Thr Val
310                 315                 320                 325

ttg ttg acg atc cca gtt gcc gcc atc agc tac acc ttc atc gaa gag    1123
Leu Leu Thr Ile Pro Val Ala Ala Ile Ser Tyr Thr Phe Ile Glu Glu
                330                 335                 340

ccc atc agc ggt gga ccc ggc gcg cca ttc agg ctg ggg gtc gtt agg    1171
Pro Ile Ser Gly Gly Pro Gly Ala Pro Phe Arg Leu Gly Val Val Arg
            345                 350                 355

att cac cat ttt tct ggg ggt agg tct gga aaa tgatgaattg gcaccacgtc 1224
Ile His His Phe Ser Gly Gly Arg Ser Gly Lys
        360                 365

aag                                                                1227


<210> 116
<211> 368
<212> PRT
<213> Corynebacterium glutamicum

<400> 116
Met Ser Thr Gln Ser Tyr Ala Pro Ile Arg His Arg Gly Phe Ile Ser
  1               5                  10                  15

Ser Leu Glu Gly Leu Arg Ala Ile Ala Ser Leu Gly Val Leu Ala Thr
             20                  25                  30

His Val Ala Phe Gln Thr Ser Val Asp Pro Ala Ser Asn Ile Gly Ala
         35                  40                  45

Val Leu Ala Arg Phe Asp Phe Phe Val Ala Val Phe Phe Ala Leu Ser
     50                  55                  60

Ala Phe Val Leu Trp Arg Arg Arg Ala Gly Gln Pro Val Gly Leu Tyr
 65                  70                  75                  80

Tyr Leu Lys Arg Leu Ala Arg Ile Met Pro Ala Tyr Trp Ala Thr Val
                 85                  90                  95

Ile Ala Val Leu Leu Phe Ile Pro Thr Gly Pro Trp Leu Ala Asn Leu
            100                 105                 110

Thr Met Thr Gln Ile Tyr Trp Pro Asp Gly Leu Met Thr Gly Leu Thr
        115                 120                 125

His Leu Trp Ser Leu Cys Val Glu Val Ala Phe Tyr Leu Val Met Pro
    130                 135                 140

Leu Leu Ala Trp Val Leu Asp Arg Phe Gly Arg Pro Val Arg Ile Leu
145                 150                 155                 160

Leu Ile Val Gly Gly Ala Val Leu Ser Leu Ala Trp Pro Trp Ile Pro
                165                 170                 175

Leu Val Glu His Ala Leu Asp Glu Gly Trp Ala Asn Met Gln Ile Trp
            180                 185                 190
```

```
Pro Pro Ala Tyr Ala Cys Trp Phe Ala Val Gly Met Ile Ala Ala Glu
        195                 200                 205

Ile Glu Gly Val Arg Phe Pro Arg Val Pro Ser Phe Val Trp Val Gly
    210                 215                 220

Leu Ala Leu Val Val Ala Trp Ile Ala Gly Gln Glu Trp Phe Gly Pro
225                 230                 235                 240

Leu Gly Leu Val His Pro Ser Pro Trp Glu Phe Asn Leu Arg Val Leu
                245                 250                 255

Ala Gly Thr Leu Phe Ala Val Phe Leu Val Val Pro Tyr Ala Leu Gly
            260                 265                 270

Thr Pro Ser Arg Leu Leu Asp Ser Ser Trp Met Lys Thr Leu Gly Thr
        275                 280                 285

Trp Ser Tyr Ser Ile Phe Leu Trp His Leu Pro Val Leu Thr Ile Val
    290                 295                 300

Phe Pro Leu Leu Gly Leu Pro Leu Phe Ser Gly Asn Phe Leu Leu Val
305                 310                 315                 320

Phe Ile Val Thr Val Leu Leu Thr Ile Pro Val Ala Ala Ile Ser Tyr
                325                 330                 335

Thr Phe Ile Glu Glu Pro Ile Ser Gly Gly Pro Gly Ala Pro Phe Arg
            340                 345                 350

Leu Gly Val Val Arg Ile His His Phe Ser Gly Gly Arg Ser Gly Lys
        355                 360                 365
```

```
<210> 117
<211> 924
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(901)
<223> RXA02150

<400> 117
gtgtttttcg gtgggctgcg atgacgcatg tccaccaaaa gagccacccc ttaaagaaat 60

taaaaagtgg ttttggtagc ttcgcagcaa aatacacatc gtg ggt aac gta ttc   115
                                            Val Gly Asn Val Phe
                                             1               5

tta gaa gtt cct aca gca gta aag cgc gaa gaa ggg gta aac cca aac   163
Leu Glu Val Pro Thr Ala Val Lys Arg Glu Glu Gly Val Asn Pro Asn
                10                  15                  20

atc atg aaa aac aac tgg tat cgg ctt ttc aag tat gtg cta att ggc   211
Ile Met Lys Asn Asn Trp Tyr Arg Leu Phe Lys Tyr Val Leu Ile Gly
            25                  30                  35
```

```
ccg ttt ttg cgt gtg tac aac cgc ccg gag atc gaa ggc aaa gaa aac    259
Pro Phe Leu Arg Val Tyr Asn Arg Pro Glu Ile Glu Gly Lys Glu Asn
         40                  45                  50

atc cct gca gaa ggt gcc gcg atc atg gcg tcc aac cac gaa gca gtg    307
Ile Pro Ala Glu Gly Ala Ala Ile Met Ala Ser Asn His Glu Ala Val
     55                  60                  65

atg gat tcc ttt tat ttt ccc ctg ctg tgc cca cgg cag ctg acc ttc    355
Met Asp Ser Phe Tyr Phe Pro Leu Leu Cys Pro Arg Gln Leu Thr Phe
 70                  75                  80                  85

cca gcg aag gcc gaa tac ttc aca tca cca ggt att aaa ggc aag atg    403
Pro Ala Lys Ala Glu Tyr Phe Thr Ser Pro Gly Ile Lys Gly Lys Met
                 90                  95                 100

cag aag tgg ttt ttt act tct gtg ggg caa gta ccc ctg gac cgc acc    451
Gln Lys Trp Phe Phe Thr Ser Val Gly Gln Val Pro Leu Asp Arg Thr
            105                 110                 115

gca gat aat gcc atg gat tct ttg atg aat acc gcc aaa atg gtg ctg    499
Ala Asp Asn Ala Met Asp Ser Leu Met Asn Thr Ala Lys Met Val Leu
        120                 125                 130

gat cgg gga gac ctc ttc ggt att tac cct gaa gga tct cgt tcg ccc    547
Asp Arg Gly Asp Leu Phe Gly Ile Tyr Pro Glu Gly Ser Arg Ser Pro
    135                 140                 145

gat ggt cgc atc tac aag ggc aaa acc gga atg gcc tat gtt gcg atg    595
Asp Gly Arg Ile Tyr Lys Gly Lys Thr Gly Met Ala Tyr Val Ala Met
150                 155                 160                 165

gaa act ggt acg aca gtt atc ccc gtt gcc atg att ggc agc cgg gac    643
Glu Thr Gly Thr Thr Val Ile Pro Val Ala Met Ile Gly Ser Arg Asp
                170                 175                 180

gcg aac cct atc gga agt tgg ttt ccg aaa ccc gca aaa gtc agg atc    691
Ala Asn Pro Ile Gly Ser Trp Phe Pro Lys Pro Ala Lys Val Arg Ile
            185                 190                 195

aag gta gga agc cca att gat ccc ctc gca ttc gtc aaa gaa cat ggg    739
Lys Val Gly Ser Pro Ile Asp Pro Leu Ala Phe Val Lys Glu His Gly
        200                 205                 210

ttg aag cct gga acc tac gaa gca gcg cgc aag ctg aca gat cac gtt    787
Leu Lys Pro Gly Thr Tyr Glu Ala Ala Arg Lys Leu Thr Asp His Val
    215                 220                 225

atg ttc att ctt gct gat ctc act ggt cag ccg tat gtt gat gcg tac    835
Met Phe Ile Leu Ala Asp Leu Thr Gly Gln Pro Tyr Val Asp Ala Tyr
230                 235                 240                 245

tct aaa gat gtg aaa aac gct ctg gag gaa gga aaa gga tac ccg gag    883
Ser Lys Asp Val Lys Asn Ala Leu Glu Glu Gly Lys Gly Tyr Pro Glu
                250                 255                 260

ggc aca gct cct tca cag taatcgggtc ttttctgtta aaa                  924
Gly Thr Ala Pro Ser Gln
            265
```

<210> 118
<211> 267
<212> PRT
<213> Corynebacterium glutamicum

<400> 118
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Val Gly Asn Val Phe Leu Glu Val Pro Thr Ala Val Lys Arg Glu Glu
 1               5                  10                  15

Gly Val Asn Pro Asn Ile Met Lys Asn Asn Trp Tyr Arg Leu Phe Lys
            20                  25                  30

Tyr Val Leu Ile Gly Pro Phe Leu Arg Val Tyr Asn Arg Pro Glu Ile
        35                  40                  45

Glu Gly Lys Glu Asn Ile Pro Ala Glu Gly Ala Ala Ile Met Ala Ser
    50                  55                  60

Asn His Glu Ala Val Met Asp Ser Phe Tyr Phe Pro Leu Leu Cys Pro
65                  70                  75                  80

Arg Gln Leu Thr Phe Pro Ala Lys Ala Glu Tyr Phe Thr Ser Pro Gly
                85                  90                  95

Ile Lys Gly Lys Met Gln Lys Trp Phe Phe Thr Ser Val Gly Gln Val
            100                 105                 110

Pro Leu Asp Arg Thr Ala Asp Asn Ala Met Asp Ser Leu Met Asn Thr
        115                 120                 125

Ala Lys Met Val Leu Asp Arg Gly Asp Leu Phe Gly Ile Tyr Pro Glu
    130                 135                 140

Gly Ser Arg Ser Pro Asp Gly Arg Ile Tyr Lys Gly Lys Thr Gly Met
145                 150                 155                 160

Ala Tyr Val Ala Met Glu Thr Gly Thr Thr Val Ile Pro Val Ala Met
                165                 170                 175

Ile Gly Ser Arg Asp Ala Asn Pro Ile Gly Ser Trp Phe Pro Lys Pro
            180                 185                 190

Ala Lys Val Arg Ile Lys Val Gly Ser Pro Ile Asp Pro Leu Ala Phe
        195                 200                 205

Val Lys Glu His Gly Leu Lys Pro Gly Thr Tyr Glu Ala Ala Arg Lys
    210                 215                 220

Leu Thr Asp His Val Met Phe Ile Leu Ala Asp Leu Thr Gly Gln Pro
225                 230                 235                 240

Tyr Val Asp Ala Tyr Ser Lys Asp Val Lys Asn Ala Leu Glu Glu Gly
                245                 250                 255

Lys Gly Tyr Pro Glu Gly Thr Ala Pro Ser Gln
            260                 265
```

<210> 119
<211> 504

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(481)
<223> RXA00607

<400> 119
cactgccagc aacgccaacg gttgaacccg aaccagaagg cgatgaagac tggcccgaac 60

ccatcaaccc cgcaggcgat aacaaagagg aggcaaaccg atg att ctc gca ctg 115
Met Ile Leu Ala Leu
1 5

aca gtc gcg ata ctt ttc ggt gga ggt gtc tac ctc att cag caa cgc 163
Thr Val Ala Ile Leu Phe Gly Gly Gly Val Tyr Leu Ile Gln Gln Arg
10 15 20

gga atg gtg cgc atc gtc ttc ggc atg tca ctg atc ggc cac gca gcg 211
Gly Met Val Arg Ile Val Phe Gly Met Ser Leu Ile Gly His Ala Ala
25 30 35

aac ctg acc atc ctg tac gcc ggt gtg ccc acg tgg cgc ggc gaa gcc 259
Asn Leu Thr Ile Leu Tyr Ala Gly Val Pro Thr Trp Arg Gly Glu Ala
40 45 50

ttc ccc gac agg acc ccg ctt acc gac gcc gcc gat cca ctc ccc cag 307
Phe Pro Asp Arg Thr Pro Leu Thr Asp Ala Ala Asp Pro Leu Pro Gln
55 60 65

gcc ttc gtc ctc acc gcc atc gtc atc gcg atg gcc acc aca acc atc 355
Ala Phe Val Leu Thr Ala Ile Val Ile Ala Met Ala Thr Thr Thr Ile
70 75 80 85

atg ttg gcc ttg gca gca ctg gga cgc agc gac gac acc cgg tcc atc 403
Met Leu Ala Leu Ala Ala Leu Gly Arg Ser Asp Asp Thr Arg Ser Ile
90 95 100

gaa cca gat gac gat caa tcg cct ttg act act agc gct cgt tca gtc 451
Glu Pro Asp Asp Asp Gln Ser Pro Leu Thr Thr Ser Ala Arg Ser Val
105 110 115

acc aac cca aca gat cag gag gat aaa gct taaatggcca tggatgttct 501
Thr Asn Pro Thr Asp Gln Glu Asp Lys Ala
120 125

cct 504

<210> 120
<211> 127
<212> PRT
<213> Corynebacterium glutamicum

<400> 120
Met Ile Leu Ala Leu Thr Val Ala Ile Leu Phe Gly Gly Gly Val Tyr
1 5 10 15

Leu Ile Gln Gln Arg Gly Met Val Arg Ile Val Phe Gly Met Ser Leu
20 25 30

Ile Gly His Ala Ala Asn Leu Thr Ile Leu Tyr Ala Gly Val Pro Thr
35 40 45

Trp Arg Gly Glu Ala Phe Pro Asp Arg Thr Pro Leu Thr Asp Ala Ala
50 55 60

Asp Pro Leu Pro Gln Ala Phe Val Leu Thr Ala Ile Val Ile Ala Met
65 70 75 80

Ala Thr Thr Thr Ile Met Leu Ala Leu Ala Ala Leu Gly Arg Ser Asp
85 90 95

Asp Thr Arg Ser Ile Glu Pro Asp Asp Asp Gln Ser Pro Leu Thr Thr
100 105 110

Ser Ala Arg Ser Val Thr Asn Pro Thr Asp Gln Glu Asp Lys Ala
115 120 125

<210> 121
<211> 1119
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1096)
<223> RXA02397

<400> 121
gtgtgaataa aacttgtttc ctggtcattt cccctactga actgcgctta tgcctatgct 60

tagaaaccag agacaagctt aagaaggaca ggggccggcc atg aat gat ttc gaa 115
Met Asn Asp Phe Glu
1 5

aca acc atc gat cgg atc tct aaa gaa caa gat ccc gca gcc cga agc 163
Thr Thr Ile Asp Arg Ile Ser Lys Glu Gln Asp Pro Ala Ala Arg Ser
10 15 20

cgc gtg gaa cag ttc att gtg gaa aca gta cgt gca cta ccc aac ttg 211
Arg Val Glu Gln Phe Ile Val Glu Thr Val Arg Ala Leu Pro Asn Leu
25 30 35

acc acc aaa caa ggt gca tcg ttg gct atc caa ctt ctt gat gcg gta 259
Thr Thr Lys Gln Gly Ala Ser Leu Ala Ile Gln Leu Leu Asp Ala Val
40 45 50

cag ctc gcg gat gcg gcg gga acc aag ggg ggt gcg tcg aca agc aat 307
Gln Leu Ala Asp Ala Ala Gly Thr Lys Gly Gly Ala Ser Thr Ser Asn
55 60 65

gct tca tcg ctg cct gac acc ttt gac gcg ctg acc agc ctg att ggc 355
Ala Ser Ser Leu Pro Asp Thr Phe Asp Ala Leu Thr Ser Leu Ile Gly
70 75 80 85

aag ctc gat gtg cgc agc gat tct gaa tgg cgc tcg ttt ggg ttc cag 403
Lys Leu Asp Val Arg Ser Asp Ser Glu Trp Arg Ser Phe Gly Phe Gln
90 95 100

```
cct tct gaa act gcg cac ccg cta atg atc gct atc cct gag att gag     451
Pro Ser Glu Thr Ala His Pro Leu Met Ile Ala Ile Pro Glu Ile Glu
            105                 110                 115

att ttt tat cag cac acc gat gtg gag ccg gga agc gat gac gcc gtg     499
Ile Phe Tyr Gln His Thr Asp Val Glu Pro Gly Ser Asp Asp Ala Val
        120                 125                 130

gcg ccg gac ttt cag gaa aat cag gat atg tgg cgc agg cgt ctc gga     547
Ala Pro Asp Phe Gln Glu Asn Gln Asp Met Trp Arg Arg Arg Leu Gly
    135                 140                 145

tct gtc acc gaa cca aac ctt ata tat aaa gag ttt tcc gga ccc ggc     595
Ser Val Thr Glu Pro Asn Leu Ile Tyr Lys Glu Phe Ser Gly Pro Gly
150                 155                 160                 165

aaa gcg cag cgt gcc gta gaa atg ctg ggc aat ctg tgg aag atc ggc     643
Lys Ala Gln Arg Ala Val Glu Met Leu Gly Asn Leu Trp Lys Ile Gly
                170                 175                 180

gtg gtg gtg agt agg aat acg gaa agt cgc ctt ggg tta act cgt gtg     691
Val Val Val Ser Arg Asn Thr Glu Ser Arg Leu Gly Leu Thr Arg Val
            185                 190                 195

gaa tac acc ccc acc cct ggc gaa gta ccc gtg ccg ctg atg tcg gag     739
Glu Tyr Thr Pro Thr Pro Gly Glu Val Pro Val Pro Leu Met Ser Glu
        200                 205                 210

aag aac tgt tgg tac agc att cgg gtg tct gaa acc att ggt gag aac     787
Lys Asn Cys Trp Tyr Ser Ile Arg Val Ser Glu Thr Ile Gly Glu Asn
    215                 220                 225

cag gtt ccg gaa att gtg cgc tgc tta ggc gag att ttc tgt ggc tat     835
Gln Val Pro Glu Ile Val Arg Cys Leu Gly Glu Ile Phe Cys Gly Tyr
230                 235                 240                 245

ctt ccc cag atg tgg ctc aaa gaa cca gta aag gcc ggc aag ttg cga     883
Leu Pro Gln Met Trp Leu Lys Glu Pro Val Lys Ala Gly Lys Leu Arg
                250                 255                 260

atc caa gaa tcg gaa gca gca gcg tat atc gcg atg gcg cga cta gat     931
Ile Gln Glu Ser Glu Ala Ala Ala Tyr Ile Ala Met Ala Arg Leu Asp
            265                 270                 275

ctt tcc cca cgc acc ggc aac acc act tgg acc aac agc tat att tcc     979
Leu Ser Pro Arg Thr Gly Asn Thr Thr Trp Thr Asn Ser Tyr Ile Ser
        280                 285                 290

acg cgt cct ctc tcc ccc gct ttt agg tgg gac gtg gtg ctg gag gct     1027
Thr Arg Pro Leu Ser Pro Ala Phe Arg Trp Asp Val Val Leu Glu Ala
    295                 300                 305

tcc cac caa ttg gag aac ctg ctg cgt gga gac aca ggg ccg gtc act     1075
Ser His Gln Leu Glu Asn Leu Leu Arg Gly Asp Thr Gly Pro Val Thr
310                 315                 320                 325

gcc aca caa tcg gca gct ggt taaccaaaag ttcacgtgga gat              1119
Ala Thr Gln Ser Ala Ala Gly
                330
```

<210> 122
<211> 332
<212> PRT
<213> Corynebacterium glutamicum

<400> 122
Met Asn Asp Phe Glu Thr Thr Ile Asp Arg Ile Ser Lys Glu Gln Asp
1 5 10 15

Pro Ala Ala Arg Ser Arg Val Glu Gln Phe Ile Val Glu Thr Val Arg
20 25 30

Ala Leu Pro Asn Leu Thr Thr Lys Gln Gly Ala Ser Leu Ala Ile Gln
35 40 45

Leu Leu Asp Ala Val Gln Leu Ala Asp Ala Ala Gly Thr Lys Gly Gly
50 55 60

Ala Ser Thr Ser Asn Ala Ser Ser Leu Pro Asp Thr Phe Asp Ala Leu
65 70 75 80

Thr Ser Leu Ile Gly Lys Leu Asp Val Arg Ser Asp Ser Glu Trp Arg
85 90 95

Ser Phe Gly Phe Gln Pro Ser Glu Thr Ala His Pro Leu Met Ile Ala
100 105 110

Ile Pro Glu Ile Glu Ile Phe Tyr Gln His Thr Asp Val Glu Pro Gly
115 120 125

Ser Asp Asp Ala Val Ala Pro Asp Phe Gln Glu Asn Gln Asp Met Trp
130 135 140

Arg Arg Arg Leu Gly Ser Val Thr Glu Pro Asn Leu Ile Tyr Lys Glu
145 150 155 160

Phe Ser Gly Pro Gly Lys Ala Gln Arg Ala Val Glu Met Leu Gly Asn
165 170 175

Leu Trp Lys Ile Gly Val Val Val Ser Arg Asn Thr Glu Ser Arg Leu
180 185 190

Gly Leu Thr Arg Val Glu Tyr Thr Pro Thr Pro Gly Glu Val Pro Val
195 200 205

Pro Leu Met Ser Glu Lys Asn Cys Trp Tyr Ser Ile Arg Val Ser Glu
210 215 220

Thr Ile Gly Glu Asn Gln Val Pro Glu Ile Val Arg Cys Leu Gly Glu
225 230 235 240

Ile Phe Cys Gly Tyr Leu Pro Gln Met Trp Leu Lys Glu Pro Val Lys
245 250 255

Ala Gly Lys Leu Arg Ile Gln Glu Ser Glu Ala Ala Ala Tyr Ile Ala
260 265 270

Met Ala Arg Leu Asp Leu Ser Pro Arg Thr Gly Asn Thr Thr Trp Thr
275 280 285

Asn Ser Tyr Ile Ser Thr Arg Pro Leu Ser Pro Ala Phe Arg Trp Asp

```
    290                 295                 300

Val Val Leu Glu Ala Ser His Gln Leu Glu Asn Leu Leu Arg Gly Asp
305                 310                 315                 320

Thr Gly Pro Val Thr Ala Thr Gln Ser Ala Ala Gly
                325                 330


<210> 123
<211> 1462
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1462)
<223> RXN03110

<400> 123
aatgagtgaa cctgcgcttg aactataccc cctggggtat tactgtagat tctcaatacc 60

ccgaggggta tctagttttt acgttgagaa ggagagctca gtg ctt att gaa cgc   115
                                            Val Leu Ile Glu Arg
                                             1               5

atc tac gac gaa gac ctt gcg cag gcc agc tat ttc att ggc tgc caa   163
Ile Tyr Asp Glu Asp Leu Ala Gln Ala Ser Tyr Phe Ile Gly Cys Gln
                10                  15                  20

gcc cac aac acc gca gtc gtg gtt gat ccg cgt cgc gat att gcc gtc   211
Ala His Asn Thr Ala Val Val Val Asp Pro Arg Arg Asp Ile Ala Val
            25                  30                  35

tat ctg gac atg gcc aag aaa aac gga atg gag att gtt gga gtt acc   259
Tyr Leu Asp Met Ala Lys Lys Asn Gly Met Glu Ile Val Gly Val Thr
        40                  45                  50

gaa acc cat atc cat gcg gac tat ttg tca gga acc cgt gag tta gct   307
Glu Thr His Ile His Ala Asp Tyr Leu Ser Gly Thr Arg Glu Leu Ala
    55                  60                  65

gct gca act aat gcc acc atg tac gtc tca ggg gag ggc ggc gcc gat   355
Ala Ala Thr Asn Ala Thr Met Tyr Val Ser Gly Glu Gly Gly Ala Asp
70                  75                  80                  85

tgg cag tat gaa ttc gac gcc gag cga ata tgc gac ggc agc gag att   403
Trp Gln Tyr Glu Phe Asp Ala Glu Arg Ile Cys Asp Gly Ser Glu Ile
                90                  95                  100

cgc ctg gga aat ctg gtg ctc aca gct gtt cac acc cca ggc cat acc   451
Arg Leu Gly Asn Leu Val Leu Thr Ala Val His Thr Pro Gly His Thr
            105                 110                 115

ccg gaa cac tta tcg ttc ctg ctg aag gac ggc gcg ttc gca gat gag   499
Pro Glu His Leu Ser Phe Leu Leu Lys Asp Gly Ala Phe Ala Asp Glu
        120                 125                 130

cca gga ttc atg ctc act ggc gat ttc gtt ttc gcg ggt gat ctt ggc   547
Pro Gly Phe Met Leu Thr Gly Asp Phe Val Phe Ala Gly Asp Leu Gly
    135                 140                 145
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cga cca gat ttg ctc gat gaa gca gct ggg gga gtg gac act cgt ttt 595
Arg Pro Asp Leu Leu Asp Glu Ala Ala Gly Gly Val Asp Thr Arg Phe
150 155 160 165

gag ggg gct cgc caa atg ttc aag agc ttg aag gaa aaa ttc ctg aca 643
Glu Gly Ala Arg Gln Met Phe Lys Ser Leu Lys Glu Lys Phe Leu Thr
170 175 180

ttg cct gat cac atc cag atc ttc cct ggt cat ggt tcc ggt tcc gcg 691
Leu Pro Asp His Ile Gln Ile Phe Pro Gly His Gly Ser Gly Ser Ala
185 190 195

tgt ggc aaa gcc ttg ggt tcg gtt cct tca aca aca ctt gga tat gaa 739
Cys Gly Lys Ala Leu Gly Ser Val Pro Ser Thr Thr Leu Gly Tyr Glu
200 205 210

cgt caa ttt gcg tgg tgg gga aag tat ctg gag gca gat gat gaa caa 787
Arg Gln Phe Ala Trp Trp Gly Lys Tyr Leu Glu Ala Asp Asp Glu Gln
215 220 225

gga ttc att gat gag ctt ctg gaa ggc caa cct gat gca cct gca tac 835
Gly Phe Ile Asp Glu Leu Leu Glu Gly Gln Pro Asp Ala Pro Ala Tyr
230 235 240 245

ttc ggc agg atg aag agg caa aat agg caa ggg ccc gca att atg ggc 883
Phe Gly Arg Met Lys Arg Gln Asn Arg Gln Gly Pro Ala Ile Met Gly
250 255 260

gct cgc gag ctg ttg cca cag ctg gaa gct tct gat ctg cac gac gtc 931
Ala Arg Glu Leu Leu Pro Gln Leu Glu Ala Ser Asp Leu His Asp Val
265 270 275

att gtt gtt gat acc cgc tca gcc gat gaa gtt cac cag ggc act gta 979
Ile Val Val Asp Thr Arg Ser Ala Asp Glu Val His Gln Gly Thr Val
280 285 290

gct ggt gca gtg aat att cct gcg ggc aat tcg atg gcg aaa ttt ggc 1027
Ala Gly Ala Val Asn Ile Pro Ala Gly Asn Ser Met Ala Lys Phe Gly
295 300 305

tcg tgg acc gtt gat ccc gag aag gat tcc cga gct ttg gtt ctg ctc 1075
Ser Trp Thr Val Asp Pro Glu Lys Asp Ser Arg Ala Leu Val Leu Leu
310 315 320 325

gcg gca agc caa att ggt gcc atg gag atg tgg gac cac atg gtt cgc 1123
Ala Ala Ser Gln Ile Gly Ala Met Glu Met Trp Asp His Met Val Arg
330 335 340

gtg gga atc gat aat gtt gct ggt ttt atc acc aac ttt gat ggg gtg 1171
Val Gly Ile Asp Asn Val Ala Gly Phe Ile Thr Asn Phe Asp Gly Val
345 350 355

gac cta gtt gca ccg caa act gtg tcc cca gat cag ctg gat gaa ttg 1219
Asp Leu Val Ala Pro Gln Thr Val Ser Pro Asp Gln Leu Asp Glu Leu
360 365 370

gaa tac gat cta ctt ctt gat gtc cgc aac cgc agt gaa gtc gaa gaa 1267
Glu Tyr Asp Leu Leu Leu Asp Val Arg Asn Arg Ser Glu Val Glu Glu
375 380 385

```
ggc tac atc cca gga gca ctc cat att aat ggt gca tcc gtg ctg tgg    1315
Gly Tyr Ile Pro Gly Ala Leu His Ile Asn Gly Ala Ser Val Leu Trp
390                 395                 400                 405

aat ctg gag aaa ctg cca cgt gac gga aag atc gtg agc tac tgc aag    1363
Asn Leu Glu Lys Leu Pro Arg Asp Gly Lys Ile Val Ser Tyr Cys Lys
                410                 415                 420

agt gga aca cgc agc tca atc gcc gca agc acc ctg cgt aat gct ggt    1411
Ser Gly Thr Arg Ser Ser Ile Ala Ala Ser Thr Leu Arg Asn Ala Gly
            425                 430                 435

ttt gat gtg gtg gaa ctt caa gga tcc tat gac aac tgg gtc cgg cac    1459
Phe Asp Val Val Glu Leu Gln Gly Ser Tyr Asp Asn Trp Val Arg His
        440                 445                 450

aac                                                                1462
Asn
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<210> 124
<211> 454
<212> PRT
<213> Corynebacterium glutamicum

<400> 124
Val Leu Ile Glu Arg Ile Tyr Asp Glu Asp Leu Ala Gln Ala Ser Tyr
  1               5                  10                  15

Phe Ile Gly Cys Gln Ala His Asn Thr Ala Val Val Val Asp Pro Arg
             20                  25                  30

Arg Asp Ile Ala Val Tyr Leu Asp Met Ala Lys Lys Asn Gly Met Glu
         35                  40                  45

Ile Val Gly Val Thr Glu Thr His Ile His Ala Asp Tyr Leu Ser Gly
     50                  55                  60

Thr Arg Glu Leu Ala Ala Ala Thr Asn Ala Thr Met Tyr Val Ser Gly
 65                  70                  75                  80

Glu Gly Gly Ala Asp Trp Gln Tyr Glu Phe Asp Ala Glu Arg Ile Cys
                 85                  90                  95

Asp Gly Ser Glu Ile Arg Leu Gly Asn Leu Val Leu Thr Ala Val His
            100                 105                 110

Thr Pro Gly His Thr Pro Glu His Leu Ser Phe Leu Leu Lys Asp Gly
        115                 120                 125

Ala Phe Ala Asp Glu Pro Gly Phe Met Leu Thr Gly Asp Phe Val Phe
    130                 135                 140

Ala Gly Asp Leu Gly Arg Pro Asp Leu Leu Asp Glu Ala Ala Gly Gly
145                 150                 155                 160

Val Asp Thr Arg Phe Glu Gly Ala Arg Gln Met Phe Lys Ser Leu Lys
                165                 170                 175

Glu Lys Phe Leu Thr Leu Pro Asp His Ile Gln Ile Phe Pro Gly His
```

```
            180                 185                 190

Gly Ser Gly Ser Ala Cys Gly Lys Ala Leu Gly Ser Val Pro Ser Thr
        195                 200                 205

Thr Leu Gly Tyr Glu Arg Gln Phe Ala Trp Trp Gly Lys Tyr Leu Glu
    210                 215                 220

Ala Asp Asp Glu Gln Gly Phe Ile Asp Glu Leu Leu Glu Gly Gln Pro
225                 230                 235                 240

Asp Ala Pro Ala Tyr Phe Gly Arg Met Lys Arg Gln Asn Arg Gln Gly
                245                 250                 255

Pro Ala Ile Met Gly Ala Arg Glu Leu Leu Pro Gln Leu Glu Ala Ser
            260                 265                 270

Asp Leu His Asp Val Ile Val Val Asp Thr Arg Ser Ala Asp Glu Val
        275                 280                 285

His Gln Gly Thr Val Ala Gly Ala Val Asn Ile Pro Ala Gly Asn Ser
    290                 295                 300

Met Ala Lys Phe Gly Ser Trp Thr Val Asp Pro Glu Lys Asp Ser Arg
305                 310                 315                 320

Ala Leu Val Leu Leu Ala Ala Ser Gln Ile Gly Ala Met Glu Met Trp
                325                 330                 335

Asp His Met Val Arg Val Gly Ile Asp Asn Val Ala Gly Phe Ile Thr
            340                 345                 350

Asn Phe Asp Gly Val Asp Leu Val Ala Pro Gln Thr Val Ser Pro Asp
        355                 360                 365

Gln Leu Asp Glu Leu Glu Tyr Asp Leu Leu Leu Asp Val Arg Asn Arg
    370                 375                 380

Ser Glu Val Glu Glu Gly Tyr Ile Pro Gly Ala Leu His Ile Asn Gly
385                 390                 395                 400

Ala Ser Val Leu Trp Asn Leu Glu Lys Leu Pro Arg Asp Gly Lys Ile
                405                 410                 415

Val Ser Tyr Cys Lys Ser Gly Thr Arg Ser Ser Ile Ala Ala Ser Thr
            420                 425                 430

Leu Arg Asn Ala Gly Phe Asp Val Val Glu Leu Gln Gly Ser Tyr Asp
        435                 440                 445

Asn Trp Val Arg His Asn
    450
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<210> 125
<211> 1023
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

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<222> (1)..(1023)
<223> FRXA00660

<400> 125
cca ggc cat acc ccg gaa cac tta tcg ttc ctg ctg aag gac ggc gcg      48
Pro Gly His Thr Pro Glu His Leu Ser Phe Leu Leu Lys Asp Gly Ala
  1               5                  10                  15

ttc gca cat gag cca gga ttc atg ctc act ggc gat ttc gtt ttc gcg      96
Phe Ala His Glu Pro Gly Phe Met Leu Thr Gly Asp Phe Val Phe Ala
             20                  25                  30

ggt gat ctt ggc cga cca gat ttg ctc gat gaa gca gct ggg gga gtg     144
Gly Asp Leu Gly Arg Pro Asp Leu Leu Asp Glu Ala Ala Gly Gly Val
         35                  40                  45

gac act cgt ttt gag ggg gct cgc caa atg ttc aag agc ttg aag gaa     192
Asp Thr Arg Phe Glu Gly Ala Arg Gln Met Phe Lys Ser Leu Lys Glu
     50                  55                  60

aaa ttc ctg aca ttg cct gat cac atc cag atc ttc cct ggt cat ggt     240
Lys Phe Leu Thr Leu Pro Asp His Ile Gln Ile Phe Pro Gly His Gly
 65                  70                  75                  80

tcc ggt tcc gcg tgt ggc aaa gcc ttg ggt tcg gtt cct tca aca aca     288
Ser Gly Ser Ala Cys Gly Lys Ala Leu Gly Ser Val Pro Ser Thr Thr
                 85                  90                  95

ctt gga tat gaa cgt caa ttt gcg tgg tgg gga aag tat ctg gag gca     336
Leu Gly Tyr Glu Arg Gln Phe Ala Trp Trp Gly Lys Tyr Leu Glu Ala
            100                 105                 110

gat gat gaa caa gga ttc att gat gag ctt ctg gaa ggc caa cct gat     384
Asp Asp Glu Gln Gly Phe Ile Asp Glu Leu Leu Glu Gly Gln Pro Asp
        115                 120                 125

gca cct gca tac ttc ggc agg atg aag agg caa aat agg caa ggg ccc     432
Ala Pro Ala Tyr Phe Gly Arg Met Lys Arg Gln Asn Arg Gln Gly Pro
    130                 135                 140

gca att atg ggc gct cgc gag ctg ttg cca cag ctg gaa gct tct gat     480
Ala Ile Met Gly Ala Arg Glu Leu Leu Pro Gln Leu Glu Ala Ser Asp
145                 150                 155                 160

ctg cac gac gtc att gtt gtt gat acc cgc tca gcc gat gaa gtt cac     528
Leu His Asp Val Ile Val Val Asp Thr Arg Ser Ala Asp Glu Val His
                165                 170                 175

cag ggc act gta gct ggt gca gtg aat att cct gcg ggc aat tcg atg     576
Gln Gly Thr Val Ala Gly Ala Val Asn Ile Pro Ala Gly Asn Ser Met
            180                 185                 190

gcg aaa ttt ggc tcg tgg acc gtt gat ccc gag aag gat tcc cga gct     624
Ala Lys Phe Gly Ser Trp Thr Val Asp Pro Glu Lys Asp Ser Arg Ala
        195                 200                 205

ttg gtt ctg ctc gcg gca agc caa att ggt gcc atg gag atg tgg gac     672
Leu Val Leu Leu Ala Ala Ser Gln Ile Gly Ala Met Glu Met Trp Asp
    210                 215                 220

cac atg gtt cgc gtg gga atc gat aat gtt gct ggt ttt atc acc aac     720
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His Met Val Arg Val Gly Ile Asp Asn Val Ala Gly Phe Ile Thr Asn
225 230 235 240

ttt gat ggg gtg gac cta gtt gca ccg caa act gtg tcc cca gat cag 768
Phe Asp Gly Val Asp Leu Val Ala Pro Gln Thr Val Ser Pro Asp Gln
245 250 255

ctg gat gaa ttg gaa tac gat cta ctt ctt gat gtc cgc aac cgc agt 816
Leu Asp Glu Leu Glu Tyr Asp Leu Leu Leu Asp Val Arg Asn Arg Ser
260 265 270

gaa gtc gaa gaa ggc tac atc cca gga gca ctc cat att aat ggt gca 864
Glu Val Glu Glu Gly Tyr Ile Pro Gly Ala Leu His Ile Asn Gly Ala
275 280 285

tcc gtg ctg tgg aat ctg gag aaa ctg cca cgt gac gga aag atc gtg 912
Ser Val Leu Trp Asn Leu Glu Lys Leu Pro Arg Asp Gly Lys Ile Val
290 295 300

agc tac tgc aag agt gga aca cgc agc tca atc gcc gca agc acc ctg 960
Ser Tyr Cys Lys Ser Gly Thr Arg Ser Ser Ile Ala Ala Ser Thr Leu
305 310 315 320

cgt aat gct ggt ttt gat gtg gtg gaa ctt caa gga tcc tat gac aac 1008
Arg Asn Ala Gly Phe Asp Val Val Glu Leu Gln Gly Ser Tyr Asp Asn
325 330 335

tgg gtc cgg cac aac 1023
Trp Val Arg His Asn
340

<210> 126
<211> 341
<212> PRT
<213> Corynebacterium glutamicum

<400> 126
Pro Gly His Thr Pro Glu His Leu Ser Phe Leu Leu Lys Asp Gly Ala
1 5 10 15

Phe Ala His Glu Pro Gly Phe Met Leu Thr Gly Asp Phe Val Phe Ala
20 25 30

Gly Asp Leu Gly Arg Pro Asp Leu Leu Asp Glu Ala Ala Gly Gly Val
35 40 45

Asp Thr Arg Phe Glu Gly Ala Arg Gln Met Phe Lys Ser Leu Lys Glu
50 55 60

Lys Phe Leu Thr Leu Pro Asp His Ile Gln Ile Phe Pro Gly His Gly
65 70 75 80

Ser Gly Ser Ala Cys Gly Lys Ala Leu Gly Ser Val Pro Ser Thr Thr
85 90 95

Leu Gly Tyr Glu Arg Gln Phe Ala Trp Trp Gly Lys Tyr Leu Glu Ala
100 105 110

Asp Asp Glu Gln Gly Phe Ile Asp Glu Leu Leu Glu Gly Gln Pro Asp
115 120 125

Ala Pro Ala Tyr Phe Gly Arg Met Lys Arg Gln Asn Arg Gln Gly Pro
    130   135   140

Ala Ile Met Gly Ala Arg Glu Leu Leu Pro Gln Leu Glu Ala Ser Asp
145   150   155   160

Leu His Asp Val Ile Val Val Asp Thr Arg Ser Ala Asp Glu Val His
                165   170   175

Gln Gly Thr Val Ala Gly Ala Val Asn Ile Pro Ala Gly Asn Ser Met
            180   185   190

Ala Lys Phe Gly Ser Trp Thr Val Asp Pro Glu Lys Asp Ser Arg Ala
        195   200   205

Leu Val Leu Leu Ala Ala Ser Gln Ile Gly Ala Met Glu Met Trp Asp
    210   215   220

His Met Val Arg Val Gly Ile Asp Asn Val Ala Gly Phe Ile Thr Asn
225   230   235   240

Phe Asp Gly Val Asp Leu Val Ala Pro Gln Thr Val Ser Pro Asp Gln
                245   250   255

Leu Asp Glu Leu Glu Tyr Asp Leu Leu Leu Asp Val Arg Asn Arg Ser
            260   265   270

Glu Val Glu Glu Gly Tyr Ile Pro Gly Ala Leu His Ile Asn Gly Ala
        275   280   285

Ser Val Leu Trp Asn Leu Glu Lys Leu Pro Arg Asp Gly Lys Ile Val
    290   295   300

Ser Tyr Cys Lys Ser Gly Thr Arg Ser Ser Ile Ala Ala Ser Thr Leu
305   310   315   320

Arg Asn Ala Gly Phe Asp Val Val Glu Leu Gln Gly Ser Tyr Asp Asn
                325   330   335

Trp Val Arg His Asn
            340

<210> 127
<211> 756
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)
<223> RXA00801

<400> 127
ggataagttt gtttctgagc gtattggtct tgatgatgtt gaagaggctt tcaacaccat 60

gaaggctggc gacgtgctgc gttctgtggt ggagatctaa atg gct cac gac gga 115
                                            Met Ala His Asp Gly
                                            1   5

ttg cgc gta gaa aac att gtc acc tca ggc atc ttt gcc ctt gat ggt 163
Leu Arg Val Glu Asn Ile Val Thr Ser Gly Ile Phe Ala Leu Asp Gly
10 15 20

ggc gaa tgg gaa gtc gac aac aac atc tgg gtt gtg gga aat gat gat 211
Gly Glu Trp Glu Val Asp Asn Asn Ile Trp Val Val Gly Asn Asp Asp
25 30 35

gag gtt ttc atc atc gat gcg gca cac act gca gca ccc atc atc gag 259
Glu Val Phe Ile Ile Asp Ala Ala His Thr Ala Ala Pro Ile Ile Glu
40 45 50

gct gtc ggt gga cgt gct gtg aag ggc att ttg tgc acc cac gca cac 307
Ala Val Gly Gly Arg Ala Val Lys Gly Ile Leu Cys Thr His Ala His
55 60 65

aat gac cac atc act gtc gca cca gag cta tcc aag gaa ttt gat gca 355
Asn Asp His Ile Thr Val Ala Pro Glu Leu Ser Lys Glu Phe Asp Ala
70 75 80 85

cca atc ttc gtg cac cca ggt gac caa atg ctg tgg gag gaa acc cac 403
Pro Ile Phe Val His Pro Gly Asp Gln Met Leu Trp Glu Glu Thr His
90 95 100

gga aac ctg acc cac gag gat ttg gca gat cag cag aag ttc caa atc 451
Gly Asn Leu Thr His Glu Asp Leu Ala Asp Gln Gln Lys Phe Gln Ile
105 110 115

gct gga act gaa ctg atc gtg ctt aat acc cct gga cac tca cct gga 499
Ala Gly Thr Glu Leu Ile Val Leu Asn Thr Pro Gly His Ser Pro Gly
120 125 130

tcc agc tgc ttc tac ctc cct gaa gca aac gag ctc ttc tct gga gac 547
Ser Ser Cys Phe Tyr Leu Pro Glu Ala Asn Glu Leu Phe Ser Gly Asp
135 140 145

act ttg ttc cag ggt ggg ccg gga gca act ggc cgt aag tac agc tcc 595
Thr Leu Phe Gln Gly Gly Pro Gly Ala Thr Gly Arg Lys Tyr Ser Ser
150 155 160 165

ttt gac acc atc att gag tcc ctc aag acc tca att ttg gat cta cca 643
Phe Asp Thr Ile Ile Glu Ser Leu Lys Thr Ser Ile Leu Asp Leu Pro
170 175 180

gcg gaa acc acc gtg cgc act ggc cat ggt gat cac acc agt gtg ggg 691
Ala Glu Thr Thr Val Arg Thr Gly His Gly Asp His Thr Ser Val Gly
185 190 195

gct gag gct cca cac ttg gag gaa tgg att aaa cgc ggg cac 733
Ala Glu Ala Pro His Leu Glu Glu Trp Ile Lys Arg Gly His
200 205 210

taagccccga acgattagta ggc 756

<210> 128
<211> 211
<212> PRT
<213> Corynebacterium glutamicum

<400> 128

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Met Ala His Asp Gly Leu Arg Val Glu Asn Ile Val Thr Ser Gly Ile
1               5                   10                  15

Phe Ala Leu Asp Gly Gly Glu Trp Glu Val Asp Asn Asn Ile Trp Val
            20                  25                  30

Val Gly Asn Asp Asp Glu Val Phe Ile Ile Asp Ala Ala His Thr Ala
        35                  40                  45

Ala Pro Ile Ile Glu Ala Val Gly Gly Arg Ala Val Lys Gly Ile Leu
    50                  55                  60

Cys Thr His Ala His Asn Asp His Ile Thr Val Ala Pro Glu Leu Ser
65                  70                  75                  80

Lys Glu Phe Asp Ala Pro Ile Phe Val His Pro Gly Asp Gln Met Leu
                85                  90                  95

Trp Glu Glu Thr His Gly Asn Leu Thr His Glu Asp Leu Ala Asp Gln
            100                 105                 110

Gln Lys Phe Gln Ile Ala Gly Thr Glu Leu Ile Val Leu Asn Thr Pro
        115                 120                 125

Gly His Ser Pro Gly Ser Ser Cys Phe Tyr Leu Pro Glu Ala Asn Glu
    130                 135                 140

Leu Phe Ser Gly Asp Thr Leu Phe Gln Gly Gly Pro Gly Ala Thr Gly
145                 150                 155                 160

Arg Lys Tyr Ser Ser Phe Asp Thr Ile Ile Glu Ser Leu Lys Thr Ser
                165                 170                 175

Ile Leu Asp Leu Pro Ala Glu Thr Thr Val Arg Thr Gly His Gly Asp
            180                 185                 190

His Thr Ser Val Gly Ala Glu Ala Pro His Leu Glu Glu Trp Ile Lys
        195                 200                 205

Arg Gly His
    210


<210> 129
<211> 966
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(943)
<223> RXA00821

<400> 129
ttaaaagctt gcttctcgac gcaaaaaccc atccggcgca tcccttcaat gttaggggtg 60

cgctgctatt tttctcccca gttctacgaa atgacttatt gtg act aag ctt gag   115
                                            Val Thr Lys Leu Glu
                                            1               5

cgc atg gag cat cct gct tac agc caa ttg cgg ccg gtt acc ccg tcc   163
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Arg Met Glu His Pro Ala Tyr Ser Gln Leu Arg Pro Val Thr Pro Ser
10 15 20

gca tct gtt gtt ttg tgc cct aat ccc ggt tac agc tcg ctg gaa ggc 211
Ala Ser Val Val Leu Cys Pro Asn Pro Gly Tyr Ser Ser Leu Glu Gly
25 30 35

act aat tct tgg gtt atc cgg gca cca gaa gac ccc cgg agc att gtc 259
Thr Asn Ser Trp Val Ile Arg Ala Pro Glu Asp Pro Arg Ser Ile Val
40 45 50

atc gat cca ggt cct gaa gat gag ggc cac ctt aac gtc ttg cat tcc 307
Ile Asp Pro Gly Pro Glu Asp Glu Gly His Leu Asn Val Leu His Ser
55 60 65

aag gct gag gag gtg ggt ttg att ctt ctg acc cac cgt cac tat gat 355
Lys Ala Glu Glu Val Gly Leu Ile Leu Leu Thr His Arg His Tyr Asp
70 75 80 85

cat gct gac ggc gca cag cgt ttc cgt cag ctg acc aat gca cct gtg 403
His Ala Asp Gly Ala Gln Arg Phe Arg Gln Leu Thr Asn Ala Pro Val
90 95 100

cgt gcg atg gac cct tcg tac tgt gct ggt gcg gag gag att cat gat 451
Arg Ala Met Asp Pro Ser Tyr Cys Ala Gly Ala Glu Glu Ile His Asp
105 110 115

ggt gag atc atc acg atc gac ggt gtc acc cca cag att gag gtg gtg 499
Gly Glu Ile Ile Thr Ile Asp Gly Val Thr Pro Gln Ile Glu Val Val
120 125 130

gcc aca cct ggt cat acc cgt gat tct gtg tct tat ttc atc tgg agt 547
Ala Thr Pro Gly His Thr Arg Asp Ser Val Ser Tyr Phe Ile Trp Ser
135 140 145

gga gtc cct cat gag tcc act ttg gag ggc atc gtt tct ggc gac acc 595
Gly Val Pro His Glu Ser Thr Leu Glu Gly Ile Val Ser Gly Asp Thr
150 155 160 165

att gcg ggt cgt cac acc acg atg att tca gag acc gac ggc gat ttg 643
Ile Ala Gly Arg His Thr Thr Met Ile Ser Glu Thr Asp Gly Asp Leu
170 175 180

ggt gag tac ctg aat tct ttg gcc att ttg gag gag cgc ggc aag gat 691
Gly Glu Tyr Leu Asn Ser Leu Ala Ile Leu Glu Glu Arg Gly Lys Asp
185 190 195

att ccg ctg ctt cca gga cat ggt cca gat gga cag gac gtg tcc tcc 739
Ile Pro Leu Leu Pro Gly His Gly Pro Asp Gly Gln Asp Val Ser Ser
200 205 210

ttc gcg cgt aag tac att gag cgt cgt gag ctg cgt ctg aac cag atc 787
Phe Ala Arg Lys Tyr Ile Glu Arg Arg Glu Leu Arg Leu Asn Gln Ile
215 220 225

cgt gag gta tgg gag acc cgt ggc cgt gac gtg tcc atg aag gat ctc 835
Arg Glu Val Trp Glu Thr Arg Gly Arg Asp Val Ser Met Lys Asp Leu
230 235 240 245

atc gac gcc atc tac gat gat gtt gat cca gtt ctg cgt ggt gca gcc 883
Ile Asp Ala Ile Tyr Asp Asp Val Asp Pro Val Leu Arg Gly Ala Ala

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                250                 255                 260

gag cag tcc act cat gtg gct att cgt tac ctg cag gct cag gaa gct    931
Glu Gln Ser Thr His Val Ala Ile Arg Tyr Leu Gln Ala Gln Glu Ala
            265                 270                 275

tcc gcc tca aac taaacacttt taactaaaca aca                          966
Ser Ala Ser Asn
        280


<210> 130
<211> 281
<212> PRT
<213> Corynebacterium glutamicum

<400> 130
Val Thr Lys Leu Glu Arg Met Glu His Pro Ala Tyr Ser Gln Leu Arg
  1               5                  10                  15

Pro Val Thr Pro Ser Ala Ser Val Val Leu Cys Pro Asn Pro Gly Tyr
             20                  25                  30

Ser Ser Leu Glu Gly Thr Asn Ser Trp Val Ile Arg Ala Pro Glu Asp
         35                  40                  45

Pro Arg Ser Ile Val Ile Asp Pro Gly Pro Glu Asp Glu Gly His Leu
     50                  55                  60

Asn Val Leu His Ser Lys Ala Glu Glu Val Gly Leu Ile Leu Leu Thr
 65                  70                  75                  80

His Arg His Tyr Asp His Ala Asp Gly Ala Gln Arg Phe Arg Gln Leu
                 85                  90                  95

Thr Asn Ala Pro Val Arg Ala Met Asp Pro Ser Tyr Cys Ala Gly Ala
            100                 105                 110

Glu Glu Ile His Asp Gly Glu Ile Ile Thr Ile Asp Gly Val Thr Pro
        115                 120                 125

Gln Ile Glu Val Val Ala Thr Pro Gly His Thr Arg Asp Ser Val Ser
    130                 135                 140

Tyr Phe Ile Trp Ser Gly Val Pro His Glu Ser Thr Leu Glu Gly Ile
145                 150                 155                 160

Val Ser Gly Asp Thr Ile Ala Gly Arg His Thr Thr Met Ile Ser Glu
                165                 170                 175

Thr Asp Gly Asp Leu Gly Glu Tyr Leu Asn Ser Leu Ala Ile Leu Glu
            180                 185                 190

Glu Arg Gly Lys Asp Ile Pro Leu Leu Pro Gly His Gly Pro Asp Gly
        195                 200                 205

Gln Asp Val Ser Ser Phe Ala Arg Lys Tyr Ile Glu Arg Arg Glu Leu
    210                 215                 220

Arg Leu Asn Gln Ile Arg Glu Val Trp Glu Thr Arg Gly Arg Asp Val
225                 230                 235                 240
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Ser Met Lys Asp Leu Ile Asp Ala Ile Tyr Asp Asp Val Asp Pro Val
                245                 250                 255

Leu Arg Gly Ala Ala Glu Gln Ser Thr His Val Ala Ile Arg Tyr Leu
            260                 265                 270

Gln Ala Gln Glu Ala Ser Ala Ser Asn
        275                 280


<210> 131
<211> 1530
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1507)
<223> RXN02966

<400> 131
aaatataccc cccagggtat cttgacagat taaagctcga tgttttaggc tctacatata 60

cccccacggg tatcccctca actttgatct aaggtgtcac atg ctt ttt gaa cgc   115
                                           Met Leu Phe Glu Arg
                                           1               5

atc tac gaa gaa ggc ctc gcc caa gcc agc tat ttc att ggc tgc caa   163
Ile Tyr Glu Glu Gly Leu Ala Gln Ala Ser Tyr Phe Ile Gly Cys Gln
                10                  15                  20

cgc gaa ggc aaa gcg att gtt gtt gat gct cgc cga gat atc cag acc   211
Arg Glu Gly Lys Ala Ile Val Val Asp Ala Arg Arg Asp Ile Gln Thr
            25                  30                  35

tat ctg gac ctt gca gca aaa aac aac atg gtc att agc gcc gta acc   259
Tyr Leu Asp Leu Ala Ala Lys Asn Asn Met Val Ile Ser Ala Val Thr
        40                  45                  50

gaa acc cat att cat gcc gat tat ctc tcc ggt act cgc gaa ctt gca   307
Glu Thr His Ile His Ala Asp Tyr Leu Ser Gly Thr Arg Glu Leu Ala
    55                  60                  65

gct gcc acc ggc gcc gag att ttc ctc tct ggc gaa ggc gga gct gat   355
Ala Ala Thr Gly Ala Glu Ile Phe Leu Ser Gly Glu Gly Gly Ala Asp
70                  75                  80                  85

tgg caa tat ggc ttt aca ggc acc acc ttg atg cac aat tcc acc atc   403
Trp Gln Tyr Gly Phe Thr Gly Thr Thr Leu Met His Asn Ser Thr Ile
                90                  95                  100

aag ctg gga aat atc acc atc aca gcc aag cac act ccc gga cac act   451
Lys Leu Gly Asn Ile Thr Ile Thr Ala Lys His Thr Pro Gly His Thr
            105                 110                 115

cca gag cac ctg tca ttt ttg att act gat ggt gcg gtc tca aag gat   499
Pro Glu His Leu Ser Phe Leu Ile Thr Asp Gly Ala Val Ser Lys Asp
        120                 125                 130

ccc ggt ttt atg ctc agc ggt gac ttc gtc ttc gta ggt gac gtg gga   547
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Pro Gly Phe Met Leu Ser Gly Asp Phe Val Phe Val Gly Asp Val Gly
    135                 140                 145

cgt cca gat tta ctt gat gag gca gct ggc ggc gtg gac acc cgc ttc     595
Arg Pro Asp Leu Leu Asp Glu Ala Ala Gly Gly Val Asp Thr Arg Phe
150                 155                 160                 165

gcc gga gca cag caa ctc ttc cat agc cta aaa gag cag ttc ctt gca     643
Ala Gly Ala Gln Gln Leu Phe His Ser Leu Lys Glu Gln Phe Leu Ala
                170                 175                 180

ctc ccc gac cac att cag gtt tat cca ggt cat ggt gct ggc agc cct     691
Leu Pro Asp His Ile Gln Val Tyr Pro Gly His Gly Ala Gly Ser Pro
            185                 190                 195

tgt ggc aag gca ttg ggc gcg atc cct agc acc acc gtg gga tat gaa     739
Cys Gly Lys Ala Leu Gly Ala Ile Pro Ser Thr Thr Val Gly Tyr Glu
        200                 205                 210

aag gct aat gcg tgg tgg gct cca tat ctg cgc agt gat gat gaa gcc     787
Lys Ala Asn Ala Trp Trp Ala Pro Tyr Leu Arg Ser Asp Asp Glu Ala
    215                 220                 225

ggc ttt gtg gaa gag ctt ctc gac ggc cag cca gat gcc cac gct tac     835
Gly Phe Val Glu Glu Leu Leu Asp Gly Gln Pro Asp Ala His Ala Tyr
230                 235                 240                 245

ttt gct cgc atg aaa aag cag aac aag cag gga cct gca gta ctt agt     883
Phe Ala Arg Met Lys Lys Gln Asn Lys Gln Gly Pro Ala Val Leu Ser
                250                 255                 260

aca tta tcc ccg ctt gtg aag cta gaa gcc gag gaa gtc gtc gaa aag     931
Thr Leu Ser Pro Leu Val Lys Leu Glu Ala Glu Glu Val Val Glu Lys
            265                 270                 275

ctt ggt tct gaa gca gta ttt gtg gat acc cgc gag caa aac caa gtc     979
Leu Gly Ser Glu Ala Val Phe Val Asp Thr Arg Glu Gln Asn Gln Val
        280                 285                 290

cat ctc gga acc gtt gtt ggg gca ttg aat att ccg cgc ggc gcc aag     1027
His Leu Gly Thr Val Val Gly Ala Leu Asn Ile Pro Arg Gly Ala Lys
    295                 300                 305

gcg tcc aat ttt gcg gcg tgg gtt att gat cct caa aag gat gct cag     1075
Ala Ser Asn Phe Ala Ala Trp Val Ile Asp Pro Gln Lys Asp Ala Gln
310                 315                 320                 325

gac ctt att gtt ttg gct ccg gac gcc aat acc gct gcg gat ttc cgc     1123
Asp Leu Ile Val Leu Ala Pro Asp Ala Asn Thr Ala Ala Asp Phe Arg
                330                 335                 340

gac gct ttg ctg cgg gtt ggc atc gac act gtg cgt tat ttc acc aac     1171
Asp Ala Leu Leu Arg Val Gly Ile Asp Thr Val Arg Tyr Phe Thr Asn
            345                 350                 355

agt atc gat gga ttg cct acc ttt gtg cca gaa ctc atc tcc ccc gct     1219
Ser Ile Asp Gly Leu Pro Thr Phe Val Pro Glu Leu Ile Ser Pro Ala
        360                 365                 370

gag cta gct gag acc aac tat gac gca ctg att gat atc cgt gca aag     1267
Glu Leu Ala Glu Thr Asn Tyr Asp Ala Leu Ile Asp Ile Arg Ala Lys
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    375                 380                 385

tcc gaa ttt gcc gct ggc agc att ccc ggc gcg cag cag ctt tct gga     1315
Ser Glu Phe Ala Ala Gly Ser Ile Pro Gly Ala Gln Gln Leu Ser Gly
390                 395                 400                 405

ggt tcg gcc atg tgg cgc ctc aat gag ctg cct gcg ggt ggc act ttg     1363
Gly Ser Ala Met Trp Arg Leu Asn Glu Leu Pro Ala Gly Gly Thr Leu
                410                 415                 420

gta acc ttc tgc caa tca gga gcg cga aat acc gtg gta gcc aat gct     1411
Val Thr Phe Cys Gln Ser Gly Ala Arg Asn Thr Val Val Ala Asn Ala
            425                 430                 435

ttg cga cgc gcc gga ttc acc gtt atc gag ctc gag ggc agc tac gcc     1459
Leu Arg Arg Ala Gly Phe Thr Val Ile Glu Leu Glu Gly Ser Tyr Ala
        440                 445                 450

gcg tgg gaa aaa tca gct gcc aat cct aaa aac ttg cag act gcc gtc     1507
Ala Trp Glu Lys Ser Ala Ala Asn Pro Lys Asn Leu Gln Thr Ala Val
    455                 460                 465

tagttttaga tccggcgctg tat                                           1530


<210> 132
<211> 469
<212> PRT
<213> Corynebacterium glutamicum

<400> 132
Met Leu Phe Glu Arg Ile Tyr Glu Glu Gly Leu Ala Gln Ala Ser Tyr
  1               5                  10                  15

Phe Ile Gly Cys Gln Arg Glu Gly Lys Ala Ile Val Val Asp Ala Arg
            20                  25                  30

Arg Asp Ile Gln Thr Tyr Leu Asp Leu Ala Ala Lys Asn Asn Met Val
        35                  40                  45

Ile Ser Ala Val Thr Glu Thr His Ile His Ala Asp Tyr Leu Ser Gly
    50                  55                  60

Thr Arg Glu Leu Ala Ala Ala Thr Gly Ala Glu Ile Phe Leu Ser Gly
 65                  70                  75                  80

Glu Gly Gly Ala Asp Trp Gln Tyr Gly Phe Thr Gly Thr Thr Leu Met
                 85                  90                  95

His Asn Ser Thr Ile Lys Leu Gly Asn Ile Thr Ile Thr Ala Lys His
            100                 105                 110

Thr Pro Gly His Thr Pro Glu His Leu Ser Phe Leu Ile Thr Asp Gly
        115                 120                 125

Ala Val Ser Lys Asp Pro Gly Phe Met Leu Ser Gly Asp Phe Val Phe
    130                 135                 140

Val Gly Asp Val Gly Arg Pro Asp Leu Leu Asp Glu Ala Ala Gly Gly
145                 150                 155                 160
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Val Asp Thr Arg Phe Ala Gly Ala Gln Gln Leu Phe His Ser Leu Lys
                165                 170                 175

Glu Gln Phe Leu Ala Leu Pro Asp His Ile Gln Val Tyr Pro Gly His
            180                 185                 190

Gly Ala Gly Ser Pro Cys Gly Lys Ala Leu Gly Ala Ile Pro Ser Thr
        195                 200                 205

Thr Val Gly Tyr Glu Lys Ala Asn Ala Trp Trp Ala Pro Tyr Leu Arg
    210                 215                 220

Ser Asp Asp Glu Ala Gly Phe Val Glu Glu Leu Leu Asp Gly Gln Pro
225                 230                 235                 240

Asp Ala His Ala Tyr Phe Ala Arg Met Lys Lys Gln Asn Lys Gln Gly
                245                 250                 255

Pro Ala Val Leu Ser Thr Leu Ser Pro Leu Val Lys Leu Glu Ala Glu
            260                 265                 270

Glu Val Val Glu Lys Leu Gly Ser Glu Ala Val Phe Val Asp Thr Arg
        275                 280                 285

Glu Gln Asn Gln Val His Leu Gly Thr Val Val Gly Ala Leu Asn Ile
    290                 295                 300

Pro Arg Gly Ala Lys Ala Ser Asn Phe Ala Ala Trp Val Ile Asp Pro
305                 310                 315                 320

Gln Lys Asp Ala Gln Asp Leu Ile Val Leu Ala Pro Asp Ala Asn Thr
                325                 330                 335

Ala Ala Asp Phe Arg Asp Ala Leu Leu Arg Val Gly Ile Asp Thr Val
            340                 345                 350

Arg Tyr Phe Thr Asn Ser Ile Asp Gly Leu Pro Thr Phe Val Pro Glu
        355                 360                 365

Leu Ile Ser Pro Ala Glu Leu Ala Glu Thr Asn Tyr Asp Ala Leu Ile
    370                 375                 380

Asp Ile Arg Ala Lys Ser Glu Phe Ala Ala Gly Ser Ile Pro Gly Ala
385                 390                 395                 400

Gln Gln Leu Ser Gly Gly Ser Ala Met Trp Arg Leu Asn Glu Leu Pro
                405                 410                 415

Ala Gly Gly Thr Leu Val Thr Phe Cys Gln Ser Gly Ala Arg Asn Thr
            420                 425                 430

Val Val Ala Asn Ala Leu Arg Arg Ala Gly Phe Thr Val Ile Glu Leu
        435                 440                 445

Glu Gly Ser Tyr Ala Ala Trp Glu Lys Ser Ala Ala Asn Pro Lys Asn
    450                 455                 460

Leu Gln Thr Ala Val
465
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<210> 133
<211> 1530
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1507)
<223> FRXA01833

<400> 133
aaatataccc cccagggtat cttgacagat taaagctcga tgttttaggc tctacatata 60

cccccacggg tatcccctca actttgatct aaggtgtcac atg ctt ttt gaa cgc   115
                                           Met Leu Phe Glu Arg
                                           1               5

atc tac gaa gaa ggc ctc gcc caa gcc agc tat ttc att ggc tgc caa   163
Ile Tyr Glu Glu Gly Leu Ala Gln Ala Ser Tyr Phe Ile Gly Cys Gln
                10                  15                  20

cgc gaa ggc aaa gcg att gtt gtt gat gct cgc cga gat atc cag acc   211
Arg Glu Gly Lys Ala Ile Val Val Asp Ala Arg Arg Asp Ile Gln Thr
            25                  30                  35

tat ctg gac ctt gca gca aaa aac aac atg gtc att agc gcc gta acc   259
Tyr Leu Asp Leu Ala Ala Lys Asn Asn Met Val Ile Ser Ala Val Thr
        40                  45                  50

gaa acc cat att cat gcc gat tat ctc tcc ggt act cgc gaa ctt gca   307
Glu Thr His Ile His Ala Asp Tyr Leu Ser Gly Thr Arg Glu Leu Ala
    55                  60                  65

gct gcc acc ggc gcc gag att ttc ctc tct ggc gaa ggc gga gct gat   355
Ala Ala Thr Gly Ala Glu Ile Phe Leu Ser Gly Glu Gly Gly Ala Asp
70                  75                  80                  85

tgg caa tat ggc ttt aca ggc acc acc ttg atg cac aat tcc acc atc   403
Trp Gln Tyr Gly Phe Thr Gly Thr Thr Leu Met His Asn Ser Thr Ile
                90                  95                  100

aag ctg gaa aat atc acc atc aca gcc aag cac act ccc gga cac act   451
Lys Leu Glu Asn Ile Thr Ile Thr Ala Lys His Thr Pro Gly His Thr
            105                 110                 115

cca gag cac ctg tca ttt ttg att act gat ggt gcg gtc tca aag gat   499
Pro Glu His Leu Ser Phe Leu Ile Thr Asp Gly Ala Val Ser Lys Asp
        120                 125                 130

ccc ggt ttt atg ctc agc ggt gac ttc gtc ttc gta ggt gac gtg gga   547
Pro Gly Phe Met Leu Ser Gly Asp Phe Val Phe Val Gly Asp Val Gly
    135                 140                 145

cgt cca gat tta ctt gat gag gca gct ggc ggc gtg gac acc cgc ttc   595
Arg Pro Asp Leu Leu Asp Glu Ala Ala Gly Gly Val Asp Thr Arg Phe
150                 155                 160                 165

gcc gga gca cag caa ctc ttc cat agc cta aaa gag cag ttc ctt gca   643
Ala Gly Ala Gln Gln Leu Phe His Ser Leu Lys Glu Gln Phe Leu Ala
                170                 175                 180
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ctc ccc gac cac att cag gtt tat cca ggt cat ggt gct ggc agc cct    691
Leu Pro Asp His Ile Gln Val Tyr Pro Gly His Gly Ala Gly Ser Pro
            185                 190                 195

tgt ggc aag gca ttg ggc gcg atc cct agc acc acc gtg gga tat gaa    739
Cys Gly Lys Ala Leu Gly Ala Ile Pro Ser Thr Thr Val Gly Tyr Glu
        200                 205                 210

aag gct aat gcg tgg tgg gct cca tat ctg cgc agt gat gat gaa gcc    787
Lys Ala Asn Ala Trp Trp Ala Pro Tyr Leu Arg Ser Asp Asp Glu Ala
    215                 220                 225

ggc ttt gtg gaa gag ctt ctc gac ggc cag cca gat gcc cac gct tac    835
Gly Phe Val Glu Glu Leu Leu Asp Gly Gln Pro Asp Ala His Ala Tyr
230                 235                 240                 245

ttt gct cgc atg aaa aag cag aac aag cag gga cct gca gta ctt agt    883
Phe Ala Arg Met Lys Lys Gln Asn Lys Gln Gly Pro Ala Val Leu Ser
                250                 255                 260

aca tta tcc ccg ctt gtg aag cta gaa gcc gag gaa gtc gtc gaa aag    931
Thr Leu Ser Pro Leu Val Lys Leu Glu Ala Glu Glu Val Val Glu Lys
            265                 270                 275

ctt ggt tct gaa gca gta ttt gtg gat acc cgc gag caa aac caa gtc    979
Leu Gly Ser Glu Ala Val Phe Val Asp Thr Arg Glu Gln Asn Gln Val
        280                 285                 290

cat ctc gga acc gtt gtt ggg gca ttg aat att ccg cgc ggc gcc aag    1027
His Leu Gly Thr Val Val Gly Ala Leu Asn Ile Pro Arg Gly Ala Lys
    295                 300                 305

gcg tcc aat ttt gcg gcg tgg gtt att gat cct caa aag gat gct cag    1075
Ala Ser Asn Phe Ala Ala Trp Val Ile Asp Pro Gln Lys Asp Ala Gln
310                 315                 320                 325

gac ctt att gtt ttg gct ccg gac gcc aat acc gct gcg gat ttc cgc    1123
Asp Leu Ile Val Leu Ala Pro Asp Ala Asn Thr Ala Ala Asp Phe Arg
                330                 335                 340

gac gct ttg ctg cgg gtt ggc atc gac act gtg cgt tat ttc acc aac    1171
Asp Ala Leu Leu Arg Val Gly Ile Asp Thr Val Arg Tyr Phe Thr Asn
            345                 350                 355

agt atc gat gga ttg cct acc ttt gtg cca gaa ctc atc tcc ccc gct    1219
Ser Ile Asp Gly Leu Pro Thr Phe Val Pro Glu Leu Ile Ser Pro Ala
        360                 365                 370

gag cta gct gag acc aac tat gac gca ctg att gat atc cgt gca aag    1267
Glu Leu Ala Glu Thr Asn Tyr Asp Ala Leu Ile Asp Ile Arg Ala Lys
    375                 380                 385

tcc gaa ttt gcc gct ggc agc att ccc ggc gcg cag cag ctt tct gga    1315
Ser Glu Phe Ala Ala Gly Ser Ile Pro Gly Ala Gln Gln Leu Ser Gly
390                 395                 400                 405

ggt tcg gcc atg tgg cgc ctc aat gag ctg cct gcg ggt ggc act ttg    1363
Gly Ser Ala Met Trp Arg Leu Asn Glu Leu Pro Ala Gly Gly Thr Leu
                410                 415                 420

gta acc ttc tgc caa tca gga gcg cga aat acc gtg gta gcc aat gct    1411
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Val Thr Phe Cys Gln Ser Gly Ala Arg Asn Thr Val Val Ala Asn Ala
            425                 430                 435

ttg cga cgc gcc gga ttc acc gtt atc gag ctc gag ggc agc tac gcc    1459
Leu Arg Arg Ala Gly Phe Thr Val Ile Glu Leu Glu Gly Ser Tyr Ala
        440                 445                 450

gcg tgg gaa aaa tca gct gcc aat cct aaa aac ttg cag act gcc gtc    1507
Ala Trp Glu Lys Ser Ala Ala Asn Pro Lys Asn Leu Gln Thr Ala Val
    455                 460                 465

tagttttaga tccggcgctg tat                                          1530


<210> 134
<211> 469
<212> PRT
<213> Corynebacterium glutamicum

<400> 134
Met Leu Phe Glu Arg Ile Tyr Glu Glu Gly Leu Ala Gln Ala Ser Tyr
  1               5                  10                  15

Phe Ile Gly Cys Gln Arg Glu Gly Lys Ala Ile Val Val Asp Ala Arg
             20                  25                  30

Arg Asp Ile Gln Thr Tyr Leu Asp Leu Ala Ala Lys Asn Asn Met Val
         35                  40                  45

Ile Ser Ala Val Thr Glu Thr His Ile His Ala Asp Tyr Leu Ser Gly
     50                  55                  60

Thr Arg Glu Leu Ala Ala Ala Thr Gly Ala Glu Ile Phe Leu Ser Gly
 65                  70                  75                  80

Glu Gly Gly Ala Asp Trp Gln Tyr Gly Phe Thr Gly Thr Thr Leu Met
                 85                  90                  95

His Asn Ser Thr Ile Lys Leu Glu Asn Ile Thr Ile Thr Ala Lys His
            100                 105                 110

Thr Pro Gly His Thr Pro Glu His Leu Ser Phe Leu Ile Thr Asp Gly
        115                 120                 125

Ala Val Ser Lys Asp Pro Gly Phe Met Leu Ser Gly Asp Phe Val Phe
    130                 135                 140

Val Gly Asp Val Gly Arg Pro Asp Leu Leu Asp Glu Ala Ala Gly Gly
145                 150                 155                 160

Val Asp Thr Arg Phe Ala Gly Ala Gln Gln Leu Phe His Ser Leu Lys
                165                 170                 175

Glu Gln Phe Leu Ala Leu Pro Asp His Ile Gln Val Tyr Pro Gly His
            180                 185                 190

Gly Ala Gly Ser Pro Cys Gly Lys Ala Leu Gly Ala Ile Pro Ser Thr
        195                 200                 205

Thr Val Gly Tyr Glu Lys Ala Asn Ala Trp Trp Ala Pro Tyr Leu Arg
    210                 215                 220
```

Ser Asp Asp Glu Ala Gly Phe Val Glu Glu Leu Leu Asp Gly Gln Pro
225 230 235 240

Asp Ala His Ala Tyr Phe Ala Arg Met Lys Lys Gln Asn Lys Gln Gly
245 250 255

Pro Ala Val Leu Ser Thr Leu Ser Pro Leu Val Lys Leu Glu Ala Glu
260 265 270

Glu Val Val Glu Lys Leu Gly Ser Glu Ala Val Phe Val Asp Thr Arg
275 280 285

Glu Gln Asn Gln Val His Leu Gly Thr Val Val Gly Ala Leu Asn Ile
290 295 300

Pro Arg Gly Ala Lys Ala Ser Asn Phe Ala Ala Trp Val Ile Asp Pro
305 310 315 320

Gln Lys Asp Ala Gln Asp Leu Ile Val Leu Ala Pro Asp Ala Asn Thr
325 330 335

Ala Ala Asp Phe Arg Asp Ala Leu Leu Arg Val Gly Ile Asp Thr Val
340 345 350

Arg Tyr Phe Thr Asn Ser Ile Asp Gly Leu Pro Thr Phe Val Pro Glu
355 360 365

Leu Ile Ser Pro Ala Glu Leu Ala Glu Thr Asn Tyr Asp Ala Leu Ile
370 375 380

Asp Ile Arg Ala Lys Ser Glu Phe Ala Ala Gly Ser Ile Pro Gly Ala
385 390 395 400

Gln Gln Leu Ser Gly Gly Ser Ala Met Trp Arg Leu Asn Glu Leu Pro
405 410 415

Ala Gly Gly Thr Leu Val Thr Phe Cys Gln Ser Gly Ala Arg Asn Thr
420 425 430

Val Val Ala Asn Ala Leu Arg Arg Ala Gly Phe Thr Val Ile Glu Leu
435 440 445

Glu Gly Ser Tyr Ala Ala Trp Glu Lys Ser Ala Ala Asn Pro Lys Asn
450 455 460

Leu Gln Thr Ala Val
465

<210> 135
<211> 675
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(652)
<223> RXA01853

<400> 135

gaatgtccaa cgtcaaaaaa attcttttct atcctaaccg tatcttcaca ccttgaggga 60

atgatggggg agcgccgctt acgcactaca ctgtttattc atg gag atc ctc gga 115
Met Glu Ile Leu Gly
1 5

ttc gcg gct ggt ccg tat aaa aca aat tgc tat gtg gtg cgc ggg gag 163
Phe Ala Ala Gly Pro Tyr Lys Thr Asn Cys Tyr Val Val Arg Gly Glu
10 15 20

aat gag gtc gcg atc att gat cct ggc atg cat gcc cac gat gat ttg 211
Asn Glu Val Ala Ile Ile Asp Pro Gly Met His Ala His Asp Asp Leu
25 30 35

gtg gaa tac atc acc acg aat aat ttg agc gtg gac aag att gtg ctc 259
Val Glu Tyr Ile Thr Thr Asn Asn Leu Ser Val Asp Lys Ile Val Leu
40 45 50

acc cac gga cac att gat cac acc cgt gat gct ggt gtt gtg gca aag 307
Thr His Gly His Ile Asp His Thr Arg Asp Ala Gly Val Val Ala Lys
55 60 65

cgt ttc aat gcg ccg gtc tat atc cat cct gat gat gcg ttt ttc ctt 355
Arg Phe Asn Ala Pro Val Tyr Ile His Pro Asp Asp Ala Phe Phe Leu
70 75 80 85

gag gtc tac aag gga tct gga aca aag acg gcc atg ctt ttc gac gcc 403
Glu Val Tyr Lys Gly Ser Gly Thr Lys Thr Ala Met Leu Phe Asp Ala
90 95 100

gac aac atg gtg tcc cct gat cct gag tca ctg cgt gat ctg gtt gat 451
Asp Asn Met Val Ser Pro Asp Pro Glu Ser Leu Arg Asp Leu Val Asp
105 110 115

ggt gag aca atc act ttg gct ggc gaa gaa ttc acg ttg aag cat gca 499
Gly Glu Thr Ile Thr Leu Ala Gly Glu Glu Phe Thr Leu Lys His Ala
120 125 130

cca ggg cat tca cct ggt tgt acg ctg atc gtc ggc aag gaa tac tgc 547
Pro Gly His Ser Pro Gly Cys Thr Leu Ile Val Gly Lys Glu Tyr Cys
135 140 145

ttt agc ggt gat gtg ttg ttc aag ggc tct att ggt cgc act gat ttt 595
Phe Ser Gly Asp Val Leu Phe Lys Gly Ser Ile Gly Arg Thr Asp Phe
150 155 160 165

gag tgg tct gat gca gat gcc atg aat gag tca cta cgc acg gca gtg 643
Glu Trp Ser Asp Ala Asp Ala Met Asn Glu Ser Leu Arg Thr Ala Val
170 175 180

ctc cca ctt tgatgatgca ttgcagattc ttc 675
Leu Pro Leu

<210> 136
<211> 184
<212> PRT
<213> Corynebacterium glutamicum

<400> 136

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Met Glu Ile Leu Gly Phe Ala Ala Gly Pro Tyr Lys Thr Asn Cys Tyr
  1               5                  10                  15

Val Val Arg Gly Glu Asn Glu Val Ala Ile Ile Asp Pro Gly Met His
            20                  25                  30

Ala His Asp Asp Leu Val Glu Tyr Ile Thr Thr Asn Asn Leu Ser Val
        35                  40                  45

Asp Lys Ile Val Leu Thr His Gly His Ile Asp His Thr Arg Asp Ala
    50                  55                  60

Gly Val Val Ala Lys Arg Phe Asn Ala Pro Val Tyr Ile His Pro Asp
 65                  70                  75                      80

Asp Ala Phe Phe Leu Glu Val Tyr Lys Gly Ser Gly Thr Lys Thr Ala
                 85                  90                  95

Met Leu Phe Asp Ala Asp Asn Met Val Ser Pro Asp Pro Glu Ser Leu
            100                 105                 110

Arg Asp Leu Val Asp Gly Glu Thr Ile Thr Leu Ala Gly Glu Glu Phe
        115                 120                 125

Thr Leu Lys His Ala Pro Gly His Ser Pro Gly Cys Thr Leu Ile Val
    130                 135                 140

Gly Lys Glu Tyr Cys Phe Ser Gly Asp Val Leu Phe Lys Gly Ser Ile
145                 150                 155                     160

Gly Arg Thr Asp Phe Glu Trp Ser Asp Ala Asp Ala Met Asn Glu Ser
                165                 170                 175

Leu Arg Thr Ala Val Leu Pro Leu
            180


<210> 137
<211> 723
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(700)
<223> RXN02424

<400> 137
agccaatgct caactgccct tcaaaatcga tttttgtcgc ttcaaaaaat acaccttcga 60

acatagcatc gaacaaggtg tttccgctag tctgaaccac atg act aac gag ctc   115
                                           Met Thr Asn Glu Leu
                                           1               5

act ctt cac cat att tcc gtg tcc caa atg gac aac aat tgc tac ctt   163
Thr Leu His His Ile Ser Val Ser Gln Met Asp Asn Asn Cys Tyr Leu
                10                  15                  20

ttg gcc gca aat ggc aac ggt tta ctc att gat gct gca gat gac gca   211
Leu Ala Ala Asn Gly Asn Gly Leu Leu Ile Asp Ala Ala Asp Asp Ala
            25                  30                  35
```

gct gca cta ctt aaa tta gcc gaa gat gcc ggt gtg acc atc acc aaa 259
Ala Ala Leu Leu Lys Leu Ala Glu Asp Ala Gly Val Thr Ile Thr Lys
40 45 50

gtg ttg acc acc cac cgc cac gca gac cac gtc cgt gca ttg ccg gag 307
Val Leu Thr Thr His Arg His Ala Asp His Val Arg Ala Leu Pro Glu
55 60 65

gtt ctc cag aag acc gga gca act cac tac gcg cct ttc ctt gag gtg 355
Val Leu Gln Lys Thr Gly Ala Thr His Tyr Ala Pro Phe Leu Glu Val
70 75 80 85

cca gct ttg ccc tcc gct gtt gat gtg gaa ctg cat cat ggt gat tca 403
Pro Ala Leu Pro Ser Ala Val Asp Val Glu Leu His His Gly Asp Ser
90 95 100

att gaa ttt gag ggt cat gta ttc cct atc agc att ctg cgc ggc cac 451
Ile Glu Phe Glu Gly His Val Phe Pro Ile Ser Ile Leu Arg Gly His
105 110 115

acc cca ggc ggt gca gta ctc acc gct gag atc gac ggt aaa act cac 499
Thr Pro Gly Gly Ala Val Leu Thr Ala Glu Ile Asp Gly Lys Thr His
120 125 130

ctt ttc gtg ggt gac agc ctc ttc ccc ggc ggt ttg ggc aaa acc agc 547
Leu Phe Val Gly Asp Ser Leu Phe Pro Gly Gly Leu Gly Lys Thr Ser
135 140 145

agc gaa ggc gac ttc gtc cga ctg ttc aac gat gtc aaa gag cgc atc 595
Ser Glu Gly Asp Phe Val Arg Leu Phe Asn Asp Val Lys Glu Arg Ile
150 155 160 165

ttt gac acc tac gac gat gac agc atc gtg tgg cca ggt cac ggc aag 643
Phe Asp Thr Tyr Asp Asp Asp Ser Ile Val Trp Pro Gly His Gly Lys
170 175 180

gaa acc acc ctt gga gcc gag cgt cca cag ctg gaa atc tgg tgg gag 691
Glu Thr Thr Leu Gly Ala Glu Arg Pro Gln Leu Glu Ile Trp Trp Glu
185 190 195

cgt cgc tgg taagcgcttt tctcaaccag gca 723
Arg Arg Trp
200

<210> 138
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 138
Met Thr Asn Glu Leu Thr Leu His His Ile Ser Val Ser Gln Met Asp
1 5 10 15

Asn Asn Cys Tyr Leu Leu Ala Ala Asn Gly Asn Gly Leu Leu Ile Asp
20 25 30

Ala Ala Asp Asp Ala Ala Ala Leu Leu Lys Leu Ala Glu Asp Ala Gly
35 40 45

Val Thr Ile Thr Lys Val Leu Thr Thr His Arg His Ala Asp His Val
50 55 60

Arg Ala Leu Pro Glu Val Leu Gln Lys Thr Gly Ala Thr His Tyr Ala
65 70 75 80

Pro Phe Leu Glu Val Pro Ala Leu Pro Ser Ala Val Asp Val Glu Leu
85 90 95

His His Gly Asp Ser Ile Glu Phe Glu Gly His Val Phe Pro Ile Ser
100 105 110

Ile Leu Arg Gly His Thr Pro Gly Gly Ala Val Leu Thr Ala Glu Ile
115 120 125

Asp Gly Lys Thr His Leu Phe Val Gly Asp Ser Leu Phe Pro Gly Gly
130 135 140

Leu Gly Lys Thr Ser Ser Glu Gly Asp Phe Val Arg Leu Phe Asn Asp
145 150 155 160

Val Lys Glu Arg Ile Phe Asp Thr Tyr Asp Asp Asp Ser Ile Val Trp
165 170 175

Pro Gly His Gly Lys Glu Thr Thr Leu Gly Ala Glu Arg Pro Gln Leu
180 185 190

Glu Ile Trp Trp Glu Arg Arg Trp
195 200

<210> 139
<211> 404
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(381)
<223> FRXA02424

<400> 139
acc gga gca act cac tac gcg cct ttc ctt gag gtg cca gct ttg ccc 48
Thr Gly Ala Thr His Tyr Ala Pro Phe Leu Glu Val Pro Ala Leu Pro
1 5 10 15

tcc gct gtt gat gtg gaa ctg cat cat ggt gat tca att gaa ttt gag 96
Ser Ala Val Asp Val Glu Leu His His Gly Asp Ser Ile Glu Phe Glu
20 25 30

ggt cat gta ttc cct atc agc att ctg cgc ggc cac acc cca ggc ggt 144
Gly His Val Phe Pro Ile Ser Ile Leu Arg Gly His Thr Pro Gly Gly
35 40 45

gca gta ctc acc gct gag atc gac ggt aaa act cac ctt ttc gtg ggt 192
Ala Val Leu Thr Ala Glu Ile Asp Gly Lys Thr His Leu Phe Val Gly
50 55 60

gac agc ctc ttc ccc ggc ggt ttg ggc aaa acc agc agc gaa ggc gac 240
Asp Ser Leu Phe Pro Gly Gly Leu Gly Lys Thr Ser Ser Glu Gly Asp
65 70 75 80

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ttc gtc cga ctg ttc aac gat gtc aaa gag cgc atc ttt gac acc tac    288
Phe Val Arg Leu Phe Asn Asp Val Lys Glu Arg Ile Phe Asp Thr Tyr
                85                  90                  95

gac gat gac agc atc gtg tgg cca ggt cac ggc aag gaa acc acc ctt    336
Asp Asp Asp Ser Ile Val Trp Pro Gly His Gly Lys Glu Thr Thr Leu
            100                 105                 110

gga gcc gag cgt cca cag ctg gaa atc tgg tgg gag cgt cgc tgg        381
Gly Ala Glu Arg Pro Gln Leu Glu Ile Trp Trp Glu Arg Arg Trp
        115                 120                 125

taagcgcttt tctcaaccag gca                                          404


<210> 140
<211> 127
<212> PRT
<213> Corynebacterium glutamicum

<400> 140
Thr Gly Ala Thr His Tyr Ala Pro Phe Leu Glu Val Pro Ala Leu Pro
  1               5                  10                  15

Ser Ala Val Asp Val Glu Leu His His Gly Asp Ser Ile Glu Phe Glu
             20                  25                  30

Gly His Val Phe Pro Ile Ser Ile Leu Arg Gly His Thr Pro Gly Gly
        35                  40                  45

Ala Val Leu Thr Ala Glu Ile Asp Gly Lys Thr His Leu Phe Val Gly
    50                  55                  60

Asp Ser Leu Phe Pro Gly Gly Leu Gly Lys Thr Ser Ser Glu Gly Asp
 65                  70                  75                  80

Phe Val Arg Leu Phe Asn Asp Val Lys Glu Arg Ile Phe Asp Thr Tyr
                85                  90                  95

Asp Asp Asp Ser Ile Val Trp Pro Gly His Gly Lys Glu Thr Thr Leu
            100                 105                 110

Gly Ala Glu Arg Pro Gln Leu Glu Ile Trp Trp Glu Arg Arg Trp
        115                 120                 125


<210> 141
<211> 882
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(859)
<223> RXN00419

<400> 141
gctggttgaa gactcgaaat gagatcgacc caaccggagt ctttgcatct gacatgtccc 60

gccgacttga gctttcttaa gaaagggctt gaactaaaca atg ctt aac gca gtg   115
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                                                      Met Leu Asn Ala Val
                                                       1               5

ggc aaa gcc caa aac att ctc ctt ctt ggt gga acc tct gag atc ggt     163
Gly Lys Ala Gln Asn Ile Leu Leu Leu Gly Gly Thr Ser Glu Ile Gly
                 10                  15                  20

att tcc att gtc tcc cgc ttc ctc aag cag ggt cca tcc cat gtg acc     211
Ile Ser Ile Val Ser Arg Phe Leu Lys Gln Gly Pro Ser His Val Thr
             25                  30                  35

ttg gca gcg cgt aaa gat tcc cca cgc gtg gac gca gca gtc gca gag     259
Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp Ala Ala Val Ala Glu
         40                  45                  50

atc aaa gca gct ggc gct gct tcc gtt gct gtt gtt gat ttc gat gcg     307
Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val Val Asp Phe Asp Ala
     55                  60                  65

ctc gac acc gaa tcc cac cct gca gcc atc gac gca gcc ttt gaa aac     355
Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp Ala Ala Phe Glu Asn
 70                  75                  80                  85

ggc gac gtt gac gta gca atc gtg gct ttc ggc atc ctc ggc gac aac     403
Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly Ile Leu Gly Asp Asn
                 90                  95                 100

gaa gca cag tgg cgc gac caa gca cta gca gtg gaa gca acc acc gtg     451
Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val Glu Ala Thr Thr Val
            105                 110                 115

aac tac acc gcc ggc gtt tcc gta ggt gta ctg ctg ggc cag aaa ttt     499
Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu Leu Gly Gln Lys Phe
        120                 125                 130

gag cag cag ggc cac ggc acc atc gtg gca ttg tcc tct gtg gca ggc     547
Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu Ser Ser Val Ala Gly
    135                 140                 145

cag cga gtc cgc cgc tcc aac ttt gtc tac ggc tcc gcc aag gca ggt     595
Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly Ser Ala Lys Ala Gly
150                 155                 160                 165

ttc gac ggt ttc tac acc cag ctc ggc gaa gcc ctg cgt gga tcc ggt     643
Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala Leu Arg Gly Ser Gly
                170                 175                 180

gcc aac gta ttg gtg gtt cgc cca ggc cag gta cgc acc aag atg tcc     691
Ala Asn Val Leu Val Val Arg Pro Gly Gln Val Arg Thr Lys Met Ser
            185                 190                 195

gca gat ggt ggc gaa gcc cca ctg acc gtc aac cgc gaa gac gtg gca     739
Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn Arg Glu Asp Val Ala
        200                 205                 210

gat gct gtt tat gat gca gtg gtg aac aag aag gac atc atc ttt gtc     787
Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys Asp Ile Ile Phe Val
    215                 220                 225

cac cca ctg ttc cag tac gtc tct ttt gcg ttc caa ttc att ccg cga     835
His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe Gln Phe Ile Pro Arg
```

```
230                 235                 240                 245

gca atc ttc cgc aag ctg ccg ttc taacggaagt tacggaagtt acg          882
Ala Ile Phe Arg Lys Leu Pro Phe
                250


<210> 142
<211> 253
<212> PRT
<213> Corynebacterium glutamicum

<400> 142
Met Leu Asn Ala Val Gly Lys Ala Gln Asn Ile Leu Leu Leu Gly Gly
  1               5                  10                  15

Thr Ser Glu Ile Gly Ile Ser Ile Val Ser Arg Phe Leu Lys Gln Gly
             20                  25                  30

Pro Ser His Val Thr Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp
         35                  40                  45

Ala Ala Val Ala Glu Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val
     50                  55                  60

Val Asp Phe Asp Ala Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp
 65                  70                  75                  80

Ala Ala Phe Glu Asn Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly
                 85                  90                  95

Ile Leu Gly Asp Asn Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val
            100                 105                 110

Glu Ala Thr Thr Val Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu
        115                 120                 125

Leu Gly Gln Lys Phe Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu
    130                 135                 140

Ser Ser Val Ala Gly Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly
145                 150                 155                 160

Ser Ala Lys Ala Gly Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala
                165                 170                 175

Leu Arg Gly Ser Gly Ala Asn Val Leu Val Val Arg Pro Gly Gln Val
            180                 185                 190

Arg Thr Lys Met Ser Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn
        195                 200                 205

Arg Glu Asp Val Ala Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys
    210                 215                 220

Asp Ile Ile Phe Val His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe
225                 230                 235                 240

Gln Phe Ile Pro Arg Ala Ile Phe Arg Lys Leu Pro Phe
                245                 250
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<210> 143
<211> 485
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(462)
<223> FRXA00419

<400> 143
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gac aac gaa gca cag tgg cgc gac caa gca cta gca gtg gaa gca acc    48
Asp Asn Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val Glu Ala Thr
  1               5                  10                  15

acc gtg aac tac acc gcc ggc gtt tcc gta ggt gta ctg ctg ggc cag    96
Thr Val Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu Leu Gly Gln
             20                  25                  30

aaa ttt gag cag cag ggc cac ggc acc atc gtg gca ttg tcc tct gtg   144
Lys Phe Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu Ser Ser Val
         35                  40                  45

gca ggc cag cga gtc cgc cgc tcc aac ttt gtc tac ggc tcc gcc aag   192
Ala Gly Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly Ser Ala Lys
     50                  55                  60

gca ggt ttc gac ggt ttc tac acc cag ctc ggc gaa gcc ctg cgt gga   240
Ala Gly Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala Leu Arg Gly
 65                  70                  75                  80

tcc ggt gcc aac gta ttg gtg gtt cgc cca ggc cag gta cgc acc aag   288
Ser Gly Ala Asn Val Leu Val Val Arg Pro Gly Gln Val Arg Thr Lys
                 85                  90                  95

atg tcc gca gat ggt ggc gaa gcc cca ctg acc gtc aac cgc gaa gac   336
Met Ser Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn Arg Glu Asp
            100                 105                 110

gtg gca gat gct gtt tat gat gca gtg gtg aac aag aag gac atc atc   384
Val Ala Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys Asp Ile Ile
        115                 120                 125

ttt gtc cac cca ctg ttc cag tac gtc tct ttt gcg ttc caa ttc att   432
Phe Val His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe Gln Phe Ile
    130                 135                 140

ccg cga gca atc ttc cgc aag ctg ccg ttc taacggaagt tacggaagtt     482
Pro Arg Ala Ile Phe Arg Lys Leu Pro Phe
145                 150

acg                                                               485
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<210> 144
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 144

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Asp Asn Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val Glu Ala Thr
 1               5                  10                  15

Thr Val Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu Leu Gly Gln
            20                  25                  30

Lys Phe Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu Ser Ser Val
        35                  40                  45

Ala Gly Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly Ser Ala Lys
    50                  55                  60

Ala Gly Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala Leu Arg Gly
65                  70                  75                      80

Ser Gly Ala Asn Val Leu Val Val Arg Pro Gly Gln Val Arg Thr Lys
                85                  90                  95

Met Ser Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn Arg Glu Asp
            100                 105                 110

Val Ala Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys Asp Ile Ile
        115                 120                 125

Phe Val His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe Gln Phe Ile
    130                 135                 140

Pro Arg Ala Ile Phe Arg Lys Leu Pro Phe
145                 150


<210> 145
<211> 259
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(259)
<223> FRXA00421

<400> 145
gctggttgaa gactcgaaat gagatcgacc caaccggagt ctttgcatct gacatgtccc 60

gccgacttga gctttcttaa gaaagggctt gaactaaaca atg ctt aac gca gtg   115
                                          Met Leu Asn Ala Val
                                           1               5

ggc aaa gcc caa aac att ctc ctt ctt ggt gga acc tct gag atc ggt   163
Gly Lys Ala Gln Asn Ile Leu Leu Leu Gly Gly Thr Ser Glu Ile Gly
                10                  15                  20

att tcc att gtc tcc cgc ttc ctc aag cag ggt cca tcc cat gtg acc   211
Ile Ser Ile Val Ser Arg Phe Leu Lys Gln Gly Pro Ser His Val Thr
            25                  30                  35

ttg gca gcg cgt aaa gat tcc cca cgc gtg gac gca gca gtc gca gag   259
Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp Ala Ala Val Ala Glu
        40                  45                  50
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<210> 146
<211> 53
<212> PRT
<213> Corynebacterium glutamicum

<400> 146
Met Leu Asn Ala Val Gly Lys Ala Gln Asn Ile Leu Leu Leu Gly Gly
1   5   10   15

Thr Ser Glu Ile Gly Ile Ser Ile Val Ser Arg Phe Leu Lys Gln Gly
            20   25   30

Pro Ser His Val Thr Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp
        35   40   45

Ala Ala Val Ala Glu
    50

<210> 147
<211> 861
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(838)
<223> RXN02923

<400> 147
gcatctacat tgaaggaatc cacggagcgc gcatcgaaga catcgttgtg gtgaatgaag 60

acggttgtga aaccctcaac aaccagccca aggaactgcg ttg agc att ctt ctc 115
                                          Leu Ser Ile Leu Leu
                                          1   5

cta ggc gga acc tct gac att gcc ggt gag att gcc acg ttg acg tgt 163
Leu Gly Gly Thr Ser Asp Ile Ala Gly Glu Ile Ala Thr Leu Thr Cys
                10   15   20

cac ggc gaa gac gtt gtt ttg gct gct cgt cga cca gag gct gca cag 211
His Gly Glu Asp Val Val Leu Ala Ala Arg Arg Pro Glu Ala Ala Gln
            25   30   35

ggc tta gcg gaa gat ctt cga cag cgc ggt gcc aca tct gtt cat gtt 259
Gly Leu Ala Glu Asp Leu Arg Gln Arg Gly Ala Thr Ser Val His Val
        40   45   50

ttg agc ttt gac gcc caa gta cta gac acg cac cga gaa ctt gtg aag 307
Leu Ser Phe Asp Ala Gln Val Leu Asp Thr His Arg Glu Leu Val Lys
    55   60   65

aaa aca caa gag cta gct ggc gag att tcc ctt gcc gtg gtt gct ttt 355
Lys Thr Gln Glu Leu Ala Gly Glu Ile Ser Leu Ala Val Val Ala Phe
70   75   80   85

ggc atc ttg gga gac caa gaa cgc gca gaa acc gat gag acc cat gcg 403
Gly Ile Leu Gly Asp Gln Glu Arg Ala Glu Thr Asp Glu Thr His Ala
                90   95   100

gta gag atc gcc acc gtg gat tac acc gct cag gtc tcc atg ctc act 451

Val Glu Ile Ala Thr Val Asp Tyr Thr Ala Gln Val Ser Met Leu Thr
105 110 115

gtg ctt gct gat gag ctc cgc gca caa act act cca gca gcg atc gtg 499
Val Leu Ala Asp Glu Leu Arg Ala Gln Thr Thr Pro Ala Ala Ile Val
120 125 130

gcg ttt tcc tcg att gct ggg tgg cgg gcg cgc cgg cct aac tat gtc 547
Ala Phe Ser Ser Ile Ala Gly Trp Arg Ala Arg Arg Pro Asn Tyr Val
135 140 145

tat gga tcc acc aag gct ggt ctc gat gca ttt tgc caa ggg ctt gca 595
Tyr Gly Ser Thr Lys Ala Gly Leu Asp Ala Phe Cys Gln Gly Leu Ala
150 155 160 165

gat agc ctg cat ggg aca cac gtg cga ttg att att gcg cgt cct ggc 643
Asp Ser Leu His Gly Thr His Val Arg Leu Ile Ile Ala Arg Pro Gly
170 175 180

ttt gtt att ggt tct atg acc acg ggg atg aag cct gct ccg atg tcg 691
Phe Val Ile Gly Ser Met Thr Thr Gly Met Lys Pro Ala Pro Met Ser
185 190 195

gtg tat cca cga gat gtt gcc gca gct gtt gtt agt gct tat acc tct 739
Val Tyr Pro Arg Asp Val Ala Ala Ala Val Val Ser Ala Tyr Thr Ser
200 205 210

aag aag agg agc acg acc ttg tgg att ccg gga cgt ctg cgg gtt ctc 787
Lys Lys Arg Ser Thr Thr Leu Trp Ile Pro Gly Arg Leu Arg Val Leu
215 220 225

gcc tgg att atg cgg atg gtt cct cgt ccg gtg tgg cgg aag atg cca 835
Ala Trp Ile Met Arg Met Val Pro Arg Pro Val Trp Arg Lys Met Pro
230 235 240 245

cgc tagataccg ttcagccctc aca 861
Arg

<210> 148
<211> 246
<212> PRT
<213> Corynebacterium glutamicum

<400> 148
Leu Ser Ile Leu Leu Leu Gly Gly Thr Ser Asp Ile Ala Gly Glu Ile
1 5 10 15

Ala Thr Leu Thr Cys His Gly Glu Asp Val Val Leu Ala Ala Arg Arg
20 25 30

Pro Glu Ala Ala Gln Gly Leu Ala Glu Asp Leu Arg Gln Arg Gly Ala
35 40 45

Thr Ser Val His Val Leu Ser Phe Asp Ala Gln Val Leu Asp Thr His
50 55 60

Arg Glu Leu Val Lys Lys Thr Gln Glu Leu Ala Gly Glu Ile Ser Leu
65 70 75 80

```
Ala Val Val Ala Phe Gly Ile Leu Gly Asp Gln Glu Arg Ala Glu Thr
                85                  90                  95

Asp Glu Thr His Ala Val Glu Ile Ala Thr Val Asp Tyr Thr Ala Gln
            100                 105                 110

Val Ser Met Leu Thr Val Leu Ala Asp Glu Leu Arg Ala Gln Thr Thr
        115                 120                 125

Pro Ala Ala Ile Val Ala Phe Ser Ser Ile Ala Gly Trp Arg Ala Arg
    130                 135                 140

Arg Pro Asn Tyr Val Tyr Gly Ser Thr Lys Ala Gly Leu Asp Ala Phe
145                 150                 155                 160

Cys Gln Gly Leu Ala Asp Ser Leu His Gly Thr His Val Arg Leu Ile
                165                 170                 175

Ile Ala Arg Pro Gly Phe Val Ile Gly Ser Met Thr Thr Gly Met Lys
            180                 185                 190

Pro Ala Pro Met Ser Val Tyr Pro Arg Asp Val Ala Ala Ala Val Val
        195                 200                 205

Ser Ala Tyr Thr Ser Lys Lys Arg Ser Thr Thr Leu Trp Ile Pro Gly
    210                 215                 220

Arg Leu Arg Val Leu Ala Trp Ile Met Arg Met Val Pro Arg Pro Val
225                 230                 235                 240

Trp Arg Lys Met Pro Arg
                245


<210> 149
<211> 1203
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1180)
<223> RXN02922

<400> 149
cccaccgcgg cgcaagctac cgcctaggcg ctcggaactc caccgccact attgatctca 60

gttccatatc cgcccaacta gtttcccagg gagcccactc atg atc tca ccg caa    115
                                            Met Ile Ser Pro Gln
                                            1               5

aca atc atc gac aat ctt gct cca gtc ctc gcg gag atc gca gca acg    163
Thr Ile Ile Asp Asn Leu Ala Pro Val Leu Ala Glu Ile Ala Ala Thr
                10                  15                  20

gct gcg cag cgc gaa cag gat cga gaa ttc agc cgt gat ttg gca aag    211
Ala Ala Gln Arg Glu Gln Asp Arg Glu Phe Ser Arg Asp Leu Ala Lys
            25                  30                  35

cag ctt agt gcc ggt ggg ttc act aaa ctc cgc att cca gtt gaa ttt    259
Gln Leu Ser Ala Gly Gly Phe Thr Lys Leu Arg Ile Pro Val Glu Phe
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        40                  45                  50

ggc ggt ttg ggt ttt agc ctt cca gaa gca ttt gag gtg ctg gtg gca    307
Gly Gly Leu Gly Phe Ser Leu Pro Glu Ala Phe Glu Val Leu Val Ala
     55                  60                  65

gcg gcc gct gca gat tca aat atc gcg cag gga ttg cgg cct cac ttc    355
Ala Ala Ala Ala Asp Ser Asn Ile Ala Gln Gly Leu Arg Pro His Phe
 70                  75                  80                  85

ttg gca gtg gag agc tta ttg atc gct cct tat tca gag cac cgc acc    403
Leu Ala Val Glu Ser Leu Leu Ile Ala Pro Tyr Ser Glu His Arg Thr
                 90                  95                 100

aag tgg ctg cga aaa atc gct gag aaa ggc gtg gtc att ggc aat gcg    451
Lys Trp Leu Arg Lys Ile Ala Glu Lys Gly Val Val Ile Gly Asn Ala
            105                 110                 115

ttg act gaa gtg gga aac aag cca ggt gag ctg aaa acc aag atc cga    499
Leu Thr Glu Val Gly Asn Lys Pro Gly Glu Leu Lys Thr Lys Ile Arg
            120                 125                 130

aag gaa ggc gag tct tac gtt ctc agc gac acc aag ttc tat tcc acg    547
Lys Glu Gly Glu Ser Tyr Val Leu Ser Asp Thr Lys Phe Tyr Ser Thr
    135                 140                 145

ggc agt ctt tac gcc gac tgg att caa gta cat gcg aaa gat gag gaa    595
Gly Ser Leu Tyr Ala Asp Trp Ile Gln Val His Ala Lys Asp Glu Glu
150                 155                 160                 165

gat caa gat gtt ttc gcc ttt gtt gat cgc gac gca tca ggc gtt gtt    643
Asp Gln Asp Val Phe Ala Phe Val Asp Arg Asp Ala Ser Gly Val Val
                170                 175                 180

ttg gtg gat tac tgg gac gaa ttt ggg caa caa cta ttt gcc tcc gga    691
Leu Val Asp Tyr Trp Asp Glu Phe Gly Gln Gln Leu Phe Ala Ser Gly
            185                 190                 195

acc agc ttc ttt gaa aaa gtc gtg gta gat cca ctg gac att gtc acc    739
Thr Ser Phe Phe Glu Lys Val Val Val Asp Pro Leu Asp Ile Val Thr
        200                 205                 210

cgt gat tac acc gca ccc agc gct ttc cag gcg ctg gcg cag tca cat    787
Arg Asp Tyr Thr Ala Pro Ser Ala Phe Gln Ala Leu Ala Gln Ser His
    215                 220                 225

cat ttg tct acg ttg act ggt att tcg cag gca atc acc cgt gac att    835
His Leu Ser Thr Leu Thr Gly Ile Ser Gln Ala Ile Thr Arg Asp Ile
230                 235                 240                 245

gtt acc tat gta caa aac cgc acc cgt att ttc agc cac gga agt ggt    883
Val Thr Tyr Val Gln Asn Arg Thr Arg Ile Phe Ser His Gly Ser Gly
                250                 255                 260

gac ctt cca cgc ttt gat ccg cag gtg caa cag gtg gtg ggt gag gtg    931
Asp Leu Pro Arg Phe Asp Pro Gln Val Gln Gln Val Val Gly Glu Val
            265                 270                 275

aaa gcc aag tcg tat gca gtc gag aaa atc ttt cag ggt ttc gca caa    979
Lys Ala Lys Ser Tyr Ala Val Glu Lys Ile Phe Gln Gly Phe Ala Gln
        280                 285                 290
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gaa ctg gat ctt gtc gtc gat aag gca aaa gcc ggc act gct acg gag    1027
Glu Leu Asp Leu Val Val Asp Lys Ala Lys Ala Gly Thr Ala Thr Glu
    295                 300                 305

gtc gat ctg gcc gct gtc gac ctg agc gcc tac caa gcc cag tta gcg    1075
Val Asp Leu Ala Ala Val Asp Leu Ser Ala Tyr Gln Ala Gln Leu Ala
310                 315                 320                 325

gtg gca cct ttg gtg ctg agc cag gcc acc cag gcc ttt gag gtt ggc    1123
Val Ala Pro Leu Val Leu Ser Gln Ala Thr Gln Ala Phe Glu Val Gly
                330                 335                 340

gca gat gcc tta aac ggc ggc cac gtg gct gcc caa tac acg atc gga    1171
Ala Asp Ala Leu Asn Gly Gly His Val Ala Ala Gln Tyr Thr Ile Gly
            345                 350                 355

tcc ttg tca tgagccaaga aattttgagc cat                              1203
Ser Leu Ser
        360


<210> 150
<211> 360
<212> PRT
<213> Corynebacterium glutamicum

<400> 150
Met Ile Ser Pro Gln Thr Ile Ile Asp Asn Leu Ala Pro Val Leu Ala
  1               5                  10                  15

Glu Ile Ala Ala Thr Ala Ala Gln Arg Glu Gln Asp Arg Glu Phe Ser
             20                  25                  30

Arg Asp Leu Ala Lys Gln Leu Ser Ala Gly Gly Phe Thr Lys Leu Arg
         35                  40                  45

Ile Pro Val Glu Phe Gly Gly Leu Gly Phe Ser Leu Pro Glu Ala Phe
     50                  55                  60

Glu Val Leu Val Ala Ala Ala Ala Ala Asp Ser Asn Ile Ala Gln Gly
 65                  70                  75                  80

Leu Arg Pro His Phe Leu Ala Val Glu Ser Leu Leu Ile Ala Pro Tyr
                 85                  90                  95

Ser Glu His Arg Thr Lys Trp Leu Arg Lys Ile Ala Glu Lys Gly Val
            100                 105                 110

Val Ile Gly Asn Ala Leu Thr Glu Val Gly Asn Lys Pro Gly Glu Leu
        115                 120                 125

Lys Thr Lys Ile Arg Lys Glu Gly Glu Ser Tyr Val Leu Ser Asp Thr
    130                 135                 140

Lys Phe Tyr Ser Thr Gly Ser Leu Tyr Ala Asp Trp Ile Gln Val His
145                 150                 155                 160

Ala Lys Asp Glu Glu Asp Gln Asp Val Phe Ala Phe Val Asp Arg Asp
                165                 170                 175
```

```
Ala Ser Gly Val Val Leu Val Asp Tyr Trp Asp Glu Phe Gly Gln Gln
            180                 185                 190

Leu Phe Ala Ser Gly Thr Ser Phe Phe Glu Lys Val Val Val Asp Pro
        195                 200                 205

Leu Asp Ile Val Thr Arg Asp Tyr Thr Ala Pro Ser Ala Phe Gln Ala
    210                 215                 220

Leu Ala Gln Ser His His Leu Ser Thr Leu Thr Gly Ile Ser Gln Ala
225                 230                 235                 240

Ile Thr Arg Asp Ile Val Thr Tyr Val Gln Asn Arg Thr Arg Ile Phe
                245                 250                 255

Ser His Gly Ser Gly Asp Leu Pro Arg Phe Asp Pro Gln Val Gln Gln
            260                 265                 270

Val Val Gly Glu Val Lys Ala Lys Ser Tyr Ala Val Glu Lys Ile Phe
        275                 280                 285

Gln Gly Phe Ala Gln Glu Leu Asp Leu Val Val Asp Lys Ala Lys Ala
    290                 295                 300

Gly Thr Ala Thr Glu Val Asp Leu Ala Ala Val Asp Leu Ser Ala Tyr
305                 310                 315                 320

Gln Ala Gln Leu Ala Val Ala Pro Leu Val Leu Ser Gln Ala Thr Gln
                325                 330                 335

Ala Phe Glu Val Gly Ala Asp Ala Leu Asn Gly Gly His Val Ala Ala
            340                 345                 350

Gln Tyr Thr Ile Gly Ser Leu Ser
        355                 360


<210> 151
<211> 516
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(493)
<223> RXN03065

<400> 151
gacggcgcca actctgcatt cttcgcctca gcgtgcgtgg cagtgtttgc actgatcgtg 60

ggcttctttg taaagaggcc agcccgctaa gctaggtcgc atg atc agc att gga    115
                                            Met Ile Ser Ile Gly
                                             1               5

acc gac ctc gtt cac att tcg gcg ttc gca gag cag ctt gca cag ccg    163
Thr Asp Leu Val His Ile Ser Ala Phe Ala Glu Gln Leu Ala Gln Pro
                10                  15                  20

gga agt tcc ttc atg gag gtg ttt tcc gca ggg gag cgt cgt aaa gca    211
Gly Ser Ser Phe Met Glu Val Phe Ser Ala Gly Glu Arg Arg Lys Ala
            25                  30                  35
```

```
aat gaa cgc cag gca agc cgc tac gcc gag cat ttg gcg ggg cgg tgg    259
Asn Glu Arg Gln Ala Ser Arg Tyr Ala Glu His Leu Ala Gly Arg Trp
         40                  45                  50

gcg gca aaa gaa tcc ttt att aag gcc tgg tca cag gcc att tat ggc    307
Ala Ala Lys Glu Ser Phe Ile Lys Ala Trp Ser Gln Ala Ile Tyr Gly
     55                  60                  65

cag cca ccc gtg atc gcc gaa gaa gcc gtg gtg tgg cgg gac atc gaa    355
Gln Pro Pro Val Ile Ala Glu Glu Ala Val Val Trp Arg Asp Ile Glu
 70                  75                  80                  85

gtt cgc gca gac gcg tgg ggg cgc gtc gcg atc gaa ttg gcg ccc gaa    403
Val Arg Ala Asp Ala Trp Gly Arg Val Ala Ile Glu Leu Ala Pro Glu
                 90                  95                 100

ttg gcc gca gtg gtc cgg gaa tcc atc ggg gag ttt tcc agc agc ttg    451
Leu Ala Ala Val Val Arg Glu Ser Ile Gly Glu Phe Ser Ser Ser Leu
            105                 110                 115

agc atc agc cac gac ggc gac tac gcg gtg gaa cgt gcg tgt            493
Ser Ile Ser His Asp Gly Asp Tyr Ala Val Glu Arg Ala Cys
        120                 125                 130

tgactatcca gtagccacgg aga                                          516


<210> 152
<211> 131
<212> PRT
<213> Corynebacterium glutamicum

<400> 152
Met Ile Ser Ile Gly Thr Asp Leu Val His Ile Ser Ala Phe Ala Glu
  1               5                  10                  15

Gln Leu Ala Gln Pro Gly Ser Ser Phe Met Glu Val Phe Ser Ala Gly
             20                  25                  30

Glu Arg Arg Lys Ala Asn Glu Arg Gln Ala Ser Arg Tyr Ala Glu His
         35                  40                  45

Leu Ala Gly Arg Trp Ala Ala Lys Glu Ser Phe Ile Lys Ala Trp Ser
     50                  55                  60

Gln Ala Ile Tyr Gly Gln Pro Pro Val Ile Ala Glu Glu Ala Val Val
 65                  70                  75                  80

Trp Arg Asp Ile Glu Val Arg Ala Asp Ala Trp Gly Arg Val Ala Ile
                 85                  90                  95

Glu Leu Ala Pro Glu Leu Ala Ala Val Val Arg Glu Ser Ile Gly Glu
            100                 105                 110

Phe Ser Ser Ser Leu Ser Ile Ser His Asp Gly Asp Tyr Ala Val Glu
        115                 120                 125

Arg Ala Cys
    130
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<210> 153
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> RXN03132

<400> 153
taacttattt atacataaaa acacaataaa aaccgcacac gcggcgaaac ttcaataaat 60

ccctagactg caaaaaatgg ttaggctaac cttatttcca atg aat gtg aat caa   115
                                           Met Asn Val Asn Gln
                                            1               5

cag ttg gga gcc cgc acc gcc atg aac cac cct gag acc gca acc gtc   163
Gln Leu Gly Ala Arg Thr Ala Met Asn His Pro Glu Thr Ala Thr Val
                10                  15                  20

ctt cgc tcc atc tct gac atg gtt agc acc gaa acc aat ccg cgc cgt   211
Leu Arg Ser Ile Ser Asp Met Val Ser Thr Glu Thr Asn Pro Arg Arg
            25                  30                  35

aaa agc cgc ctc gag cag ctc att tac gcc acc gcc agc gcc tgg ccc   259
Lys Ser Arg Leu Glu Gln Leu Ile Tyr Ala Thr Ala Ser Ala Trp Pro
        40                  45                  50

cac tac ccc att gcc cac gca gcc cag gcc gcg gtg caa tta gcc agg   307
His Tyr Pro Ile Ala His Ala Ala Gln Ala Ala Val Gln Leu Ala Arg
    55                  60                  65

cca atg cgg gtt ttt gag ctc cag agc ttt gaa ggc gtc aag cac gca   355
Pro Met Arg Val Phe Glu Leu Gln Ser Phe Glu Gly Val Lys His Ala
70                  75                  80                  85

ctc cac cac atc gat ctt cgc ccc gcc ctc gaa tgg gac atc atg gga   403
Leu His His Ile Asp Leu Arg Pro Ala Leu Glu Trp Asp Ile Met Gly
                90                  95                  100

ttt ccc gaa tcc ccc gac acg ctg ccc att ttg ctc agt gac ctg cgc   451
Phe Pro Glu Ser Pro Asp Thr Leu Pro Ile Leu Leu Ser Asp Leu Arg
            105                 110                 115

gac ccc cct tac gcc acc act gct gtg cca cct caa tcc acg cca cgc   499
Asp Pro Pro Tyr Ala Thr Thr Ala Val Pro Pro Gln Ser Thr Pro Arg
        120                 125                 130

tcc gct cac cga tcc aca cat tgacgcttcc aggcgccacc gcg             543
Ser Ala His Arg Ser Thr His
    135                 140


<210> 154
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 154
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Met Asn Val Asn Gln Gln Leu Gly Ala Arg Thr Ala Met Asn His Pro
1 5 10 15

Glu Thr Ala Thr Val Leu Arg Ser Ile Ser Asp Met Val Ser Thr Glu
20 25 30

Thr Asn Pro Arg Arg Lys Ser Arg Leu Glu Gln Leu Ile Tyr Ala Thr
35 40 45

Ala Ser Ala Trp Pro His Tyr Pro Ile Ala His Ala Ala Gln Ala Ala
50 55 60

Val Gln Leu Ala Arg Pro Met Arg Val Phe Glu Leu Gln Ser Phe Glu
65 70 75 80

Gly Val Lys His Ala Leu His His Ile Asp Leu Arg Pro Ala Leu Glu
85 90 95

Trp Asp Ile Met Gly Phe Pro Glu Ser Pro Asp Thr Leu Pro Ile Leu
100 105 110

Leu Ser Asp Leu Arg Asp Pro Pro Tyr Ala Thr Thr Ala Val Pro Pro
115 120 125

Gln Ser Thr Pro Arg Ser Ala His Arg Ser Thr His
130 135 140

<210> 155
<211> 461
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(438)
<223> RXN03157

<400> 155
ggc cac ctc gac atc gtg acc cgc gcc gcc gcg caa ttt agc gaa gtc 48
Gly His Leu Asp Ile Val Thr Arg Ala Ala Ala Gln Phe Ser Glu Val
1 5 10 15

acc atc ttg gtc acc gcc aac ccc aac aaa aac tca gga ctg ttc acc 96
Thr Ile Leu Val Thr Ala Asn Pro Asn Lys Asn Ser Gly Leu Phe Thr
20 25 30

gtc gca gaa cgc atg gat ctc atc cgc gaa tcc acc gca cac ctg gac 144
Val Ala Glu Arg Met Asp Leu Ile Arg Glu Ser Thr Ala His Leu Asp
35 40 45

aac gta aaa gta gac act tgg gcc tca ctg ctc gtg gat tac acc acc 192
Asn Val Lys Val Asp Thr Trp Ala Ser Leu Leu Val Asp Tyr Thr Thr
50 55 60

gaa cat ggc atc ggc gcc cta gtc aaa ggc ctg cga agc tcc ctc gac 240
Glu His Gly Ile Gly Ala Leu Val Lys Gly Leu Arg Ser Ser Leu Asp
65 70 75 80

tac gaa tac gag ctc ccc atg gca cag atg aac agg cga ctc acg ggc 288
Tyr Glu Tyr Glu Leu Pro Met Ala Gln Met Asn Arg Arg Leu Thr Gly

85 90 95

gta gac acc ttc ttc ctc ctc acc gac gag aaa tac ggc tac gtc agc 336
Val Asp Thr Phe Phe Leu Leu Thr Asp Glu Lys Tyr Gly Tyr Val Ser
100 105 110

tcc aca ctg tgc aaa gaa gtt gcc cgc ttc ggt ggc gat gtc tcc ggc 384
Ser Thr Leu Cys Lys Glu Val Ala Arg Phe Gly Gly Asp Val Ser Gly
115 120 125

ctc cta cct gag gta gtg gca aaa gcc gtg aca gaa aaa tac agc aac 432
Leu Leu Pro Glu Val Val Ala Lys Ala Val Thr Glu Lys Tyr Ser Asn
130 135 140

cag cac tagtttcttt tgcatcaagc gtc 461
Gln His
145

<210> 156
<211> 146
<212> PRT
<213> Corynebacterium glutamicum

<400> 156
Gly His Leu Asp Ile Val Thr Arg Ala Ala Ala Gln Phe Ser Glu Val
1 5 10 15

Thr Ile Leu Val Thr Ala Asn Pro Asn Lys Asn Ser Gly Leu Phe Thr
20 25 30

Val Ala Glu Arg Met Asp Leu Ile Arg Glu Ser Thr Ala His Leu Asp
35 40 45

Asn Val Lys Val Asp Thr Trp Ala Ser Leu Leu Val Asp Tyr Thr Thr
50 55 60

Glu His Gly Ile Gly Ala Leu Val Lys Gly Leu Arg Ser Ser Leu Asp
65 70 75 80

Tyr Glu Tyr Glu Leu Pro Met Ala Gln Met Asn Arg Arg Leu Thr Gly
85 90 95

Val Asp Thr Phe Phe Leu Leu Thr Asp Glu Lys Tyr Gly Tyr Val Ser
100 105 110

Ser Thr Leu Cys Lys Glu Val Ala Arg Phe Gly Gly Asp Val Ser Gly
115 120 125

Leu Leu Pro Glu Val Val Ala Lys Ala Val Thr Glu Lys Tyr Ser Asn
130 135 140

Gln His
145

<210> 157
<211> 1206
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1183)
<223> RXN00934

<400> 157
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aaatgttcac aaaccggtgg cattacagga ggacaattag gtg cga att gga atg 115
Val Arg Ile Gly Met
1 5

gtc tgc ccg tac tcc ttc gat gag ccg ggc ggt gtt caa gcg cat atc 163
Val Cys Pro Tyr Ser Phe Asp Glu Pro Gly Gly Val Gln Ala His Ile
10 15 20

ctt gac tta gcg cga acc ttc att gcc caa ggc cat gag gtt cag gtg 211
Leu Asp Leu Ala Arg Thr Phe Ile Ala Gln Gly His Glu Val Gln Val
25 30 35

ctt ggt ccg tgt agt gcg gat acg cag gtg ccc gat ttc gtg gtg cgc 259
Leu Gly Pro Cys Ser Ala Asp Thr Gln Val Pro Asp Phe Val Val Arg
40 45 50

ggt ggt ggc agc atc ccg att ccg tac aat ggc tcg gtt gcc cgc ttg 307
Gly Gly Gly Ser Ile Pro Ile Pro Tyr Asn Gly Ser Val Ala Arg Leu
55 60 65

agc ttt ggg ccg aaa atg ttc aag gcc gtg cgc acg ttc ctc cgc gaa 355
Ser Phe Gly Pro Lys Met Phe Lys Ala Val Arg Thr Phe Leu Arg Glu
70 75 80 85

ggc aac ttc gat gtg ctg cat atc cat gaa ccg aat tca cca agt ttt 403
Gly Asn Phe Asp Val Leu His Ile His Glu Pro Asn Ser Pro Ser Phe
90 95 100

tcc atg gcg gcg cta cgc ttt gcg gaa ggc ccc atc gtt gct act tac 451
Ser Met Ala Ala Leu Arg Phe Ala Glu Gly Pro Ile Val Ala Thr Tyr
105 110 115

cac gcc tcc agt agc gga tcg aag ctg ctc aag gct ttc tta cca gtg 499
His Ala Ser Ser Ser Gly Ser Lys Leu Leu Lys Ala Phe Leu Pro Val
120 125 130

ctt tcg ccc atg ctg gag aaa gtg cgc gca ggc atc gcc gtg tct gaa 547
Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly Ile Ala Val Ser Glu
135 140 145

atg gct cgg cgc tgg cag gtg gag caa gtc ggc ggc gat ccc gtg ctg 595
Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly Gly Asp Pro Val Leu
150 155 160 165

atc ccc aac ggg gta gag acc tcc atg ttc aaa gcc gcg cgc caa atc 643
Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys Ala Ala Arg Gln Ile
170 175 180

gaa ccg aat gat cct gta gag atc gtc ttt ttg ggt cgc ctc gat gag 691
Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu Gly Arg Leu Asp Glu
185 190 195

tcc cgc aaa ggc ctc gac atc ctc ctg cgc gct ctg acc agg ctg gat 739

Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala Leu Thr Arg Leu Asp
        200   205   210

cgc ccg ttt acc tgc acc gtc att ggc ggc ggc acc ccg cga gaa gtc   787
Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly Thr Pro Arg Glu Val
    215   220   225

gcc ggc atc aac ttt gtg ggc cgc gtc agc gat gag gaa aag gca gca   835
Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp Glu Glu Lys Ala Ala
230   235   240   245

atc tta ggt cgc gca gac atc tat gtc gca ccc aac acc ggc ggc gaa   883
Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro Asn Thr Gly Gly Glu
                250   255   260

agc ttc ggc atc gtg cta gtt gaa gcg atg gcc gcg gga tgc gct gtc   931
Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala Ala Gly Cys Ala Val
            265   270   275

gtc gcc agc gac cta gaa gcg ttc tcc ctg gtc acc gat tct gaa gcc   979
Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val Thr Asp Ser Glu Ala
        280   285   290

gca cag cca gcg ggc gtg cta ttt aaa acc ggc tca gac gcc gac cta   1027
Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly Ser Asp Ala Asp Leu
    295   300   305

gcc aaa aaa ctt caa gcg ctt atc gac gac ccc tcc tcc cgt tcc acg   1075
Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro Ser Ser Arg Ser Thr
310   315   320   325

ctt atc gcc gcg ggg cta aag cgc gca aac gcc tac gac tgg tcg aca   1123
Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala Tyr Asp Trp Ser Thr
                330   335   340

gta tcc acc cag gtc atg gca gtc tat gaa acc att gcg atc gac aaa   1171
Val Ser Thr Gln Val Met Ala Val Tyr Glu Thr Ile Ala Ile Asp Lys
            345   350   355

gtg agg ctt gga tgacccttgt ttacctcctc atc   1206
Val Arg Leu Gly
        360

<210> 158
<211> 361
<212> PRT
<213> Corynebacterium glutamicum

<400> 158
Val Arg Ile Gly Met Val Cys Pro Tyr Ser Phe Asp Glu Pro Gly Gly
1   5   10   15

Val Gln Ala His Ile Leu Asp Leu Ala Arg Thr Phe Ile Ala Gln Gly
            20   25   30

His Glu Val Gln Val Leu Gly Pro Cys Ser Ala Asp Thr Gln Val Pro
        35   40   45

Asp Phe Val Val Arg Gly Gly Gly Ser Ile Pro Ile Pro Tyr Asn Gly
    50   55   60

Ser Val Ala Arg Leu Ser Phe Gly Pro Lys Met Phe Lys Ala Val Arg
65 70 75 80

Thr Phe Leu Arg Glu Gly Asn Phe Asp Val Leu His Ile His Glu Pro
85 90 95

Asn Ser Pro Ser Phe Ser Met Ala Ala Leu Arg Phe Ala Glu Gly Pro
100 105 110

Ile Val Ala Thr Tyr His Ala Ser Ser Ser Gly Ser Lys Leu Leu Lys
115 120 125

Ala Phe Leu Pro Val Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly
130 135 140

Ile Ala Val Ser Glu Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly
145 150 155 160

Gly Asp Pro Val Leu Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys
165 170 175

Ala Ala Arg Gln Ile Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu
180 185 190

Gly Arg Leu Asp Glu Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala
195 200 205

Leu Thr Arg Leu Asp Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly
210 215 220

Thr Pro Arg Glu Val Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp
225 230 235 240

Glu Glu Lys Ala Ala Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro
245 250 255

Asn Thr Gly Gly Glu Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala
260 265 270

Ala Gly Cys Ala Val Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val
275 280 285

Thr Asp Ser Glu Ala Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly
290 295 300

Ser Asp Ala Asp Leu Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro
305 310 315 320

Ser Ser Arg Ser Thr Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala
325 330 335

Tyr Asp Trp Ser Thr Val Ser Thr Gln Val Met Ala Val Tyr Glu Thr
340 345 350

Ile Ala Ile Asp Lys Val Arg Leu Gly
355 360

<210> 159
<211> 1320

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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1297)
<223> RXN00792

<400> 159
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gcggccacgt ggctgcccaa tacacgatcg gatccttgtc atg agc caa gaa att   115
                                            Met Ser Gln Glu Ile
                                            1               5

ttg agc cat ttt gca ccc gca tta gag cgc att cga agc ggc gcc gtc   163
Leu Ser His Phe Ala Pro Ala Leu Glu Arg Ile Arg Ser Gly Ala Val
                10                  15                  20

gag cgc gaa cag cag cgc gcc ttg cca gtg gaa gag att aaa gag ctg   211
Glu Arg Glu Gln Gln Arg Ala Leu Pro Val Glu Glu Ile Lys Glu Leu
            25                  30                  35

gta gag cta ggt ttt act ggg ctt cga gtg ccc gaa gaa cta ggc ggt   259
Val Glu Leu Gly Phe Thr Gly Leu Arg Val Pro Glu Glu Leu Gly Gly
        40                  45                  50

gcg ggc gct tcc ctg gaa agc gta gtt gag tta ctg atc gag atc gcg   307
Ala Gly Ala Ser Leu Glu Ser Val Val Glu Leu Leu Ile Glu Ile Ala
    55                  60                  65

ggc gcc gat tcc aat atc gcc caa gcc ctg cgc gga cat ttt gcc ttc   355
Gly Ala Asp Ser Asn Ile Ala Gln Ala Leu Arg Gly His Phe Ala Phe
70                  75                  80                  85

gtg gaa cta ctc ctg gaa gcg ccg gag agc gaa ttc cgc acc cat tgg   403
Val Glu Leu Leu Leu Glu Ala Pro Glu Ser Glu Phe Arg Thr His Trp
                90                  95                  100

ctg cgc gaa gtc gcc acc gga aga ctt gtg ggc aac gcc gaa agt gag   451
Leu Arg Glu Val Ala Thr Gly Arg Leu Val Gly Asn Ala Glu Ser Glu
            105                 110                 115

aaa cgc ggc gtt tac ggc gat ccg cag acc ttc atc gat gag gtg gag   499
Lys Arg Gly Val Tyr Gly Asp Pro Gln Thr Phe Ile Asp Glu Val Glu
        120                 125                 130

act gaa aac gga ccg att ttc gtg ctc aac ggc act aag ttt tat acc   547
Thr Glu Asn Gly Pro Ile Phe Val Leu Asn Gly Thr Lys Phe Tyr Thr
    135                 140                 145

acc ggc acc tat ttt gcg gac tac acc tgg acc acc gcg ctg ctg cgc   595
Thr Gly Thr Tyr Phe Ala Asp Tyr Thr Trp Thr Thr Ala Leu Leu Arg
150                 155                 160                 165

aac ctt aac ggc caa gaa act ttg gtc agt ttg ccg gtc gat ctg cac   643
Asn Leu Asn Gly Gln Glu Thr Leu Val Ser Leu Pro Val Asp Leu His
                170                 175                 180

gcg ccg ggc gtg gat gtt gct gat gat tgg agc ggg ttt ggg caa aag   691
Ala Pro Gly Val Asp Val Ala Asp Asp Trp Ser Gly Phe Gly Gln Lys
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            185                 190                 195

ctc acc gcc tct gga acg acc acg ttt aaa gac ctg gag gtg gat ccg    739
Leu Thr Ala Ser Gly Thr Thr Thr Phe Lys Asp Leu Glu Val Asp Pro
        200                 205                 210

cgg tgg atc att cca cgc act gat gcg ccc acg ctg gtg tgg acg tat    787
Arg Trp Ile Ile Pro Arg Thr Asp Ala Pro Thr Leu Val Trp Thr Tyr
    215                 220                 225

ctg cag ctg agc ctg ctg acc gtg ctg gtt ggc agt gcc gca gca gct    835
Leu Gln Leu Ser Leu Leu Thr Val Leu Val Gly Ser Ala Ala Ala Ala
230                 235                 240                 245

gtc gat gag gtg gtt gcc cgc gcc caa tcc tcc acc aga aat gcg tgg    883
Val Asp Glu Val Val Ala Arg Ala Gln Ser Ser Thr Arg Asn Ala Trp
                250                 255                 260

aac cct ggc gtc gag cgc cgc agc gat ccg gcc gca acc ata gcg atc    931
Asn Pro Gly Val Glu Arg Arg Ser Asp Pro Ala Ala Thr Ile Ala Ile
            265                 270                 275

ggc gac gca cgc agc cga gtc acc gtt att cgt gga gcg ctt ctc gac    979
Gly Asp Ala Arg Ser Arg Val Thr Val Ile Arg Gly Ala Leu Leu Asp
        280                 285                 290

gcc acc cgc cac gtt tcc aac gcc gcc acg atc gta acc ccc gaa gcc    1027
Ala Thr Arg His Val Ser Asn Ala Ala Thr Ile Val Thr Pro Glu Ala
    295                 300                 305

ttc aac gag gcg gac gct att gtt gca gcg ctc tgg ccc atc gtc tcc    1075
Phe Asn Glu Ala Asp Ala Ile Val Ala Ala Leu Trp Pro Ile Val Ser
310                 315                 320                 325

gga caa gct ttg gtg gtg aca tcc aac gtt ttc gat gcg gtg ggt gca    1123
Gly Gln Ala Leu Val Val Thr Ser Asn Val Phe Asp Ala Val Gly Ala
                330                 335                 340

tct gca gtg ctt ggt gag cat tcc att gat cgc cac tgg cgc aat gtg    1171
Ser Ala Val Leu Gly Glu His Ser Ile Asp Arg His Trp Arg Asn Val
            345                 350                 355

cgt acc gtg tcc tca aac aac ccg gtg ttc ctg gcc aag aat gca gtg    1219
Arg Thr Val Ser Ser Asn Asn Pro Val Phe Leu Ala Lys Asn Ala Val
        360                 365                 370

ggg gag tat gcc ctc aac ggc act cct gtg ggt acc aac att ggt aaa    1267
Gly Glu Tyr Ala Leu Asn Gly Thr Pro Val Gly Thr Asn Ile Gly Lys
    375                 380                 385

gca ctg agc cgt ccg gtg agc cta agc agc tagacgtgtg atttcgctgg      1317
Ala Leu Ser Arg Pro Val Ser Leu Ser Ser
390                 395

ttt                                                                1320
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<210> 160
<211> 399
<212> PRT
<213> Corynebacterium glutamicum

<400> 160

Met Ser Gln Glu Ile Leu Ser His Phe Ala Pro Ala Leu Glu Arg Ile
1 5 10 15

Arg Ser Gly Ala Val Glu Arg Glu Gln Gln Arg Ala Leu Pro Val Glu
20 25 30

Glu Ile Lys Glu Leu Val Glu Leu Gly Phe Thr Gly Leu Arg Val Pro
35 40 45

Glu Glu Leu Gly Gly Ala Gly Ala Ser Leu Glu Ser Val Val Glu Leu
50 55 60

Leu Ile Glu Ile Ala Gly Ala Asp Ser Asn Ile Ala Gln Ala Leu Arg
65 70 75 80

Gly His Phe Ala Phe Val Glu Leu Leu Leu Glu Ala Pro Glu Ser Glu
85 90 95

Phe Arg Thr His Trp Leu Arg Glu Val Ala Thr Gly Arg Leu Val Gly
100 105 110

Asn Ala Glu Ser Glu Lys Arg Gly Val Tyr Gly Asp Pro Gln Thr Phe
115 120 125

Ile Asp Glu Val Glu Thr Glu Asn Gly Pro Ile Phe Val Leu Asn Gly
130 135 140

Thr Lys Phe Tyr Thr Thr Gly Thr Tyr Phe Ala Asp Tyr Thr Trp Thr
145 150 155 160

Thr Ala Leu Leu Arg Asn Leu Asn Gly Gln Glu Thr Leu Val Ser Leu
165 170 175

Pro Val Asp Leu His Ala Pro Gly Val Asp Val Ala Asp Asp Trp Ser
180 185 190

Gly Phe Gly Gln Lys Leu Thr Ala Ser Gly Thr Thr Thr Phe Lys Asp
195 200 205

Leu Glu Val Asp Pro Arg Trp Ile Ile Pro Arg Thr Asp Ala Pro Thr
210 215 220

Leu Val Trp Thr Tyr Leu Gln Leu Ser Leu Leu Thr Val Leu Val Gly
225 230 235 240

Ser Ala Ala Ala Ala Val Asp Glu Val Val Ala Arg Ala Gln Ser Ser
245 250 255

Thr Arg Asn Ala Trp Asn Pro Gly Val Glu Arg Arg Ser Asp Pro Ala
260 265 270

Ala Thr Ile Ala Ile Gly Asp Ala Arg Ser Arg Val Thr Val Ile Arg
275 280 285

Gly Ala Leu Leu Asp Ala Thr Arg His Val Ser Asn Ala Ala Thr Ile
290 295 300

Val Thr Pro Glu Ala Phe Asn Glu Ala Asp Ala Ile Val Ala Ala Leu
305 310 315 320

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Trp Pro Ile Val Ser Gly Gln Ala Leu Val Val Thr Ser Asn Val Phe
                325                 330                 335

Asp Ala Val Gly Ala Ser Ala Val Leu Gly Glu His Ser Ile Asp Arg
            340                 345                 350

His Trp Arg Asn Val Arg Thr Val Ser Ser Asn Asn Pro Val Phe Leu
        355                 360                 365

Ala Lys Asn Ala Val Gly Glu Tyr Ala Leu Asn Gly Thr Pro Val Gly
    370                 375                 380

Thr Asn Ile Gly Lys Ala Leu Ser Arg Pro Val Ser Leu Ser Ser
385                 390                 395


<210> 161
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> RXN00931

<400> 161
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gtaacctcac cgaagtgcat aaattaattg ggagtgatca gtg aaa act att gaa    115
                                           Val Lys Thr Ile Glu
                                           1               5

gat att ttg acc ttg gaa gaa atc gac cgc gat att tac cgt ggt ccc    163
Asp Ile Leu Thr Leu Glu Glu Ile Asp Arg Asp Ile Tyr Arg Gly Pro
                10                  15                  20

gtt atc gaa tct tat tta gcc agg act ttc ggt ggc cag gtc gct gcc    211
Val Ile Glu Ser Tyr Leu Ala Arg Thr Phe Gly Gly Gln Val Ala Ala
            25                  30                  35

caa gct tta gta gca gca acg cat act gtt gat aaa gcc ttt act gtg    259
Gln Ala Leu Val Ala Ala Thr His Thr Val Asp Lys Ala Phe Thr Val
        40                  45                  50

cat tct ttg cat ggc tac ttt ata gct cct ggt gat cca aca gca ccc    307
His Ser Leu His Gly Tyr Phe Ile Ala Pro Gly Asp Pro Thr Ala Pro
    55                  60                  65

gca att tat tta gtg gat cga gtt cgc gac gga aaa agc tac gtc acc    355
Ala Ile Tyr Leu Val Asp Arg Val Arg Asp Gly Lys Ser Tyr Val Thr
70                  75                  80                  85

cgc tcg gtg cgt ggc atc caa gac ggc gaa gta atc ttc agc atg cag    403
Arg Ser Val Arg Gly Ile Gln Asp Gly Glu Val Ile Phe Ser Met Gln
                90                  95                  100

gcc agc ttt cat cgt ggg gat gaa ggc att gag cac atg gac aag atg    451
Ala Ser Phe His Arg Gly Asp Glu Gly Ile Glu His Met Asp Lys Met
            105                 110                 115
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cgt aaa gtt cca gct cct gat gag atc aag gga aca gta gaa cgt atg    499
Arg Lys Val Pro Ala Pro Asp Glu Ile Lys Gly Thr Val Glu Arg Met
        120                 125                 130

ccg atc tca agt agg cga gtg ctt gat gaa tgg gcg gaa tgg gat atc    547
Pro Ile Ser Ser Arg Arg Val Leu Asp Glu Trp Ala Glu Trp Asp Ile
    135                 140                 145

cgc gtt att ccg cag gat caa tta gaa ctc agc gat ttc acc gct act    595
Arg Val Ile Pro Gln Asp Gln Leu Glu Leu Ser Asp Phe Thr Ala Thr
150                 155                 160                 165

gag caa gct gtg tgg att cgg tgc acc gct gat ctt ccg gat aat ccc    643
Glu Gln Ala Val Trp Ile Arg Cys Thr Ala Asp Leu Pro Asp Asn Pro
                170                 175                 180

acc ttc cac cag tgc tca ctg act tat ctg tcc gat atg act ttg ctg    691
Thr Phe His Gln Cys Ser Leu Thr Tyr Leu Ser Asp Met Thr Leu Leu
            185                 190                 195

cat agt gcc ctg gtg cca cac cca ggt gag aaa atg cag atg gcc tca    739
His Ser Ala Leu Val Pro His Pro Gly Glu Lys Met Gln Met Ala Ser
        200                 205                 210

ctt gat cac gct gtg tgg ttc ctg cgt ccc ttc cgc gtc gat gaa tgg    787
Leu Asp His Ala Val Trp Phe Leu Arg Pro Phe Arg Val Asp Glu Trp
    215                 220                 225

ttg ctt tat gat cag cgc tct cca tcg gcc tca agt ggg cga gcc ttg    835
Leu Leu Tyr Asp Gln Arg Ser Pro Ser Ala Ser Ser Gly Arg Ala Leu
230                 235                 240                 245

act cac ggg cgg ctt ttc aac cag cag gga gat ttg gtc gct att gtc    883
Thr His Gly Arg Leu Phe Asn Gln Gln Gly Asp Leu Val Ala Ile Val
                250                 255                 260

aat caa gag gga atg acc cgc aca ctc cac gag ggt gcg caa tca att    931
Asn Gln Glu Gly Met Thr Arg Thr Leu His Glu Gly Ala Gln Ser Ile
            265                 270                 275

ccg atg cgc aaa gac taaaatgcag cgaacttgaa gat                       969
Pro Met Arg Lys Asp
        280


<210> 162
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 162
Val Lys Thr Ile Glu Asp Ile Leu Thr Leu Glu Glu Ile Asp Arg Asp
  1               5                  10                  15

Ile Tyr Arg Gly Pro Val Ile Glu Ser Tyr Leu Ala Arg Thr Phe Gly
             20                  25                  30

Gly Gln Val Ala Ala Gln Ala Leu Val Ala Ala Thr His Thr Val Asp
         35                  40                  45
```

```
Lys Ala Phe Thr Val His Ser Leu His Gly Tyr Phe Ile Ala Pro Gly
    50                  55                  60

Asp Pro Thr Ala Pro Ala Ile Tyr Leu Val Asp Arg Val Arg Asp Gly
65                  70                  75                  80

Lys Ser Tyr Val Thr Arg Ser Val Arg Gly Ile Gln Asp Gly Glu Val
                85                  90                  95

Ile Phe Ser Met Gln Ala Ser Phe His Arg Gly Asp Glu Gly Ile Glu
            100                 105                 110

His Met Asp Lys Met Arg Lys Val Pro Ala Pro Asp Glu Ile Lys Gly
        115                 120                 125

Thr Val Glu Arg Met Pro Ile Ser Ser Arg Arg Val Leu Asp Glu Trp
    130                 135                 140

Ala Glu Trp Asp Ile Arg Val Ile Pro Gln Asp Gln Leu Glu Leu Ser
145                 150                 155                 160

Asp Phe Thr Ala Thr Glu Gln Ala Val Trp Ile Arg Cys Thr Ala Asp
                165                 170                 175

Leu Pro Asp Asn Pro Thr Phe His Gln Cys Ser Leu Thr Tyr Leu Ser
            180                 185                 190

Asp Met Thr Leu Leu His Ser Ala Leu Val Pro His Pro Gly Glu Lys
        195                 200                 205

Met Gln Met Ala Ser Leu Asp His Ala Val Trp Phe Leu Arg Pro Phe
    210                 215                 220

Arg Val Asp Glu Trp Leu Leu Tyr Asp Gln Arg Ser Pro Ser Ala Ser
225                 230                 235                 240

Ser Gly Arg Ala Leu Thr His Gly Arg Leu Phe Asn Gln Gln Gly Asp
                245                 250                 255

Leu Val Ala Ile Val Asn Gln Glu Gly Met Thr Arg Thr Leu His Glu
            260                 265                 270

Gly Ala Gln Ser Ile Pro Met Arg Lys Asp
        275                 280


<210> 163
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> FRXA00931

<400> 163
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gtaacctcac cgaagtgcat aaattaattg ggagtgatca gtg aaa act att gaa   115
                                           Val Lys Thr Ile Glu
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                                                    1               5

gat att ttg acc ttg gaa gaa atc gac cgc gat att tac cgt ggt ccc    163
Asp Ile Leu Thr Leu Glu Glu Ile Asp Arg Asp Ile Tyr Arg Gly Pro
                10                  15                  20

gtt atc gaa tct tat tta gcc agg act ttc ggt ggc cag gtc gct gcc    211
Val Ile Glu Ser Tyr Leu Ala Arg Thr Phe Gly Gly Gln Val Ala Ala
            25                  30                  35

caa gct tta gta gca gca acg cat act gtt gat aaa gcc ttt act gtg    259
Gln Ala Leu Val Ala Ala Thr His Thr Val Asp Lys Ala Phe Thr Val
        40                  45                  50

cat tct ttg cat ggc tac ttt ata gct cct ggt gat cca aca gca ccc    307
His Ser Leu His Gly Tyr Phe Ile Ala Pro Gly Asp Pro Thr Ala Pro
    55                  60                  65

gca att tat tta gtg gat cga gtt cgc gac gga aaa agc tac gtc acc    355
Ala Ile Tyr Leu Val Asp Arg Val Arg Asp Gly Lys Ser Tyr Val Thr
70                  75                  80                  85

cgc tcg gtg cgt ggc atc caa gac ggc gaa gta atc ttc agc atg cag    403
Arg Ser Val Arg Gly Ile Gln Asp Gly Glu Val Ile Phe Ser Met Gln
                90                  95                  100

gcc agc ttt cat cgt ggg gat gaa ggc att gag cac atg gac aag atg    451
Ala Ser Phe His Arg Gly Asp Glu Gly Ile Glu His Met Asp Lys Met
            105                 110                 115

cgt aaa gtt cca gct cct gat gag atc aag gga aca gta gaa cgt atg    499
Arg Lys Val Pro Ala Pro Asp Glu Ile Lys Gly Thr Val Glu Arg Met
        120                 125                 130

ccg atc tca agt agg cga gtg ctt gat gaa tgg gcg gaa tgg gat atc    547
Pro Ile Ser Ser Arg Arg Val Leu Asp Glu Trp Ala Glu Trp Asp Ile
    135                 140                 145

cgc gtt att ccg cag gat caa tta gaa ctc agc gat ttc acc gct act    595
Arg Val Ile Pro Gln Asp Gln Leu Glu Leu Ser Asp Phe Thr Ala Thr
150                 155                 160                 165

gag caa gct gtg tgg att cgg tgc acc gct gat ctt ccg gat aat ccc    643
Glu Gln Ala Val Trp Ile Arg Cys Thr Ala Asp Leu Pro Asp Asn Pro
                170                 175                 180

acc ttc cac cag tgc tca ctg act tat ctg tcc gat atg act ttg ctg    691
Thr Phe His Gln Cys Ser Leu Thr Tyr Leu Ser Asp Met Thr Leu Leu
            185                 190                 195

cat agt gcc ctg gtg cca cac cca ggt gag aaa atg cag atg gcc tca    739
His Ser Ala Leu Val Pro His Pro Gly Glu Lys Met Gln Met Ala Ser
        200                 205                 210

ctt gat cac gct gtg tgg ttc ctg cgt ccc ttc cgc gtc gat gaa tgg    787
Leu Asp His Ala Val Trp Phe Leu Arg Pro Phe Arg Val Asp Glu Trp
    215                 220                 225

ttg ctt tat gat cag cgc tct cca tcg gcc tca agt ggg cga gcc ttg    835
Leu Leu Tyr Asp Gln Arg Ser Pro Ser Ala Ser Ser Gly Arg Ala Leu
230                 235                 240                 245
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```
act cac ggg cgg ctt ttc aac cag cag gga gat ttg gtc gct att gtc    883
Thr His Gly Arg Leu Phe Asn Gln Gln Gly Asp Leu Val Ala Ile Val
                250                 255                 260

aat caa gag gga atg acc cgc aca ctc cac gag ggt gcg caa tca att    931
Asn Gln Glu Gly Met Thr Arg Thr Leu His Glu Gly Ala Gln Ser Ile
            265                 270                 275

ccg atg cgc aaa gac taaaatgcag cgaacttgaa gat                      969
Pro Met Arg Lys Asp
        280


<210> 164
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 164
Val Lys Thr Ile Glu Asp Ile Leu Thr Leu Glu Glu Ile Asp Arg Asp
  1               5                  10                  15

Ile Tyr Arg Gly Pro Val Ile Glu Ser Tyr Leu Ala Arg Thr Phe Gly
             20                  25                  30

Gly Gln Val Ala Ala Gln Ala Leu Val Ala Ala Thr His Thr Val Asp
         35                  40                  45

Lys Ala Phe Thr Val His Ser Leu His Gly Tyr Phe Ile Ala Pro Gly
     50                  55                  60

Asp Pro Thr Ala Pro Ala Ile Tyr Leu Val Asp Arg Val Arg Asp Gly
 65                  70                  75                  80

Lys Ser Tyr Val Thr Arg Ser Val Arg Gly Ile Gln Asp Gly Glu Val
                 85                  90                  95

Ile Phe Ser Met Gln Ala Ser Phe His Arg Gly Asp Glu Gly Ile Glu
            100                 105                 110

His Met Asp Lys Met Arg Lys Val Pro Ala Pro Asp Glu Ile Lys Gly
        115                 120                 125

Thr Val Glu Arg Met Pro Ile Ser Ser Arg Arg Val Leu Asp Glu Trp
    130                 135                 140

Ala Glu Trp Asp Ile Arg Val Ile Pro Gln Asp Gln Leu Glu Leu Ser
145                 150                 155                 160

Asp Phe Thr Ala Thr Glu Gln Ala Val Trp Ile Arg Cys Thr Ala Asp
                165                 170                 175

Leu Pro Asp Asn Pro Thr Phe His Gln Cys Ser Leu Thr Tyr Leu Ser
            180                 185                 190

Asp Met Thr Leu Leu His Ser Ala Leu Val Pro His Pro Gly Glu Lys
        195                 200                 205

Met Gln Met Ala Ser Leu Asp His Ala Val Trp Phe Leu Arg Pro Phe
    210                 215                 220
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Arg Val Asp Glu Trp Leu Leu Tyr Asp Gln Arg Ser Pro Ser Ala Ser
225                 230                 235                 240

Ser Gly Arg Ala Leu Thr His Gly Arg Leu Phe Asn Gln Gln Gly Asp
                245                 250                 255

Leu Val Ala Ile Val Asn Gln Glu Gly Met Thr Arg Thr Leu His Glu
            260                 265                 270

Gly Ala Gln Ser Ile Pro Met Arg Lys Asp
        275                 280


<210> 165
<211> 510
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(487)
<223> RXN01421

<400> 165
ttgatgcacg tgcagaaatc gtcggcggtc cgtggcaccc atctgttaag ggagactcgg 60

ttactgcagg gatcctgcga gatcgagtaa acgcctaaag atg acg tcg aaa agc   115
                                            Met Thr Ser Lys Ser
                                            1               5

att agc ggc aag cgc ccg aat ctg ccg tcg ctc act gga gcg cgg tgg   163
Ile Ser Gly Lys Arg Pro Asn Leu Pro Ser Leu Thr Gly Ala Arg Trp
                10                  15                  20

ctc gcg gcg ctc gct gtt tat ttt ttg cat gcg ttg gtg ttt ttg tcg   211
Leu Ala Ala Leu Ala Val Tyr Phe Leu His Ala Leu Val Phe Leu Ser
            25                  30                  35

gtg tat ccg ttc cag cag tcg gaa ctg ttt gcc aca atc cat aaa ttt   259
Val Tyr Pro Phe Gln Gln Ser Glu Leu Phe Ala Thr Ile His Lys Phe
        40                  45                  50

gtc ccc atg cag ctg ggt tca gct ggt gta acc ttc ttc ttt atc ttg   307
Val Pro Met Gln Leu Gly Ser Ala Gly Val Thr Phe Phe Phe Ile Leu
    55                  60                  65

tcc gga ttt ttg atc tat tgg tca aat agc cag ctc aag ggc atg aag   355
Ser Gly Phe Leu Ile Tyr Trp Ser Asn Ser Gln Leu Lys Gly Met Lys
70                  75                  80                  85

aat gtg ctg tat tac tgc aag cgc cgc atc acc aag att tat ccc atg   403
Asn Val Leu Tyr Tyr Cys Lys Arg Arg Ile Thr Lys Ile Tyr Pro Met
                90                  95                  100

cac ttg att gcg ttg ccg atg ttt att gag gcg tcg gcg aag ttc acg   451
His Leu Ile Ala Leu Pro Met Phe Ile Glu Ala Ser Ala Lys Phe Thr
            105                 110                 115

act aca ggc att acc tgg gtg ctg att ttg cgc gag taaagctgtg        497
Thr Thr Gly Ile Thr Trp Val Leu Ile Leu Arg Glu
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120 125

gctgcggaat gcg 510

<210> 166
<211> 129
<212> PRT
<213> Corynebacterium glutamicum

<400> 166
Met Thr Ser Lys Ser Ile Ser Gly Lys Arg Pro Asn Leu Pro Ser Leu
1 5 10 15

Thr Gly Ala Arg Trp Leu Ala Ala Leu Ala Val Tyr Phe Leu His Ala
20 25 30

Leu Val Phe Leu Ser Val Tyr Pro Phe Gln Gln Ser Glu Leu Phe Ala
35 40 45

Thr Ile His Lys Phe Val Pro Met Gln Leu Gly Ser Ala Gly Val Thr
50 55 60

Phe Phe Phe Ile Leu Ser Gly Phe Leu Ile Tyr Trp Ser Asn Ser Gln
65 70 75 80

Leu Lys Gly Met Lys Asn Val Leu Tyr Tyr Cys Lys Arg Arg Ile Thr
85 90 95

Lys Ile Tyr Pro Met His Leu Ile Ala Leu Pro Met Phe Ile Glu Ala
100 105 110

Ser Ala Lys Phe Thr Thr Thr Gly Ile Thr Trp Val Leu Ile Leu Arg
115 120 125

Glu

<210> 167
<211> 930
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(907)
<223> RXN02342

<400> 167
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aaagcgcgct tttcgacgcg accccactac attggcttcc atg aac gtt gac att 115
Met Asn Val Asp Ile
1 5

tca cga tcc aga gag ccg cta aac gtt gag ctc ctg aag gaa aaa ttg 163
Ser Arg Ser Arg Glu Pro Leu Asn Val Glu Leu Leu Lys Glu Lys Leu
10 15 20

ctc caa aac ggt gac ttt ggc cag gtc att tac gaa aaa gtg aca ggc 211

Leu Gln Asn Gly Asp Phe Gly Gln Val Ile Tyr Glu Lys Val Thr Gly
25 30 35

tcc act aat gct gac ttg ctg gca ctt gca ggt tct ggc gct cca aac 259
Ser Thr Asn Ala Asp Leu Leu Ala Leu Ala Gly Ser Gly Ala Pro Asn
40 45 50

tgg acg gtg aaa act gtc gag ttt caa gat cat gcg cgt ggg cga ctc 307
Trp Thr Val Lys Thr Val Glu Phe Gln Asp His Ala Arg Gly Arg Leu
55 60 65

ggc cgc ccg tgg tct gcc cct gag ggt tcc caa aca atc gtg tct gtg 355
Gly Arg Pro Trp Ser Ala Pro Glu Gly Ser Gln Thr Ile Val Ser Val
70 75 80 85

ctc gtt caa cta tct att gat caa gtg gac cgg att ggc act att cca 403
Leu Val Gln Leu Ser Ile Asp Gln Val Asp Arg Ile Gly Thr Ile Pro
90 95 100

ctc gcg gcg gga ctc gct gtc atg gat gcg ttg aat gac ctc ggt gtg 451
Leu Ala Ala Gly Leu Ala Val Met Asp Ala Leu Asn Asp Leu Gly Val
105 110 115

gaa ggt gcc gga ctg aaa tgg ccc aac gat gtt caa atc cac ggc aag 499
Glu Gly Ala Gly Leu Lys Trp Pro Asn Asp Val Gln Ile His Gly Lys
120 125 130

aaa ctc tgc ggc atc ctg gtg gaa gcc acc ggc ttt gat tcc acc cca 547
Lys Leu Cys Gly Ile Leu Val Glu Ala Thr Gly Phe Asp Ser Thr Pro
135 140 145

aca gtt gtc atc ggt tgg ggc act aat atc agc ctg act aaa gag gag 595
Thr Val Val Ile Gly Trp Gly Thr Asn Ile Ser Leu Thr Lys Glu Glu
150 155 160 165

ctt cct gtt cct cat gca act tcc ctc gca ttg gaa ggt gtt gaa gtc 643
Leu Pro Val Pro His Ala Thr Ser Leu Ala Leu Glu Gly Val Glu Val
170 175 180

gac aga acc aca ttc ctt att aat atg ctc aca cat ctg cat act cga 691
Asp Arg Thr Thr Phe Leu Ile Asn Met Leu Thr His Leu His Thr Arg
185 190 195

ctg gac cag tgg cag ggt cca agt gtg gat tgg ctc gat gat tac cgt 739
Leu Asp Gln Trp Gln Gly Pro Ser Val Asp Trp Leu Asp Asp Tyr Arg
200 205 210

gcg gta tgt tcc agt att ggc caa gat gtt cga gtg ctt cta cct ggg 787
Ala Val Cys Ser Ser Ile Gly Gln Asp Val Arg Val Leu Leu Pro Gly
215 220 225

gat aaa gaa ctc tta ggt gaa gcg atc ggt gtc gcg act ggc gga gaa 835
Asp Lys Glu Leu Leu Gly Glu Ala Ile Gly Val Ala Thr Gly Gly Glu
230 235 240 245

att cgt gtt cgc gat gct tcg ggc acc gtt cac acc ctc aac gcc ggt 883
Ile Arg Val Arg Asp Ala Ser Gly Thr Val His Thr Leu Asn Ala Gly
250 255 260

gaa att acg cac ctt cgc ctg cag taaggtgacg gtatggggaa ttc 930
Glu Ile Thr His Leu Arg Leu Gln

265

<210> 168
<211> 269
<212> PRT
<213> Corynebacterium glutamicum

<400> 168
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Met Asn Val Asp Ile Ser Arg Ser Arg Glu Pro Leu Asn Val Glu Leu
 1               5                  10                  15

Leu Lys Glu Lys Leu Leu Gln Asn Gly Asp Phe Gly Gln Val Ile Tyr
            20                  25                  30

Glu Lys Val Thr Gly Ser Thr Asn Ala Asp Leu Leu Ala Leu Ala Gly
        35                  40                  45

Ser Gly Ala Pro Asn Trp Thr Val Lys Thr Val Glu Phe Gln Asp His
    50                  55                  60

Ala Arg Gly Arg Leu Gly Arg Pro Trp Ser Ala Pro Glu Gly Ser Gln
65                  70                  75                  80

Thr Ile Val Ser Val Leu Val Gln Leu Ser Ile Asp Gln Val Asp Arg
                85                  90                  95

Ile Gly Thr Ile Pro Leu Ala Ala Gly Leu Ala Val Met Asp Ala Leu
            100                 105                 110

Asn Asp Leu Gly Val Glu Gly Ala Gly Leu Lys Trp Pro Asn Asp Val
        115                 120                 125

Gln Ile His Gly Lys Lys Leu Cys Gly Ile Leu Val Glu Ala Thr Gly
    130                 135                 140

Phe Asp Ser Thr Pro Thr Val Val Ile Gly Trp Gly Thr Asn Ile Ser
145                 150                 155                 160

Leu Thr Lys Glu Glu Leu Pro Val Pro His Ala Thr Ser Leu Ala Leu
                165                 170                 175

Glu Gly Val Glu Val Asp Arg Thr Thr Phe Leu Ile Asn Met Leu Thr
            180                 185                 190

His Leu His Thr Arg Leu Asp Gln Trp Gln Gly Pro Ser Val Asp Trp
        195                 200                 205

Leu Asp Asp Tyr Arg Ala Val Cys Ser Ser Ile Gly Gln Asp Val Arg
    210                 215                 220

Val Leu Leu Pro Gly Asp Lys Glu Leu Leu Gly Glu Ala Ile Gly Val
225                 230                 235                 240

Ala Thr Gly Gly Glu Ile Arg Val Arg Asp Ala Ser Gly Thr Val His
                245                 250                 255

Thr Leu Asn Ala Gly Glu Ile Thr His Leu Arg Leu Gln
            260                 265
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<210> 169
<211> 2762
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(2739)
<223> RXN00563

<400> 169
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ttc tac aag gat ctc tac gca cgt tcc gca cgc ggc acg gca gca ctg     48
Phe Tyr Lys Asp Leu Tyr Ala Arg Ser Ala Arg Gly Thr Ala Ala Leu
  1               5                  10                  15

tgg atc gtg gcg gct aac ttg agc tcc tac tca gac atc gac gcc atc     96
Trp Ile Val Ala Ala Asn Leu Ser Ser Tyr Ser Asp Ile Asp Ala Ile
             20                  25                  30

atc aac tgg gtc gga tcc gag cag acc acc acc gtc aac ggc gca tcc    144
Ile Asn Trp Val Gly Ser Glu Gln Thr Thr Thr Val Asn Gly Ala Ser
         35                  40                  45

aag ctg gtc aag cca gct ttg gtc cct acc ttg ctg ttc cca ttc gcg    192
Lys Leu Val Lys Pro Ala Leu Val Pro Thr Leu Leu Phe Pro Phe Ala
     50                  55                  60

gca cct cgc gtg tcc gga tcc atg gca gat gca ggc cca cag gca gaa    240
Ala Pro Arg Val Ser Gly Ser Met Ala Asp Ala Gly Pro Gln Ala Glu
 65                  70                  75                  80

tcc cag atg cga ctt ctg ctc tgg tct gtt gag cgc ctc atc gca ggt    288
Ser Gln Met Arg Leu Leu Leu Trp Ser Val Glu Arg Leu Ile Ala Gly
                 85                  90                  95

ctt gcg cca ttg ggc tcc tcc atc aac gtg ggt cac cgc ctg cac gtg    336
Leu Ala Pro Leu Gly Ser Ser Ile Asn Val Gly His Arg Leu His Val
            100                 105                 110

gtc atc cca ggt tca cca aac cgt gga cgc ttc ggt ggc gat ggt gca    384
Val Ile Pro Gly Ser Pro Asn Arg Gly Arg Phe Gly Gly Asp Gly Ala
        115                 120                 125

tac ggt gaa tcc aag gca gct ctc gac gcc gtg gtt acc cgt tgg aac    432
Tyr Gly Glu Ser Lys Ala Ala Leu Asp Ala Val Val Thr Arg Trp Asn
    130                 135                 140

gca gag caa gct gca tgg gga gca cac acc tcc ctc gtg cac gct cac    480
Ala Glu Gln Ala Ala Trp Gly Ala His Thr Ser Leu Val His Ala His
145                 150                 155                 160

atc ggt tgg gtt cgc ggc acc ggc ctc atg ggc ggc aac gat cct ttg    528
Ile Gly Trp Val Arg Gly Thr Gly Leu Met Gly Gly Asn Asp Pro Leu
                165                 170                 175

gtc aag gca gct gaa gaa gca ggc gtg gaa acc tac tcc acc caa gaa    576
Val Lys Ala Ala Glu Glu Ala Gly Val Glu Thr Tyr Ser Thr Gln Glu
            180                 185                 190

att gca gag aaa ctg ctg tcc cag gca act tcc act gtt cgc gag cag    624
Ile Ala Glu Lys Leu Leu Ser Gln Ala Thr Ser Thr Val Arg Glu Gln
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        195                 200                 205

gca gca tcc gcg cca atc acc gtc gac ttc act ggc gga ctt ggt gaa     672
Ala Ala Ser Ala Pro Ile Thr Val Asp Phe Thr Gly Gly Leu Gly Glu
    210                 215                 220

tct gat ctg aac ctg gcg gaa atg gca cgt gca gaa gca gct aag gca     720
Ser Asp Leu Asn Leu Ala Glu Met Ala Arg Ala Glu Ala Ala Lys Ala
225                 230                 235                 240

gct aac gca cca gtg gtt gag gct cca cgc aca gtg gca gca ctg cca     768
Ala Asn Ala Pro Val Val Glu Ala Pro Arg Thr Val Ala Ala Leu Pro
                245                 250                 255

act cct tac cga cca gtg gtt caa acc acc cct gat ttc gca ggt caa     816
Thr Pro Tyr Arg Pro Val Val Gln Thr Thr Pro Asp Phe Ala Gly Gln
            260                 265                 270

gtc acc caa aac ctt gac gag atg gtc gtc atc gtt ggc gcc ggc gag     864
Val Thr Gln Asn Leu Asp Glu Met Val Val Ile Val Gly Ala Gly Glu
        275                 280                 285

ctc ggc cca ctg ggt tct gca cgt acg cgt ttc gac gcc gaa ctc aac     912
Leu Gly Pro Leu Gly Ser Ala Arg Thr Arg Phe Asp Ala Glu Leu Asn
    290                 295                 300

ggt tcc ctc tcc gcc gcg ggt gtc atc gaa ctt gca tgg acg atg gga     960
Gly Ser Leu Ser Ala Ala Gly Val Ile Glu Leu Ala Trp Thr Met Gly
305                 310                 315                 320

ctt atc cac tgg gat gaa gat cca aag cca ggc tgg tac gac gac tcc     1008
Leu Ile His Trp Asp Glu Asp Pro Lys Pro Gly Trp Tyr Asp Asp Ser
                325                 330                 335

gac gac gca gtg gcc gaa gaa gac atc ttc gac cgc tac cac gac gaa     1056
Asp Asp Ala Val Ala Glu Glu Asp Ile Phe Asp Arg Tyr His Asp Glu
            340                 345                 350

gtc atg gca cgc gtt ggt gtc cgc aag tac aat gac atg cct gag tac     1104
Val Met Ala Arg Val Gly Val Arg Lys Tyr Asn Asp Met Pro Glu Tyr
        355                 360                 365

ggc atg atc gac aac ttt gca cca gag ctg acc acc gtc tac ctc gac     1152
Gly Met Ile Asp Asn Phe Ala Pro Glu Leu Thr Thr Val Tyr Leu Asp
    370                 375                 380

cag gac ctc acc ttc aac gtg gga tcc cgc gaa gag gca ctg acc tac     1200
Gln Asp Leu Thr Phe Asn Val Gly Ser Arg Glu Glu Ala Leu Thr Tyr
385                 390                 395                 400

gtc gac tcc gag cca gaa ctc acc ttt gct tct ttc gac gaa gca gca     1248
Val Asp Ser Glu Pro Glu Leu Thr Phe Ala Ser Phe Asp Glu Ala Ala
                405                 410                 415

ggg gag tgg aag gtc act cgc aag gca ggc tcc gca atc cgc gta cct     1296
Gly Glu Trp Lys Val Thr Arg Lys Ala Gly Ser Ala Ile Arg Val Pro
            420                 425                 430

cgc cgc atg gcg atg acc cgc ttc gtt ggt gga cag gtt cct aag gac     1344
Arg Arg Met Ala Met Thr Arg Phe Val Gly Gly Gln Val Pro Lys Asp
        435                 440                 445
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ttc gac cca gct gtg tgg ggc att cca gct gac atg gtg gac aac ctg 1392
Phe Asp Pro Ala Val Trp Gly Ile Pro Ala Asp Met Val Asp Asn Leu
450 455 460

gac acc gtc gcg ctg tgg aac att gtc tgt act gtc gac gcc ttc ctg 1440
Asp Thr Val Ala Leu Trp Asn Ile Val Cys Thr Val Asp Ala Phe Leu
465 470 475 480

tcc gct gga ttc acc cca gca gag ctg ctt gct tcc gtt cac cca gca 1488
Ser Ala Gly Phe Thr Pro Ala Glu Leu Leu Ala Ser Val His Pro Ala
485 490 495

cgc gtg tcc tct acc caa ggc acc ggc atg ggc ggc atg gaa tcc ctc 1536
Arg Val Ser Ser Thr Gln Gly Thr Gly Met Gly Gly Met Glu Ser Leu
500 505 510

cgt ggc atc tac gtc gac cgc att ctg gca gag cca cgc gcc aac gac 1584
Arg Gly Ile Tyr Val Asp Arg Ile Leu Ala Glu Pro Arg Ala Asn Asp
515 520 525

gtt ctg cag gaa gca ctg ccc aac gtt gtt gca gct cac gtc atg cag 1632
Val Leu Gln Glu Ala Leu Pro Asn Val Val Ala Ala His Val Met Gln
530 535 540

tcc tac gtc ggt ggc tac gga cag atg atc cac cca gtc gca gct tgt 1680
Ser Tyr Val Gly Gly Tyr Gly Gln Met Ile His Pro Val Ala Ala Cys
545 550 555 560

gca acc gca gct gtt tct gtg gaa gaa gca ctg gac aag atc cgc atc 1728
Ala Thr Ala Ala Val Ser Val Glu Glu Ala Leu Asp Lys Ile Arg Ile
565 570 575

ggc aag tcc gac ttc gtt gtc gca ggt ggc ttc gat gcc ctg tcc gtt 1776
Gly Lys Ser Asp Phe Val Val Ala Gly Gly Phe Asp Ala Leu Ser Val
580 585 590

gaa ggc atc acc ggc ttc ggc gac atg gca gca acc gcc gac tcc gca 1824
Glu Gly Ile Thr Gly Phe Gly Asp Met Ala Ala Thr Ala Asp Ser Ala
595 600 605

gag atg gaa ggc aag gga att gag cac cgc ttc ttc tcc cgc gcc aac 1872
Glu Met Glu Gly Lys Gly Ile Glu His Arg Phe Phe Ser Arg Ala Asn
610 615 620

gac cgg cgc cgc ggt gga ttc atc gaa tcc gaa ggt ggc gga acc gtc 1920
Asp Arg Arg Arg Gly Gly Phe Ile Glu Ser Glu Gly Gly Gly Thr Val
625 630 635 640

ctt ctg gca cgc gga tca ctc gca gct gac ctg ggc ctt cca gta ctc 1968
Leu Leu Ala Arg Gly Ser Leu Ala Ala Asp Leu Gly Leu Pro Val Leu
645 650 655

ggt gtc atc gga ttc gca gag tcc ttt gca gat ggt gcc cac acc tcc 2016
Gly Val Ile Gly Phe Ala Glu Ser Phe Ala Asp Gly Ala His Thr Ser
660 665 670

atc cca gcc cca ggc ctc ggt gcc ctt ggt gct gct cgc gat ggt gtg 2064
Ile Pro Ala Pro Gly Leu Gly Ala Leu Gly Ala Ala Arg Asp Gly Val
675 680 685

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gaa tct cgc ctt gca gta gca ctg cgt tcc gtc ggt gtc tct gct gat    2112
Glu Ser Arg Leu Ala Val Ala Leu Arg Ser Val Gly Val Ser Ala Asp
    690                 695                 700

gag atc tcc att atc tcc aag cac gac acc tcc acc aac gcg aat gat    2160
Glu Ile Ser Ile Ile Ser Lys His Asp Thr Ser Thr Asn Ala Asn Asp
705                 710                 715                 720

cca aac gag tcc gac ctg cac gag cgc atc gca tcc gct atc ggt cgt    2208
Pro Asn Glu Ser Asp Leu His Glu Arg Ile Ala Ser Ala Ile Gly Arg
                725                 730                 735

gca gac ggc aac ccg atg tac gtg att tcc cag aag tca ctc acc gga    2256
Ala Asp Gly Asn Pro Met Tyr Val Ile Ser Gln Lys Ser Leu Thr Gly
            740                 745                 750

cac gcc aag ggt ggt gca gca gca ttc cag atg atc ggt ctc acc cag    2304
His Ala Lys Gly Gly Ala Ala Ala Phe Gln Met Ile Gly Leu Thr Gln
        755                 760                 765

gtc ctc cga tcc gga ctg gtg cca gcc aac cgc gca ctc gac tgc gtt    2352
Val Leu Arg Ser Gly Leu Val Pro Ala Asn Arg Ala Leu Asp Cys Val
    770                 775                 780

gac cca gta ctg tcc aag cat tcc cac ctc gtc tgg ctg cgc aag cca    2400
Asp Pro Val Leu Ser Lys His Ser His Leu Val Trp Leu Arg Lys Pro
785                 790                 795                 800

cta gac ctt cgt gcg aag gca cca aag gca ggt ctt gtt acc tcc ctt    2448
Leu Asp Leu Arg Ala Lys Ala Pro Lys Ala Gly Leu Val Thr Ser Leu
                805                 810                 815

ggc ttc gga cac gtc tcc gct ctg gtt gcg att gtt cac cca gac gcc    2496
Gly Phe Gly His Val Ser Ala Leu Val Ala Ile Val His Pro Asp Ala
            820                 825                 830

ttc tat gag gca gtt cgt gtg gca cgt ggt gct gag gca gct gac gta    2544
Phe Tyr Glu Ala Val Arg Val Ala Arg Gly Ala Glu Ala Ala Asp Val
        835                 840                 845

tgg cgc gca tcc gcg atc gct cgc gaa gaa gca ggc ctt cgt acc atc    2592
Trp Arg Ala Ser Ala Ile Ala Arg Glu Glu Ala Gly Leu Arg Thr Ile
    850                 855                 860

gtc gcc ggt atg cac ggt ggc gta ctg tac gaa cgc cca gtc gag cgc    2640
Val Ala Gly Met His Gly Gly Val Leu Tyr Glu Arg Pro Val Glu Arg
865                 870                 875                 880

aac ctc ggt gtc cac gga gac gca gct aag gaa gtt gaa gct gca gtc    2688
Asn Leu Gly Val His Gly Asp Ala Ala Lys Glu Val Glu Ala Ala Val
                885                 890                 895

ctc ctg gat tcc cgc gcc cgc cta gtt gac ggt gtc ctc cgc gcc gaa    2736
Leu Leu Asp Ser Arg Ala Arg Leu Val Asp Gly Val Leu Arg Ala Glu
            900                 905                 910

ggc tagttggtta ttgcgttgag ccc                                      2762
Gly
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<210> 170
<211> 913
<212> PRT
<213> Corynebacterium glutamicum

<400> 170
Phe Tyr Lys Asp Leu Tyr Ala Arg Ser Ala Arg Gly Thr Ala Ala Leu
1 5 10 15

Trp Ile Val Ala Ala Asn Leu Ser Ser Tyr Ser Asp Ile Asp Ala Ile
20 25 30

Ile Asn Trp Val Gly Ser Glu Gln Thr Thr Thr Val Asn Gly Ala Ser
35 40 45

Lys Leu Val Lys Pro Ala Leu Val Pro Thr Leu Leu Phe Pro Phe Ala
50 55 60

Ala Pro Arg Val Ser Gly Ser Met Ala Asp Ala Gly Pro Gln Ala Glu
65 70 75 80

Ser Gln Met Arg Leu Leu Leu Trp Ser Val Glu Arg Leu Ile Ala Gly
85 90 95

Leu Ala Pro Leu Gly Ser Ser Ile Asn Val Gly His Arg Leu His Val
100 105 110

Val Ile Pro Gly Ser Pro Asn Arg Gly Arg Phe Gly Gly Asp Gly Ala
115 120 125

Tyr Gly Glu Ser Lys Ala Ala Leu Asp Ala Val Val Thr Arg Trp Asn
130 135 140

Ala Glu Gln Ala Ala Trp Gly Ala His Thr Ser Leu Val His Ala His
145 150 155 160

Ile Gly Trp Val Arg Gly Thr Gly Leu Met Gly Gly Asn Asp Pro Leu
165 170 175

Val Lys Ala Ala Glu Glu Ala Gly Val Glu Thr Tyr Ser Thr Gln Glu
180 185 190

Ile Ala Glu Lys Leu Leu Ser Gln Ala Thr Ser Thr Val Arg Glu Gln
195 200 205

Ala Ala Ser Ala Pro Ile Thr Val Asp Phe Thr Gly Gly Leu Gly Glu
210 215 220

Ser Asp Leu Asn Leu Ala Glu Met Ala Arg Ala Glu Ala Ala Lys Ala
225 230 235 240

Ala Asn Ala Pro Val Val Glu Ala Pro Arg Thr Val Ala Ala Leu Pro
245 250 255

Thr Pro Tyr Arg Pro Val Val Gln Thr Thr Pro Asp Phe Ala Gly Gln
260 265 270

Val Thr Gln Asn Leu Asp Glu Met Val Val Ile Val Gly Ala Gly Glu
275 280 285

Leu Gly Pro Leu Gly Ser Ala Arg Thr Arg Phe Asp Ala Glu Leu Asn

290 295 300

Gly Ser Leu Ser Ala Ala Gly Val Ile Glu Leu Ala Trp Thr Met Gly
305 310 315 320

Leu Ile His Trp Asp Glu Asp Pro Lys Pro Gly Trp Tyr Asp Asp Ser
325 330 335

Asp Asp Ala Val Ala Glu Glu Asp Ile Phe Asp Arg Tyr His Asp Glu
340 345 350

Val Met Ala Arg Val Gly Val Arg Lys Tyr Asn Asp Met Pro Glu Tyr
355 360 365

Gly Met Ile Asp Asn Phe Ala Pro Glu Leu Thr Thr Val Tyr Leu Asp
370 375 380

Gln Asp Leu Thr Phe Asn Val Gly Ser Arg Glu Glu Ala Leu Thr Tyr
385 390 395 400

Val Asp Ser Glu Pro Glu Leu Thr Phe Ala Ser Phe Asp Glu Ala Ala
405 410 415

Gly Glu Trp Lys Val Thr Arg Lys Ala Gly Ser Ala Ile Arg Val Pro
420 425 430

Arg Arg Met Ala Met Thr Arg Phe Val Gly Gly Gln Val Pro Lys Asp
435 440 445

Phe Asp Pro Ala Val Trp Gly Ile Pro Ala Asp Met Val Asp Asn Leu
450 455 460

Asp Thr Val Ala Leu Trp Asn Ile Val Cys Thr Val Asp Ala Phe Leu
465 470 475 480

Ser Ala Gly Phe Thr Pro Ala Glu Leu Leu Ala Ser Val His Pro Ala
485 490 495

Arg Val Ser Ser Thr Gln Gly Thr Gly Met Gly Gly Met Glu Ser Leu
500 505 510

Arg Gly Ile Tyr Val Asp Arg Ile Leu Ala Glu Pro Arg Ala Asn Asp
515 520 525

Val Leu Gln Glu Ala Leu Pro Asn Val Val Ala Ala His Val Met Gln
530 535 540

Ser Tyr Val Gly Gly Tyr Gly Gln Met Ile His Pro Val Ala Ala Cys
545 550 555 560

Ala Thr Ala Ala Val Ser Val Glu Glu Ala Leu Asp Lys Ile Arg Ile
565 570 575

Gly Lys Ser Asp Phe Val Val Ala Gly Gly Phe Asp Ala Leu Ser Val
580 585 590

Glu Gly Ile Thr Gly Phe Gly Asp Met Ala Ala Thr Ala Asp Ser Ala
595 600 605

Glu Met Glu Gly Lys Gly Ile Glu His Arg Phe Phe Ser Arg Ala Asn
610 615 620

Asp Arg Arg Arg Gly Gly Phe Ile Glu Ser Glu Gly Gly Gly Thr Val
625 630 635 640

Leu Leu Ala Arg Gly Ser Leu Ala Ala Asp Leu Gly Leu Pro Val Leu
645 650 655

Gly Val Ile Gly Phe Ala Glu Ser Phe Ala Asp Gly Ala His Thr Ser
660 665 670

Ile Pro Ala Pro Gly Leu Gly Ala Leu Gly Ala Ala Arg Asp Gly Val
675 680 685

Glu Ser Arg Leu Ala Val Ala Leu Arg Ser Val Gly Val Ser Ala Asp
690 695 700

Glu Ile Ser Ile Ile Ser Lys His Asp Thr Ser Thr Asn Ala Asn Asp
705 710 715 720

Pro Asn Glu Ser Asp Leu His Glu Arg Ile Ala Ser Ala Ile Gly Arg
725 730 735

Ala Asp Gly Asn Pro Met Tyr Val Ile Ser Gln Lys Ser Leu Thr Gly
740 745 750

His Ala Lys Gly Gly Ala Ala Ala Phe Gln Met Ile Gly Leu Thr Gln
755 760 765

Val Leu Arg Ser Gly Leu Val Pro Ala Asn Arg Ala Leu Asp Cys Val
770 775 780

Asp Pro Val Leu Ser Lys His Ser His Leu Val Trp Leu Arg Lys Pro
785 790 795 800

Leu Asp Leu Arg Ala Lys Ala Pro Lys Ala Gly Leu Val Thr Ser Leu
805 810 815

Gly Phe Gly His Val Ser Ala Leu Val Ala Ile Val His Pro Asp Ala
820 825 830

Phe Tyr Glu Ala Val Arg Val Ala Arg Gly Ala Glu Ala Ala Asp Val
835 840 845

Trp Arg Ala Ser Ala Ile Ala Arg Glu Glu Ala Gly Leu Arg Thr Ile
850 855 860

Val Ala Gly Met His Gly Gly Val Leu Tyr Glu Arg Pro Val Glu Arg
865 870 875 880

Asn Leu Gly Val His Gly Asp Ala Ala Lys Glu Val Glu Ala Ala Val
885 890 895

Leu Leu Asp Ser Arg Ala Arg Leu Val Asp Gly Val Leu Arg Ala Glu
900 905 910

Gly

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<223> RXN02168

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ggtccaagaa gcccattcca agacttagga gctttatttc gtg agt att tct tca 115
Val Ser Ile Ser Ser
1 5

ctg aca ccg ctg cac tct ttc aaa gag cca gca att ctg tac gcc ggt 163
Leu Thr Pro Leu His Ser Phe Lys Glu Pro Ala Ile Leu Tyr Ala Gly
10 15 20

cag gct tct gcc tgg cag cag gtg atc gct gat tcc agc gaa gac cac 211
Gln Ala Ser Ala Trp Gln Gln Val Ile Ala Asp Ser Ser Glu Asp His
25 30 35

atc acc gca acg cac ctg cgc gag ctc ctg tct cgc tcc cgt gca aag 259
Ile Thr Ala Thr His Leu Arg Glu Leu Leu Ser Arg Ser Arg Ala Lys
40 45 50

act gca cct ttc gct cgc caa atc acc gcc atc gtg cct ggc tca ctt 307
Thr Ala Pro Phe Ala Arg Gln Ile Thr Ala Ile Val Pro Gly Ser Leu
55 60 65

gct cgt ctt gag gaa ctg acc cgc gaa gac gca caa atc ggt gca gac 355
Ala Arg Leu Glu Glu Leu Thr Arg Glu Asp Ala Gln Ile Gly Ala Asp
70 75 80 85

atc gac gca cag cct gcc gtt tcc att cca ggc att ctg ctg gga cag 403
Ile Asp Ala Gln Pro Ala Val Ser Ile Pro Gly Ile Leu Leu Gly Gln
90 95 100

atc gct gca acc cgt cag ctg cgt gac ctc gga ctc gat gtc gca gca 451
Ile Ala Ala Thr Arg Gln Leu Arg Asp Leu Gly Leu Asp Val Ala Ala
105 110 115

gct tcc cgc ctt gga cac tcc cag ggc att ttg ggc gtt gaa gca gta 499
Ala Ser Arg Leu Gly His Ser Gln Gly Ile Leu Gly Val Glu Ala Val
120 125 130

gac aat gaa gaa gac gtt tta gct ttc gcc atc ctg ctg ggc gca gca 547
Asp Asn Glu Glu Asp Val Leu Ala Phe Ala Ile Leu Leu Gly Ala Ala
135 140 145

gct tcc cag ttc gct ggc aag ggc gca cat atg ctc tct gtt cgc ggc 595
Ala Ser Gln Phe Ala Gly Lys Gly Ala His Met Leu Ser Val Arg Gly
150 155 160 165

ctg tcc cgt gag atc atc cag gac acc atc gct ggt gtc gat ggg gta 643
Leu Ser Arg Glu Ile Ile Gln Asp Thr Ile Ala Gly Val Asp Gly Val
170 175 180

gag gtc tcc ctg cgc aac gct cgt gca cac ttt gtt gtc tct ggt aag 691
Glu Val Ser Leu Arg Asn Ala Arg Ala His Phe Val Val Ser Gly Lys

185 190 195

cca gag gca ctg aag aag gct gct gct gct cta cag cgc gca gct gat 739
Pro Glu Ala Leu Lys Lys Ala Ala Ala Ala Leu Gln Arg Ala Ala Asp
200 205 210

gtt tac aac gaa gac atc aac gaa aag cgc aag ggt gga tcc ctg gca 787
Val Tyr Asn Glu Asp Ile Asn Glu Lys Arg Lys Gly Gly Ser Leu Ala
215 220 225

gag cct aag ttt gac tac ttg gat gtg gcc att cct ttc cac cac tcc 835
Glu Pro Lys Phe Asp Tyr Leu Asp Val Ala Ile Pro Phe His His Ser
230 235 240 245

tcc atg cag gac gca gcc gac ttg gct gtc gag tgg gca acc acc tgt 883
Ser Met Gln Asp Ala Ala Asp Leu Ala Val Glu Trp Ala Thr Thr Cys
250 255 260

ggc cta aac gtc aac gcg cgc gcg ttg gca gaa gca att cta gtt aac 931
Gly Leu Asn Val Asn Ala Arg Ala Leu Ala Glu Ala Ile Leu Val Asn
265 270 275

cca gct gac tgg gtt gag cag atc gca aac ctc aag gct gat tac gtt 979
Pro Ala Asp Trp Val Glu Gln Ile Ala Asn Leu Lys Ala Asp Tyr Val
280 285 290

ctt tcc ctc gat gca ggc gtc agc cgt ttc acc gct cca ttg cta gac 1027
Leu Ser Leu Asp Ala Gly Val Ser Arg Phe Thr Ala Pro Leu Leu Asp
295 300 305

ggt cgc gga atc tct ttg gtt cct gcg ttc tcc gct gca gag cgc gac 1075
Gly Arg Gly Ile Ser Leu Val Pro Ala Phe Ser Ala Ala Glu Arg Asp
310 315 320 325

aac ttg gct cgc cct ggc ttc cac gtt cct acc gct gag gat tgg tcc 1123
Asn Leu Ala Arg Pro Gly Phe His Val Pro Thr Ala Glu Asp Trp Ser
330 335 340

gag ttc gct cca aag ctg gtt aag ctt cca aac ggt gag cac aag gtt 1171
Glu Phe Ala Pro Lys Leu Val Lys Leu Pro Asn Gly Glu His Lys Val
345 350 355

ctc acc ggg ttc tcc cgc ctg act ggt tat tcc cca atc gtc ctg gct 1219
Leu Thr Gly Phe Ser Arg Leu Thr Gly Tyr Ser Pro Ile Val Leu Ala
360 365 370

ggc atg acc cca acc acc gtt gat cct gag atc gtt gca gct gca gcg 1267
Gly Met Thr Pro Thr Thr Val Asp Pro Glu Ile Val Ala Ala Ala Ala
375 380 385

aac gct gga cac tgg gcc gaa atg gcc ggt ggc gga cag tac tct gaa 1315
Asn Ala Gly His Trp Ala Glu Met Ala Gly Gly Gly Gln Tyr Ser Glu
390 395 400 405

gaa gtc ttc acc aag aac aag gaa aag ctc gtt tcc ctg ctc aag gtt 1363
Glu Val Phe Thr Lys Asn Lys Glu Lys Leu Val Ser Leu Leu Lys Val
410 415 420

gga cgc tcc gca cag ttc aac tcc atg ttc ttc gac cgc tac atg tgg 1411
Gly Arg Ser Ala Gln Phe Asn Ser Met Phe Phe Asp Arg Tyr Met Trp
425 430 435

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aac ctg cag ttc ggt gca cag cgc atc gtt tcc aag gca cgt gca acc    1459
Asn Leu Gln Phe Gly Ala Gln Arg Ile Val Ser Lys Ala Arg Ala Thr
        440                 445                 450

ggt acc tcc atc aac ggt gtt gtt gtc tcc gct ggt atc cca gag gtt    1507
Gly Thr Ser Ile Asn Gly Val Val Val Ser Ala Gly Ile Pro Glu Val
    455                 460                 465

gag gaa gca act gag ctg atc aac gat ctg aac gct gat ggc ttc cca    1555
Glu Glu Ala Thr Glu Leu Ile Asn Asp Leu Asn Ala Asp Gly Phe Pro
470                 475                 480                 485

tac gtt gca ttc aag cca ggc acc gtg gat cag atc cgc gca acc ctg    1603
Tyr Val Ala Phe Lys Pro Gly Thr Val Asp Gln Ile Arg Ala Thr Leu
                490                 495                 500

aag att gct gat gca aac cca gag acc aag atc atc atc cag atc gag    1651
Lys Ile Ala Asp Ala Asn Pro Glu Thr Lys Ile Ile Ile Gln Ile Glu
            505                 510                 515

gac gga cac gct ggt ggc cac cac tcc tgg gtc aac ttg gac gat ctg    1699
Asp Gly His Ala Gly Gly His His Ser Trp Val Asn Leu Asp Asp Leu
        520                 525                 530

ctc ctg acc acc tac gca gag ctg cgt tcc cgc aag aac gtt gtc gtc    1747
Leu Leu Thr Thr Tyr Ala Glu Leu Arg Ser Arg Lys Asn Val Val Val
    535                 540                 545

atg atc ggt ggc ggc atc gga acc cct gca aag gct gct tac tac ctg    1795
Met Ile Gly Gly Gly Ile Gly Thr Pro Ala Lys Ala Ala Tyr Tyr Leu
550                 555                 560                 565

acc ggt gaa tgg tcc acc gat ttg ggc ttc cca gca atg cca gtg gac    1843
Thr Gly Glu Trp Ser Thr Asp Leu Gly Phe Pro Ala Met Pro Val Asp
                570                 575                 580

ggc atc ctc gtg ggt acc gct gcc atg gca acc aag gaa gca acc act    1891
Gly Ile Leu Val Gly Thr Ala Ala Met Ala Thr Lys Glu Ala Thr Thr
            585                 590                 595

tct cct cag gtc aag cag gca ctg gtc gac acc cca ggt gtt gat cca    1939
Ser Pro Gln Val Lys Gln Ala Leu Val Asp Thr Pro Gly Val Asp Pro
        600                 605                 610

cac gac gct ggc ggc tgg gtt ggc cgt ggc gat gct cgt ggt ggc gtg    1987
His Asp Ala Gly Gly Trp Val Gly Arg Gly Asp Ala Arg Gly Gly Val
    615                 620                 625

acc tct ggt ctg tca cac ctg cac gct gac atg tac gag ctg gac aac    2035
Thr Ser Gly Leu Ser His Leu His Ala Asp Met Tyr Glu Leu Asp Asn
630                 635                 640                 645

gat tct gct gca gct tcc cgc ctg atc tct tcc atc gat tct gat gat    2083
Asp Ser Ala Ala Ala Ser Arg Leu Ile Ser Ser Ile Asp Ser Asp Asp
                650                 655                 660

tac gca gat cac cgc gaa gag ctc atc gag gct atc aac aag acc gct    2131
Tyr Ala Asp His Arg Glu Glu Leu Ile Glu Ala Ile Asn Lys Thr Ala
            665                 670                 675
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aag cct ttc ttc ggc gag gtc gaa gag atg act tac gca gag tgg atc    2179
Lys Pro Phe Phe Gly Glu Val Glu Glu Met Thr Tyr Ala Glu Trp Ile
        680                 685                 690

cag cgt tgg gtt gag ctt gct tac cca act cag gac cca acc tgg gat    2227
Gln Arg Trp Val Glu Leu Ala Tyr Pro Thr Gln Asp Pro Thr Trp Asp
    695                 700                 705

gat cgt ttc ctc gat ttg gtt cac cgc att gaa gct cgt ctc aac gag    2275
Asp Arg Phe Leu Asp Leu Val His Arg Ile Glu Ala Arg Leu Asn Glu
710                 715                 720                 725

gca gag cac ggc gcc atc acc aca ctg ttc cca gac cat gcg tct gtg    2323
Ala Glu His Gly Ala Ile Thr Thr Leu Phe Pro Asp His Ala Ser Val
                730                 735                 740

gaa aat gag gaa gag gcc gtc gaa aag ctt ctt gct gct tac ccg cag    2371
Glu Asn Glu Glu Glu Ala Val Glu Lys Leu Leu Ala Ala Tyr Pro Gln
            745                 750                 755

gcc cgc gag atc cag gtc tct gcg cgc gac gcc gcg tgg ttt att ggt    2419
Ala Arg Glu Ile Gln Val Ser Ala Arg Asp Ala Ala Trp Phe Ile Gly
        760                 765                 770

ctg tgc cgc aag cac cac aag cct atg cct tgg gtt cca gca atc gat    2467
Leu Cys Arg Lys His His Lys Pro Met Pro Trp Val Pro Ala Ile Asp
    775                 780                 785

gct gac cta gca cgc tgg tgg ggc ctt gac acc ctg tgg cag tcc cag    2515
Ala Asp Leu Ala Arg Trp Trp Gly Leu Asp Thr Leu Trp Gln Ser Gln
790                 795                 800                 805

aac gag cgc tac ggc gcg aac tca gtc cgc gtt atc cca gga cca gtc    2563
Asn Glu Arg Tyr Gly Ala Asn Ser Val Arg Val Ile Pro Gly Pro Val
                810                 815                 820

tcc gtc gcc ggc atc gac cgt gtt gac gag cca gtt gca gag ctg ctc    2611
Ser Val Ala Gly Ile Asp Arg Val Asp Glu Pro Val Ala Glu Leu Leu
            825                 830                 835

ggc cgc ttc gaa gct gcc tgc gtt gac gct ctc gac ggc gag cca gaa    2659
Gly Arg Phe Glu Ala Ala Cys Val Asp Ala Leu Asp Gly Glu Pro Glu
        840                 845                 850

gag atc ttc gct cgc ctc aat gag tcc aag aac gag cgc gaa ttc ctg    2707
Glu Ile Phe Ala Arg Leu Asn Glu Ser Lys Asn Glu Arg Glu Phe Leu
    855                 860                 865

ctg gct acc cca cac atc gtg tgg cac ggc aac ctg atc gac aac cca    2755
Leu Ala Thr Pro His Ile Val Trp His Gly Asn Leu Ile Asp Asn Pro
870                 875                 880                 885

gct cac gtc ctc aac gag ggt gct ttc gag ctc atc gag gag gat ggc    2803
Ala His Val Leu Asn Glu Gly Ala Phe Glu Leu Ile Glu Glu Asp Gly
                890                 895                 900

tac tgg gtc atc cgt atc ctg gct gat tcc tac ttc gac gat ctg cca    2851
Tyr Trp Val Ile Arg Ile Leu Ala Asp Ser Tyr Phe Asp Asp Leu Pro
            905                 910                 915

gtt gag cag cgc cca tac ctg gtt cag cat gtt gac atc cca gtt gag    2899
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Val Glu Gln Arg Pro Tyr Leu Val Gln His Val Asp Ile Pro Val Glu
        920                 925                 930

ctg ggt gac gct ggt tgaaccggtg gtttcccaat tgg                    2937
Leu Gly Asp Ala Gly
    935


<210> 172
<211> 938
<212> PRT
<213> Corynebacterium glutamicum

<400> 172
Val Ser Ile Ser Ser Leu Thr Pro Leu His Ser Phe Lys Glu Pro Ala
  1               5                  10                  15

Ile Leu Tyr Ala Gly Gln Ala Ser Ala Trp Gln Gln Val Ile Ala Asp
             20                  25                  30

Ser Ser Glu Asp His Ile Thr Ala Thr His Leu Arg Glu Leu Leu Ser
        35                  40                  45

Arg Ser Arg Ala Lys Thr Ala Pro Phe Ala Arg Gln Ile Thr Ala Ile
    50                  55                  60

Val Pro Gly Ser Leu Ala Arg Leu Glu Glu Leu Thr Arg Glu Asp Ala
 65                  70                  75                  80

Gln Ile Gly Ala Asp Ile Asp Ala Gln Pro Ala Val Ser Ile Pro Gly
                 85                  90                  95

Ile Leu Leu Gly Gln Ile Ala Ala Thr Arg Gln Leu Arg Asp Leu Gly
            100                 105                 110

Leu Asp Val Ala Ala Ala Ser Arg Leu Gly His Ser Gln Gly Ile Leu
        115                 120                 125

Gly Val Glu Ala Val Asp Asn Glu Glu Asp Val Leu Ala Phe Ala Ile
    130                 135                 140

Leu Leu Gly Ala Ala Ala Ser Gln Phe Ala Gly Lys Gly Ala His Met
145                 150                 155                 160

Leu Ser Val Arg Gly Leu Ser Arg Glu Ile Ile Gln Asp Thr Ile Ala
                165                 170                 175

Gly Val Asp Gly Val Glu Val Ser Leu Arg Asn Ala Arg Ala His Phe
            180                 185                 190

Val Val Ser Gly Lys Pro Glu Ala Leu Lys Lys Ala Ala Ala Ala Leu
        195                 200                 205

Gln Arg Ala Ala Asp Val Tyr Asn Glu Asp Ile Asn Glu Lys Arg Lys
    210                 215                 220

Gly Gly Ser Leu Ala Glu Pro Lys Phe Asp Tyr Leu Asp Val Ala Ile
225                 230                 235                 240

Pro Phe His His Ser Ser Met Gln Asp Ala Ala Asp Leu Ala Val Glu
                245                 250                 255
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Trp Ala Thr Thr Cys Gly Leu Asn Val Asn Ala Arg Ala Leu Ala Glu
260 265 270

Ala Ile Leu Val Asn Pro Ala Asp Trp Val Glu Gln Ile Ala Asn Leu
275 280 285

Lys Ala Asp Tyr Val Leu Ser Leu Asp Ala Gly Val Ser Arg Phe Thr
290 295 300

Ala Pro Leu Leu Asp Gly Arg Gly Ile Ser Leu Val Pro Ala Phe Ser
305 310 315 320

Ala Ala Glu Arg Asp Asn Leu Ala Arg Pro Gly Phe His Val Pro Thr
325 330 335

Ala Glu Asp Trp Ser Glu Phe Ala Pro Lys Leu Val Lys Leu Pro Asn
340 345 350

Gly Glu His Lys Val Leu Thr Gly Phe Ser Arg Leu Thr Gly Tyr Ser
355 360 365

Pro Ile Val Leu Ala Gly Met Thr Pro Thr Thr Val Asp Pro Glu Ile
370 375 380

Val Ala Ala Ala Ala Asn Ala Gly His Trp Ala Glu Met Ala Gly Gly
385 390 395 400

Gly Gln Tyr Ser Glu Glu Val Phe Thr Lys Asn Lys Glu Lys Leu Val
405 410 415

Ser Leu Leu Lys Val Gly Arg Ser Ala Gln Phe Asn Ser Met Phe Phe
420 425 430

Asp Arg Tyr Met Trp Asn Leu Gln Phe Gly Ala Gln Arg Ile Val Ser
435 440 445

Lys Ala Arg Ala Thr Gly Thr Ser Ile Asn Gly Val Val Val Ser Ala
450 455 460

Gly Ile Pro Glu Val Glu Glu Ala Thr Glu Leu Ile Asn Asp Leu Asn
465 470 475 480

Ala Asp Gly Phe Pro Tyr Val Ala Phe Lys Pro Gly Thr Val Asp Gln
485 490 495

Ile Arg Ala Thr Leu Lys Ile Ala Asp Ala Asn Pro Glu Thr Lys Ile
500 505 510

Ile Ile Gln Ile Glu Asp Gly His Ala Gly Gly His His Ser Trp Val
515 520 525

Asn Leu Asp Asp Leu Leu Leu Thr Thr Tyr Ala Glu Leu Arg Ser Arg
530 535 540

Lys Asn Val Val Val Met Ile Gly Gly Gly Ile Gly Thr Pro Ala Lys
545 550 555 560

Ala Ala Tyr Tyr Leu Thr Gly Glu Trp Ser Thr Asp Leu Gly Phe Pro
565 570 575

Ala Met Pro Val Asp Gly Ile Leu Val Gly Thr Ala Ala Met Ala Thr
580 585 590

Lys Glu Ala Thr Thr Ser Pro Gln Val Lys Gln Ala Leu Val Asp Thr
595 600 605

Pro Gly Val Asp Pro His Asp Ala Gly Gly Trp Val Gly Arg Gly Asp
610 615 620

Ala Arg Gly Gly Val Thr Ser Gly Leu Ser His Leu His Ala Asp Met
625 630 635 640

Tyr Glu Leu Asp Asn Asp Ser Ala Ala Ala Ser Arg Leu Ile Ser Ser
645 650 655

Ile Asp Ser Asp Asp Tyr Ala Asp His Arg Glu Glu Leu Ile Glu Ala
660 665 670

Ile Asn Lys Thr Ala Lys Pro Phe Phe Gly Glu Val Glu Glu Met Thr
675 680 685

Tyr Ala Glu Trp Ile Gln Arg Trp Val Glu Leu Ala Tyr Pro Thr Gln
690 695 700

Asp Pro Thr Trp Asp Asp Arg Phe Leu Asp Leu Val His Arg Ile Glu
705 710 715 720

Ala Arg Leu Asn Glu Ala Glu His Gly Ala Ile Thr Thr Leu Phe Pro
725 730 735

Asp His Ala Ser Val Glu Asn Glu Glu Glu Ala Val Glu Lys Leu Leu
740 745 750

Ala Ala Tyr Pro Gln Ala Arg Glu Ile Gln Val Ser Ala Arg Asp Ala
755 760 765

Ala Trp Phe Ile Gly Leu Cys Arg Lys His His Lys Pro Met Pro Trp
770 775 780

Val Pro Ala Ile Asp Ala Asp Leu Ala Arg Trp Trp Gly Leu Asp Thr
785 790 795 800

Leu Trp Gln Ser Gln Asn Glu Arg Tyr Gly Ala Asn Ser Val Arg Val
805 810 815

Ile Pro Gly Pro Val Ser Val Ala Gly Ile Asp Arg Val Asp Glu Pro
820 825 830

Val Ala Glu Leu Leu Gly Arg Phe Glu Ala Ala Cys Val Asp Ala Leu
835 840 845

Asp Gly Glu Pro Glu Glu Ile Phe Ala Arg Leu Asn Glu Ser Lys Asn
850 855 860

Glu Arg Glu Phe Leu Leu Ala Thr Pro His Ile Val Trp His Gly Asn
865 870 875 880

Leu Ile Asp Asn Pro Ala His Val Leu Asn Glu Gly Ala Phe Glu Leu
885 890 895

Ile Glu Glu Asp Gly Tyr Trp Val Ile Arg Ile Leu Ala Asp Ser Tyr

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            900                 905                 910

Phe Asp Asp Leu Pro Val Glu Gln Arg Pro Tyr Leu Val Gln His Val
        915                 920                 925

Asp Ile Pro Val Glu Leu Gly Asp Ala Gly
    930                 935


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<213> Corynebacterium glutamicum

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<222> (101)..(898)
<223> RXN01090

<400> 173
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taaccacgaa cgttttaaag aagccacgaa ggagcctgac atg gcg tta cca cta   115
                                           Met Ala Leu Pro Leu
                                           1               5

ccc agc aag agc gct cga gca ctt gtt act ggg gca agc caa ggc att   163
Pro Ser Lys Ser Ala Arg Ala Leu Val Thr Gly Ala Ser Gln Gly Ile
                10                  15                  20

ggc ctc gcc atc gcc aaa gat ttg gcg cgg tat ggg cac aac ctc att   211
Gly Leu Ala Ile Ala Lys Asp Leu Ala Arg Tyr Gly His Asn Leu Ile
            25                  30                  35

ttg gtt gct cgc cgc gag gat gtc ctc aaa gag atc gcc gca gat cta   259
Leu Val Ala Arg Arg Glu Asp Val Leu Lys Glu Ile Ala Ala Asp Leu
        40                  45                  50

gag aag aag cac ggc gtg atc gtt gag gtc cgc ccg gtg gat ttg agt   307
Glu Lys Lys His Gly Val Ile Val Glu Val Arg Pro Val Asp Leu Ser
    55                  60                  65

gat gag cca gcc cgc aag gtg ttg atc gat gag atc aag aca agg gaa   355
Asp Glu Pro Ala Arg Lys Val Leu Ile Asp Glu Ile Lys Thr Arg Glu
70                  75                  80                  85

atc aac atc atc att aac tct gct ggc atc gca agc ttt ggg ccg ttc   403
Ile Asn Ile Ile Ile Asn Ser Ala Gly Ile Ala Ser Phe Gly Pro Phe
                90                  95                  100

aag gac cag gat tgg tct tat gag act gcc cag ttc tca ctt aat gcc   451
Lys Asp Gln Asp Trp Ser Tyr Glu Thr Ala Gln Phe Ser Leu Asn Ala
            105                 110                 115

aca gcc gtt ttt gag ctc acc cac gcg gtg ttg ggt ggc atg att gac   499
Thr Ala Val Phe Glu Leu Thr His Ala Val Leu Gly Gly Met Ile Asp
        120                 125                 130

cgt ggc acg ggc gct att tgc aat gtg gga tct gcg gct ggc aat gtg   547
Arg Gly Thr Gly Ala Ile Cys Asn Val Gly Ser Ala Ala Gly Asn Val
    135                 140                 145
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cca atc ccc aac aac gcc acg tat gtg ctc acc aag gct ggc gtg aac    595
Pro Ile Pro Asn Asn Ala Thr Tyr Val Leu Thr Lys Ala Gly Val Asn
150                 155                 160                 165

gcg ttc acc gag gca atg cat tat gag ctg cgc gga act ggt gtg gcg    643
Ala Phe Thr Glu Ala Met His Tyr Glu Leu Arg Gly Thr Gly Val Ala
                170                 175                 180

tgt act ttg ctc gca ccg gga cct gtc cgt gag gcg gag atc cct gag    691
Cys Thr Leu Leu Ala Pro Gly Pro Val Arg Glu Ala Glu Ile Pro Glu
            185                 190                 195

tct gag aag tcg atc gtg gac aag gtt gtc cct gat ttc ttg tgg acc    739
Ser Glu Lys Ser Ile Val Asp Lys Val Val Pro Asp Phe Leu Trp Thr
        200                 205                 210

acc tat gag tcc tgc tcc gca gag acc ttg cgt gcg ctg tct aag aat    787
Thr Tyr Glu Ser Cys Ser Ala Glu Thr Leu Arg Ala Leu Ser Lys Asn
    215                 220                 225

cag cgt cgc gtt gtt cca ggt ccg ctg tcc aag gcc atg aat ttt gtg    835
Gln Arg Arg Val Val Pro Gly Pro Leu Ser Lys Ala Met Asn Phe Val
230                 235                 240                 245

tcc tct gtt gct cca acc gct gtg ctc tcc cct gtt atg ggc tgg gtt    883
Ser Ser Val Ala Pro Thr Ala Val Leu Ser Pro Val Met Gly Trp Val
                250                 255                 260

tat aag aag atg ggt tagtttttaa aagtgtctga atc                      921
Tyr Lys Lys Met Gly
            265


<210> 174
<211> 266
<212> PRT
<213> Corynebacterium glutamicum

<400> 174
Met Ala Leu Pro Leu Pro Ser Lys Ser Ala Arg Ala Leu Val Thr Gly
  1               5                  10                  15

Ala Ser Gln Gly Ile Gly Leu Ala Ile Ala Lys Asp Leu Ala Arg Tyr
             20                  25                  30

Gly His Asn Leu Ile Leu Val Ala Arg Arg Glu Asp Val Leu Lys Glu
         35                  40                  45

Ile Ala Ala Asp Leu Glu Lys Lys His Gly Val Ile Val Glu Val Arg
     50                  55                  60

Pro Val Asp Leu Ser Asp Glu Pro Ala Arg Lys Val Leu Ile Asp Glu
 65                  70                  75                  80

Ile Lys Thr Arg Glu Ile Asn Ile Ile Ile Asn Ser Ala Gly Ile Ala
                 85                  90                  95

Ser Phe Gly Pro Phe Lys Asp Gln Asp Trp Ser Tyr Glu Thr Ala Gln
            100                 105                 110
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Phe Ser Leu Asn Ala Thr Ala Val Phe Glu Leu Thr His Ala Val Leu
        115                 120                 125

Gly Gly Met Ile Asp Arg Gly Thr Gly Ala Ile Cys Asn Val Gly Ser
    130                 135                 140

Ala Ala Gly Asn Val Pro Ile Pro Asn Asn Ala Thr Tyr Val Leu Thr
145                 150                 155                 160

Lys Ala Gly Val Asn Ala Phe Thr Glu Ala Met His Tyr Glu Leu Arg
                165                 170                 175

Gly Thr Gly Val Ala Cys Thr Leu Leu Ala Pro Gly Pro Val Arg Glu
            180                 185                 190

Ala Glu Ile Pro Glu Ser Glu Lys Ser Ile Val Asp Lys Val Val Pro
        195                 200                 205

Asp Phe Leu Trp Thr Thr Tyr Glu Ser Cys Ser Ala Glu Thr Leu Arg
    210                 215                 220

Ala Leu Ser Lys Asn Gln Arg Arg Val Val Pro Gly Pro Leu Ser Lys
225                 230                 235                 240

Ala Met Asn Phe Val Ser Ser Val Ala Pro Thr Ala Val Leu Ser Pro
                245                 250                 255

Val Met Gly Trp Val Tyr Lys Lys Met Gly
            260                 265


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<211> 1293
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(1270)
<223> RXN02062

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tcgctgcgca actgttttta gatggctaat ctttgaaatt atg aga gtc gga atg   115
                                           Met Arg Val Gly Met
                                            1               5

atg aca aga gag tat cca cca gag gtt tac ggc ggc gct ggc gtg cac   163
Met Thr Arg Glu Tyr Pro Pro Glu Val Tyr Gly Gly Ala Gly Val His
                10                  15                  20

gtc acc gaa ttg acc cga ttc atg cgt gag atc gct gaa gtt gat gtt   211
Val Thr Glu Leu Thr Arg Phe Met Arg Glu Ile Ala Glu Val Asp Val
            25                  30                  35

cac tgc atg ggt gca cct cgc gat atg gag gga gtt ttc gtc cac ggc   259
His Cys Met Gly Ala Pro Arg Asp Met Glu Gly Val Phe Val His Gly
        40                  45                  50

gtc gat cct gcc ttg gaa agc gcg aac cct gcg att aag aca ctg tcc   307
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Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala Ile Lys Thr Leu Ser
     55                  60                  65

acc ggt tta cgc atg gca gaa gct gca aac aac gtg gat gtc gtg cac     355
Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn Val Asp Val Val His
 70                  75                  80                  85

tca cac act tgg tat gca ggt ctt ggc ggc cac ctt gca gct cgt ctc     403
Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His Leu Ala Ala Arg Leu
                 90                  95                 100

cac ggc att cct cac gtg gct acc gcg cac tct ttg gag cca gat cgc     451
His Gly Ile Pro His Val Ala Thr Ala His Ser Leu Glu Pro Asp Arg
            105                 110                 115

cca tgg aag cgt gag cag ctt ggc ggt gga tac gac gtg tcc tcc tgg     499
Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr Asp Val Ser Ser Trp
        120                 125                 130

tct gaa aaa aat gcc atg gaa tac gct gac gcg gtc atc gct gtg tcg     547
Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala Val Ile Ala Val Ser
    135                 140                 145

gct cgc atg aaa gat tcc atc ctc gct gcg tac cct cgc atc gag ccg     595
Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr Pro Arg Ile Glu Pro
150                 155                 160                 165

gac aac gtg cgt gtt gtc ctc aac ggc atc gac act gag ttg tgg cag     643
Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp Thr Glu Leu Trp Gln
                170                 175                 180

cct cgc ccg act ttc gat gac gcg gaa gat tcc gta ctc cgc tcc cta     691
Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser Val Leu Arg Ser Leu
            185                 190                 195

ggc gtt gac cca cag cgg ccc atc gtc gca ttt gtc ggc cgc atc acc     739
Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe Val Gly Arg Ile Thr
        200                 205                 210

cgc caa aaa ggc gtc gag cac ctc atc aag gca gca gcg ctt ttc gac     787
Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala Ala Ala Leu Phe Asp
    215                 220                 225

gag tcc gtg cag ctt gtg ctc tgt gcc ggc gcg cca gac acc ccc gaa     835
Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala Pro Asp Thr Pro Glu
230                 235                 240                 245

atc gca gct cgc acc acc gcc ctg gtg gaa gaa ctc cag gca aag cgc     883
Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Glu Leu Gln Ala Lys Arg
                250                 255                 260

gaa ggc att ttc tgg gtt cag gac atg ctg ggc aag gac aaa atc caa     931
Glu Gly Ile Phe Trp Val Gln Asp Met Leu Gly Lys Asp Lys Ile Gln
            265                 270                 275

gag att ctc acc gct gct gac acc ttc gtg tgc cca tcc att tac gag     979
Glu Ile Leu Thr Ala Ala Asp Thr Phe Val Cys Pro Ser Ile Tyr Glu
        280                 285                 290

cca ctg ggc atc gtg aac ttg gaa gca atg gcc tgc aac acc gca gtt    1027
Pro Leu Gly Ile Val Asn Leu Glu Ala Met Ala Cys Asn Thr Ala Val
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295 300 305

gtc gca tcc gac gtt gga ggc atc cct gag gtt gtt gtc gac ggc acc 1075
Val Ala Ser Asp Val Gly Gly Ile Pro Glu Val Val Val Asp Gly Thr
310 315 320 325

acc ggc gcc ctc gtt cac tac gac gaa aat gat gtc gaa acc ttc gag 1123
Thr Gly Ala Leu Val His Tyr Asp Glu Asn Asp Val Glu Thr Phe Glu
330 335 340

cgc gat atc gcc gaa gcg gtg aat aaa atg gtc gct gat cga gag acc 1171
Arg Asp Ile Ala Glu Ala Val Asn Lys Met Val Ala Asp Arg Glu Thr
345 350 355

gca gcc aaa ttt ggt ctc gca ggg cgc gaa cgt gct atc aat gat ttc 1219
Ala Ala Lys Phe Gly Leu Ala Gly Arg Glu Arg Ala Ile Asn Asp Phe
360 365 370

tcc tgg gca acg att gct cag cag acc att gat gtg tac aaa tcc ttg 1267
Ser Trp Ala Thr Ile Ala Gln Gln Thr Ile Asp Val Tyr Lys Ser Leu
375 380 385

atg taaaaccgaa agccggggaa cct 1293
Met
390

<210> 176
<211> 390
<212> PRT
<213> Corynebacterium glutamicum

<400> 176
Met Arg Val Gly Met Met Thr Arg Glu Tyr Pro Pro Glu Val Tyr Gly
1 5 10 15

Gly Ala Gly Val His Val Thr Glu Leu Thr Arg Phe Met Arg Glu Ile
20 25 30

Ala Glu Val Asp Val His Cys Met Gly Ala Pro Arg Asp Met Glu Gly
35 40 45

Val Phe Val His Gly Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala
50 55 60

Ile Lys Thr Leu Ser Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn
65 70 75 80

Val Asp Val Val His Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His
85 90 95

Leu Ala Ala Arg Leu His Gly Ile Pro His Val Ala Thr Ala His Ser
100 105 110

Leu Glu Pro Asp Arg Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr
115 120 125

Asp Val Ser Ser Trp Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala
130 135 140

Val Ile Ala Val Ser Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr

145 150 155 160

Pro Arg Ile Glu Pro Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp
165 170 175

Thr Glu Leu Trp Gln Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser
180 185 190

Val Leu Arg Ser Leu Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe
195 200 205

Val Gly Arg Ile Thr Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala
210 215 220

Ala Ala Leu Phe Asp Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala
225 230 235 240

Pro Asp Thr Pro Glu Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Glu
245 250 255

Leu Gln Ala Lys Arg Glu Gly Ile Phe Trp Val Gln Asp Met Leu Gly
260 265 270

Lys Asp Lys Ile Gln Glu Ile Leu Thr Ala Ala Asp Thr Phe Val Cys
275 280 285

Pro Ser Ile Tyr Glu Pro Leu Gly Ile Val Asn Leu Glu Ala Met Ala
290 295 300

Cys Asn Thr Ala Val Val Ala Ser Asp Val Gly Gly Ile Pro Glu Val
305 310 315 320

Val Val Asp Gly Thr Thr Gly Ala Leu Val His Tyr Asp Glu Asn Asp
325 330 335

Val Glu Thr Phe Glu Arg Asp Ile Ala Glu Ala Val Asn Lys Met Val
340 345 350

Ala Asp Arg Glu Thr Ala Ala Lys Phe Gly Leu Ala Gly Arg Glu Arg
355 360 365

Ala Ile Asn Asp Phe Ser Trp Ala Thr Ile Ala Gln Gln Thr Ile Asp
370 375 380

Val Tyr Lys Ser Leu Met
385 390

<210> 177
<211> 1266
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1243)
<223> RXN02148

<400> 177
gcctcagact acggaatccc tgtgcaggtg gtatctgttg attcagcacc gttttatggt 60

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gcgcgtcgct actaagaaat agttcgtcag gagaatcttt gtg tct gca tcc cga   115
                                            Val Ser Ala Ser Arg
                                             1               5

aaa act ctc gtt gtg acc aat gat ttt cct cca cgg atc ggc gga atc   163
Lys Thr Leu Val Val Thr Asn Asp Phe Pro Pro Arg Ile Gly Gly Ile
                 10                  15                  20

caa agc tat ttg agg gat ttc atc gct act caa gat cct gag tcg atc   211
Gln Ser Tyr Leu Arg Asp Phe Ile Ala Thr Gln Asp Pro Glu Ser Ile
             25                  30                  35

gtg gtg ttt gcg tcg act caa aac gct gag gaa gcg cat gcc tac gac   259
Val Val Phe Ala Ser Thr Gln Asn Ala Glu Glu Ala His Ala Tyr Asp
         40                  45                  50

aag act ttg gac tat gag gtc att agg tgg cct cgt tcg gtg atg ctg   307
Lys Thr Leu Asp Tyr Glu Val Ile Arg Trp Pro Arg Ser Val Met Leu
     55                  60                  65

ccc acc cca aca acg gca cac gct atg gcg gag atc att cgt gag cga   355
Pro Thr Pro Thr Thr Ala His Ala Met Ala Glu Ile Ile Arg Glu Arg
 70                  75                  80                  85

gag atc gat aat gtg tgg ttc ggt gct gcg gct ccg ttg gcg ttg atg   403
Glu Ile Asp Asn Val Trp Phe Gly Ala Ala Ala Pro Leu Ala Leu Met
                 90                  95                 100

gca ggc aca gcg aag cag gca ggt gcg agc aag gtt att gcc tcc act   451
Ala Gly Thr Ala Lys Gln Ala Gly Ala Ser Lys Val Ile Ala Ser Thr
            105                 110                 115

cat ggg cat gag gtg ggg tgg tca atg ctt cct gga tcg aga caa tcg   499
His Gly His Glu Val Gly Trp Ser Met Leu Pro Gly Ser Arg Gln Ser
        120                 125                 130

ttg cgc aaa atc ggc act gag gtg gac gtg ctg act tat atc tcg cag   547
Leu Arg Lys Ile Gly Thr Glu Val Asp Val Leu Thr Tyr Ile Ser Gln
    135                 140                 145

tac acg ctg cgc aga ttc aaa agt gct ttt gga tcg cac ccg act ttt   595
Tyr Thr Leu Arg Arg Phe Lys Ser Ala Phe Gly Ser His Pro Thr Phe
150                 155                 160                 165

gaa cat ttg cct tcc ggc gtg gac gtt aag aga ttc act ccg gcc acg   643
Glu His Leu Pro Ser Gly Val Asp Val Lys Arg Phe Thr Pro Ala Thr
                170                 175                 180

cca gag gac aaa agc gca aca agg aaa aag cta gga ttc acg gac acc   691
Pro Glu Asp Lys Ser Ala Thr Arg Lys Lys Leu Gly Phe Thr Asp Thr
            185                 190                 195

acc ccg gtt att gcc tgt aac tcg cgt tta gtg ccg agg aaa ggc cag   739
Thr Pro Val Ile Ala Cys Asn Ser Arg Leu Val Pro Arg Lys Gly Gln
        200                 205                 210

gac tcg ctg atc aag gcg atg cca cag gtg att gcg gcg cgc cca gat   787
Asp Ser Leu Ile Lys Ala Met Pro Gln Val Ile Ala Ala Arg Pro Asp
    215                 220                 225

gcg cag ttg ctc att gtg ggc agt ggg cga tac gag tcg act ttg cgg   835
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Ala Gln Leu Leu Ile Val Gly Ser Gly Arg Tyr Glu Ser Thr Leu Arg
230 235 240 245

cgc ctt gcc act gac gtg agc cag aac gtg aaa ttc ctt ggg cgc ctt 883
Arg Leu Ala Thr Asp Val Ser Gln Asn Val Lys Phe Leu Gly Arg Leu
250 255 260

gaa tat caa gat atg atc aac acg ctt gcc gcc gca gat att ttc gcg 931
Glu Tyr Gln Asp Met Ile Asn Thr Leu Ala Ala Ala Asp Ile Phe Ala
265 270 275

atg cca gcg cgc acc cgc ggt ggc gga ctt gat gtt gaa ggc ttg ggc 979
Met Pro Ala Arg Thr Arg Gly Gly Gly Leu Asp Val Glu Gly Leu Gly
280 285 290

att gtc tat ctc gag gca caa gcc tgc gga gtg ccg gtg ata gcc ggc 1027
Ile Val Tyr Leu Glu Ala Gln Ala Cys Gly Val Pro Val Ile Ala Gly
295 300 305

acc tct ggc ggc gcg cca gag acg gtg act ccg gca act ggc ctg gtt 1075
Thr Ser Gly Gly Ala Pro Glu Thr Val Thr Pro Ala Thr Gly Leu Val
310 315 320 325

gtg gag ggg tcg gac gtc gat aag ctg tct gag ctt tta att gag ctt 1123
Val Glu Gly Ser Asp Val Asp Lys Leu Ser Glu Leu Leu Ile Glu Leu
330 335 340

ctc gac gat ccg atc cgc cgc gcc gcg atg ggc gct gca ggt agg gcg 1171
Leu Asp Asp Pro Ile Arg Arg Ala Ala Met Gly Ala Ala Gly Arg Ala
345 350 355

cat gtg gag gcc gaa tgg tcg tgg gaa atc atg ggg gag cgg ttg acc 1219
His Val Glu Ala Glu Trp Ser Trp Glu Ile Met Gly Glu Arg Leu Thr
360 365 370

aat att ttg cag agt gaa cca cga tgatggttgg acagctgttg ata 1266
Asn Ile Leu Gln Ser Glu Pro Arg
375 380

<210> 178
<211> 381
<212> PRT
<213> Corynebacterium glutamicum

<400> 178
Val Ser Ala Ser Arg Lys Thr Leu Val Val Thr Asn Asp Phe Pro Pro
1 5 10 15

Arg Ile Gly Gly Ile Gln Ser Tyr Leu Arg Asp Phe Ile Ala Thr Gln
20 25 30

Asp Pro Glu Ser Ile Val Val Phe Ala Ser Thr Gln Asn Ala Glu Glu
35 40 45

Ala His Ala Tyr Asp Lys Thr Leu Asp Tyr Glu Val Ile Arg Trp Pro
50 55 60

Arg Ser Val Met Leu Pro Thr Pro Thr Thr Ala His Ala Met Ala Glu
65 70 75 80

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Ile Ile Arg Glu Arg Glu Ile Asp Asn Val Trp Phe Gly Ala Ala Ala
                85                  90                  95

Pro Leu Ala Leu Met Ala Gly Thr Ala Lys Gln Ala Gly Ala Ser Lys
            100                 105                 110

Val Ile Ala Ser Thr His Gly His Glu Val Gly Trp Ser Met Leu Pro
        115                 120                 125

Gly Ser Arg Gln Ser Leu Arg Lys Ile Gly Thr Glu Val Asp Val Leu
    130                 135                 140

Thr Tyr Ile Ser Gln Tyr Thr Leu Arg Arg Phe Lys Ser Ala Phe Gly
145                 150                 155                 160

Ser His Pro Thr Phe Glu His Leu Pro Ser Gly Val Asp Val Lys Arg
                165                 170                 175

Phe Thr Pro Ala Thr Pro Glu Asp Lys Ser Ala Thr Arg Lys Lys Leu
            180                 185                 190

Gly Phe Thr Asp Thr Thr Pro Val Ile Ala Cys Asn Ser Arg Leu Val
        195                 200                 205

Pro Arg Lys Gly Gln Asp Ser Leu Ile Lys Ala Met Pro Gln Val Ile
    210                 215                 220

Ala Ala Arg Pro Asp Ala Gln Leu Leu Ile Val Gly Ser Gly Arg Tyr
225                 230                 235                 240

Glu Ser Thr Leu Arg Arg Leu Ala Thr Asp Val Ser Gln Asn Val Lys
                245                 250                 255

Phe Leu Gly Arg Leu Glu Tyr Gln Asp Met Ile Asn Thr Leu Ala Ala
            260                 265                 270

Ala Asp Ile Phe Ala Met Pro Ala Arg Thr Arg Gly Gly Gly Leu Asp
        275                 280                 285

Val Glu Gly Leu Gly Ile Val Tyr Leu Glu Ala Gln Ala Cys Gly Val
    290                 295                 300

Pro Val Ile Ala Gly Thr Ser Gly Gly Ala Pro Glu Thr Val Thr Pro
305                 310                 315                 320

Ala Thr Gly Leu Val Val Glu Gly Ser Asp Val Asp Lys Leu Ser Glu
                325                 330                 335

Leu Leu Ile Glu Leu Leu Asp Asp Pro Ile Arg Arg Ala Ala Met Gly
            340                 345                 350

Ala Ala Gly Arg Ala His Val Glu Ala Glu Trp Ser Trp Glu Ile Met
        355                 360                 365

Gly Glu Arg Leu Thr Asn Ile Leu Gln Ser Glu Pro Arg
    370                 375                 380
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<210> 179
<211> 1287
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1264)
<223> RXN02595

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ttcgcggatt tgtgcggggg agtgggtggg agagaaaacg gtg atc gtt gtg gcc 115
Val Ile Val Val Ala
1 5

atg gct tcc att atg gct tgt tta aaa gca gct aga ctg aat aac cct 163
Met Ala Ser Ile Met Ala Cys Leu Lys Ala Ala Arg Leu Asn Asn Pro
10 15 20

atg aag atc ctt ttg ttg tgc tgg cgt gat acc act cat cct caa ggt 211
Met Lys Ile Leu Leu Leu Cys Trp Arg Asp Thr Thr His Pro Gln Gly
25 30 35

ggc gga agt gaa cgc tat ctg gag cgg gtg ggt gag ttt ttg gcg gat 259
Gly Gly Ser Glu Arg Tyr Leu Glu Arg Val Gly Glu Phe Leu Ala Asp
40 45 50

cag ggc cat gag gtg gtg ttt cgt act gct ggg cac acg gat gcg cca 307
Gln Gly His Glu Val Val Phe Arg Thr Ala Gly His Thr Asp Ala Pro
55 60 65

cgg cgt tct ttc cgc gat ggt gtg agg tat tcc agg agc ggt ggg aag 355
Arg Arg Ser Phe Arg Asp Gly Val Arg Tyr Ser Arg Ser Gly Gly Lys
70 75 80 85

ttt agt gtg tat ccc aag gcg tgg gtg gcc atg atg ttg ggt cgt gtg 403
Phe Ser Val Tyr Pro Lys Ala Trp Val Ala Met Met Leu Gly Arg Val
90 95 100

ggg att ggc acg ttt tcc aag gtt gat gtg gtg gtg gat acg cag aat 451
Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val Val Asp Thr Gln Asn
105 110 115

ggc att ccg ttt ttt gga aag ttt ttc tcc ggt aag ccg act gtg ttg 499
Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly Lys Pro Thr Val Leu
120 125 130

ctc acg cat cat tgc cat aag gag cag tgg ccg gtg gtg ggt cgg gtg 547
Leu Thr His His Cys His Lys Glu Gln Trp Pro Val Val Gly Arg Val
135 140 145

ctg gcg aag gtt ggt tgg ctg att gag agc cag atc gcg ccg cgc gct 595
Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln Ile Ala Pro Arg Ala
150 155 160 165

tac aaa act gcg ccg tat gtg act gtt tca gag ccg agc gct gag gag 643
Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu Pro Ser Ala Glu Glu
170 175 180

ctc att gcg ttg ggt gtg gat cag cag cgg att cat atc gtg cgc aat 691
Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile His Ile Val Arg Asn
185 190 195

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ggc gtg gat ccc gtg ccg ctg cac acg ccg aag ctg gat cgc gat ggc     739
Gly Val Asp Pro Val Pro Leu His Thr Pro Lys Leu Asp Arg Asp Gly
        200                 205                 210

cag cat gcg gtg acg ttg tcg cgc ctg gtt ccg cac aag cag att gag     787
Gln His Ala Val Thr Leu Ser Arg Leu Val Pro His Lys Gln Ile Glu
    215                 220                 225

cat gcg atg gat gtc gtc gcg gcg ctc gac ggc gtg gtg ctg gat gta     835
His Ala Met Asp Val Val Ala Ala Leu Asp Gly Val Val Leu Asp Val
230                 235                 240                 245

gtc gaa agc ggt tgg tgg cag aag gaa ctg gtc gat tat gcc cgc acg     883
Val Glu Ser Gly Trp Trp Gln Lys Glu Leu Val Asp Tyr Ala Arg Thr
                250                 255                 260

ctg ggt gtg agc gat cgc gtg gtt ttc cac ggc cag gtc gcc gag gat     931
Leu Gly Val Ser Asp Arg Val Val Phe His Gly Gln Val Ala Glu Asp
            265                 270                 275

cac aag cac gcc ctg ttg gag cgc gcc acg att cat ctc atg cct tcg     979
His Lys His Ala Leu Leu Glu Arg Ala Thr Ile His Leu Met Pro Ser
        280                 285                 290

cgc aag gaa ggc tgg ggc ctg gcg gtc acg gag gcg gcg cag cac ggc     1027
Arg Lys Glu Gly Trp Gly Leu Ala Val Thr Glu Ala Ala Gln His Gly
    295                 300                 305

gtt ccg acg atc ggt tac cga agc tca ggc ggc ctg cgc gat tcc gtc     1075
Val Pro Thr Ile Gly Tyr Arg Ser Ser Gly Gly Leu Arg Asp Ser Val
310                 315                 320                 325

gtc gac ggc gaa acc ggc ctg ctt gtc gac tcc aag gcc gag ctt att     1123
Val Asp Gly Glu Thr Gly Leu Leu Val Asp Ser Lys Ala Glu Leu Ile
                330                 335                 340

tca gcc acc aaa acc ctg ctt atc gac gcc tcc ctc cgc tcc aag ctc     1171
Ser Ala Thr Lys Thr Leu Leu Ile Asp Ala Ser Leu Arg Ser Lys Leu
            345                 350                 355

ggc gcc agc gcg aag cag cgc gcc gaa aac tac aag tgg gac acc gcg     1219
Gly Ala Ser Ala Lys Gln Arg Ala Glu Asn Tyr Lys Trp Asp Thr Ala
        360                 365                 370

gga gcg cag ttc gag gaa cta ctt ctt ggt ctt gcg tcg aaa aag         1264
Gly Ala Gln Phe Glu Glu Leu Leu Leu Gly Leu Ala Ser Lys Lys
    375                 380                 385

tagtcccagc ggcaacgcca tcc                                           1287


<210> 180
<211> 388
<212> PRT
<213> Corynebacterium glutamicum

<400> 180
Val Ile Val Val Ala Met Ala Ser Ile Met Ala Cys Leu Lys Ala Ala
  1               5                  10                  15
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Arg Leu Asn Asn Pro Met Lys Ile Leu Leu Leu Cys Trp Arg Asp Thr
            20                  25                  30

Thr His Pro Gln Gly Gly Gly Ser Glu Arg Tyr Leu Glu Arg Val Gly
        35                  40                  45

Glu Phe Leu Ala Asp Gln Gly His Glu Val Val Phe Arg Thr Ala Gly
    50                  55                  60

His Thr Asp Ala Pro Arg Arg Ser Phe Arg Asp Gly Val Arg Tyr Ser
65                  70                  75                  80

Arg Ser Gly Gly Lys Phe Ser Val Tyr Pro Lys Ala Trp Val Ala Met
                85                  90                  95

Met Leu Gly Arg Val Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val
            100                 105                 110

Val Asp Thr Gln Asn Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly
        115                 120                 125

Lys Pro Thr Val Leu Leu Thr His His Cys His Lys Glu Gln Trp Pro
    130                 135                 140

Val Val Gly Arg Val Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln
145                 150                 155                 160

Ile Ala Pro Arg Ala Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu
                165                 170                 175

Pro Ser Ala Glu Glu Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile
            180                 185                 190

His Ile Val Arg Asn Gly Val Asp Pro Val Pro Leu His Thr Pro Lys
        195                 200                 205

Leu Asp Arg Asp Gly Gln His Ala Val Thr Leu Ser Arg Leu Val Pro
    210                 215                 220

His Lys Gln Ile Glu His Ala Met Asp Val Val Ala Ala Leu Asp Gly
225                 230                 235                 240

Val Val Leu Asp Val Val Glu Ser Gly Trp Trp Gln Lys Glu Leu Val
                245                 250                 255

Asp Tyr Ala Arg Thr Leu Gly Val Ser Asp Arg Val Val Phe His Gly
            260                 265                 270

Gln Val Ala Glu Asp His Lys His Ala Leu Leu Glu Arg Ala Thr Ile
        275                 280                 285

His Leu Met Pro Ser Arg Lys Glu Gly Trp Gly Leu Ala Val Thr Glu
    290                 295                 300

Ala Ala Gln His Gly Val Pro Thr Ile Gly Tyr Arg Ser Ser Gly Gly
305                 310                 315                 320

Leu Arg Asp Ser Val Val Asp Gly Glu Thr Gly Leu Leu Val Asp Ser
                325                 330                 335

Lys Ala Glu Leu Ile Ser Ala Thr Lys Thr Leu Leu Ile Asp Ala Ser
```

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            340                 345                 350

Leu Arg Ser Lys Leu Gly Ala Ser Ala Lys Gln Arg Ala Glu Asn Tyr
        355                 360                 365

Lys Trp Asp Thr Ala Gly Ala Gln Phe Glu Glu Leu Leu Leu Gly Leu
    370                 375                 380

Ala Ser Lys Lys
385


<210> 181
<211> 2334
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2311)
<223> RXS00148

<400> 181
ctttgagggc agcgcgcatg cgcccgatgg ttatttgaac atgacaattg atgccgcggc 60

gacgctggct gacctgctag atgctttggg agcttaaatc atg acg tcg atc cct   115
                                            Met Thr Ser Ile Pro
                                            1               5

aat ttt tca gac atc cca ttg act gct gag aca cgt gca tcg gag tca   163
Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr Arg Ala Ser Glu Ser
                10                  15                  20

cac aac gtt gac gcc ggc aag gtg tgg aac act ccc gaa ggc att gat   211
His Asn Val Asp Ala Gly Lys Val Trp Asn Thr Pro Glu Gly Ile Asp
            25                  30                  35

gtc aag cgc gta ttc acg cag gct gac cgc gac gag gcg caa gcg gcg   259
Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp Glu Ala Gln Ala Ala
        40                  45                  50

gga cat ccg gtg gat tct ttg cca ggt caa aag cca ttt atg cgc ggg   307
Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys Pro Phe Met Arg Gly
    55                  60                  65

ccg tac cca act atg tac acc aat cag ccg tgg acg att cgc cag tac   355
Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp Thr Ile Arg Gln Tyr
70                  75                  80                  85

gca ggc ttt tca acc gcc gcg gaa tcc aat gcg ttt tat cgg agg aac   403
Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala Phe Tyr Arg Arg Asn
                90                  95                  100

ctt gct gcg ggt caa aaa ggt ttg tcg gtt gcg ttc gat cta gcg acc   451
Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala Phe Asp Leu Ala Thr
            105                 110                 115

cac cgc ggt tat gac tcg gat aat gag cgc gtg gtc ggc gat gtg ggt   499
His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val Val Gly Asp Val Gly
        120                 125                 130
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atg gcc ggc gtg gcg att gat tcg att ttg gat atg cgt cag ctg ttt     547
Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp Met Arg Gln Leu Phe
    135                 140                 145

gat ggc att gat ttg tcc agc gtg tcg gtg tcg atg acc atg aat ggc     595
Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser Met Thr Met Asn Gly
150                 155                 160                 165

gct gtg ctg ccg att ctt gcg ttc tat atc gtg gcg gct gag gaa caa     643
Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val Ala Ala Glu Glu Gln
                170                 175                 180

ggt gtg ggt ccg gag cag ctt gcg ggc acg atc cag aat gac atc ttg     691
Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile Gln Asn Asp Ile Leu
            185                 190                 195

aaa gaa ttt atg gtg cgc aac acc tat att tat ccg ccg aag ccg tcg     739
Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr Pro Pro Lys Pro Ser
        200                 205                 210

atg cgc atc att tcc aac atc ttt gag tac acc tcc ttg aag atg cca     787
Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr Ser Leu Lys Met Pro
    215                 220                 225

cgt ttt aac tcc att tcg att tct ggc tat cac atc cag gaa gcg gga     835
Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His Ile Gln Glu Ala Gly
230                 235                 240                 245

gcg act gcc gat ttg gag ctg gcc tac act ctg gcg gat ggt att gaa     883
Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu Ala Asp Gly Ile Glu
                250                 255                 260

tac atc cgt gca ggt aaa gag gta ggc ctt gac gtg gat aag ttc gcg     931
Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp Val Asp Lys Phe Ala
            265                 270                 275

cct cgt ctg tcc ttc ttc tgg ggt att tct atg tac acc ttc atg gag     979
Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met Tyr Thr Phe Met Glu
        280                 285                 290

atc gca aag ctg cgt gcg gga cga ctg ctg tgg agc gag ttg gtg gca     1027
Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp Ser Glu Leu Val Ala
    295                 300                 305

aaa ttc gat ccg aaa aac gcc aag tcc cag tcg ctg cgc acg cac tcg     1075
Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser Leu Arg Thr His Ser
310                 315                 320                 325

cag acc tct ggt tgg tcg ttg acc gcg cag gat gtg tac aac aac gtc     1123
Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp Val Tyr Asn Asn Val
                330                 335                 340

gcc cgc acc gcg att gag gcg atg gct gca acc cag ggc cac acc cag     1171
Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr Gln Gly His Thr Gln
            345                 350                 355

tcg ctg cac acc aat gca ctt gat gag gcg ttg gcg ctg ccc acc gat     1219
Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu Ala Leu Pro Thr Asp
        360                 365                 370

ttc tct gct cgt atc gcc cga aac acc cag ctg ttg ctg cag cag gaa     1267
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Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu Leu Leu Gln Gln Glu
    375                 380                 385

tct ggc acg gtg cgt cca gtt gat cca tgg gcg ggc tcc tat tac gtg     1315
Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala Gly Ser Tyr Tyr Val
390                 395                 400                 405

gag tgg ttg acc aat gag ctg gct aac cgc gcg cgc aag cac atc gat     1363
Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala Arg Lys His Ile Asp
                410                 415                 420

gag gtg gag gaa gcc ggc gga atg gcg cag gcc acc gcg cag gga att     1411
Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala Thr Ala Gln Gly Ile
            425                 430                 435

cct aag ctg cgc att gag gaa tca gcg gca cgc acc cag gct cgc att     1459
Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg Thr Gln Ala Arg Ile
        440                 445                 450

gat tcc ggc cgc cag gcg ctg atc ggc gtg aat cgc tac gtg gcg gaa     1507
Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn Arg Tyr Val Ala Glu
    455                 460                 465

gaa gat gag gaa att gaa gtc ctc aag gtt gac aac acc aag gtt cgc     1555
Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp Asn Thr Lys Val Arg
470                 475                 480                 485

gca gaa cag ttg gct aaa ctc gcg caa ctg aaa gca gag cgc aac gat     1603
Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys Ala Glu Arg Asn Asp
                490                 495                 500

gcg gaa gtc aag gct gcg ctg gat gcg ttg aca gct gct gcc cgc aac     1651
Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr Ala Ala Ala Arg Asn
            505                 510                 515

gag cat aaa gag cca ggg gat ttg gat cag aac ctg ctc aaa ctt gcc     1699
Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn Leu Leu Lys Leu Ala
        520                 525                 530

gtc gat gct gcg cgc gca aaa gct acc att gga gag atc tcc gat gct     1747
Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly Glu Ile Ser Asp Ala
    535                 540                 545

ttg gaa gtt gtc ttt ggc cgc cac gaa gca gaa atc agg acg ctg tct     1795
Leu Glu Val Val Phe Gly Arg His Glu Ala Glu Ile Arg Thr Leu Ser
550                 555                 560                 565

ggc gtg tac aag gat gag gtt gga aag gaa ggc aca gtg agc aac gtc     1843
Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly Thr Val Ser Asn Val
                570                 575                 580

gaa cgc gcg atc gcc ctg gct gac gcc ttt gag gct gag gaa ggc cgc     1891
Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu Ala Glu Glu Gly Arg
            585                 590                 595

cgc cca cgt atc ttt att gcc aag atg ggc cag gat gga cat gac cgt     1939
Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln Asp Gly His Asp Arg
        600                 605                 610

gga cag aag gtt gtc gcg tct gcc tat gct gac ctg ggc atg gac gtg     1987
Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp Leu Gly Met Asp Val
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    615                 620                 625

gat gtt gga ccg ctg ttt caa act cca gcc gaa gct gcc cgc gcc gcc     2035
Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu Ala Ala Arg Ala Ala
630                 635                 640                 645

gtg gac gcc gat gtt cac gtg gtg ggt atg tct tcg ctg gca gca ggc     2083
Val Asp Ala Asp Val His Val Val Gly Met Ser Ser Leu Ala Ala Gly
                650                 655                 660

cac ctc acc ttg ctg ccc gag ctg aag aaa gaa ctt gca gct ctt ggc     2131
His Leu Thr Leu Leu Pro Glu Leu Lys Lys Glu Leu Ala Ala Leu Gly
            665                 670                 675

cgc gat gac att ctg gtc acc gtg ggc ggc gtc att ccg ccg ggc gat     2179
Arg Asp Asp Ile Leu Val Thr Val Gly Gly Val Ile Pro Pro Gly Asp
        680                 685                 690

ttc cag gat ctc tac gat atg ggt gcc gcc gcg att tac cct tca gga     2227
Phe Gln Asp Leu Tyr Asp Met Gly Ala Ala Ala Ile Tyr Pro Ser Gly
    695                 700                 705

acc gtc atc gcg gag tcg gcg atc gat ctg atc acc cga ctc gcc gca     2275
Thr Val Ile Ala Glu Ser Ala Ile Asp Leu Ile Thr Arg Leu Ala Ala
710                 715                 720                 725

cac ctg ggc ttt gac ctg gat gtg gat gtg aat gaa tgatcacggt          2321
His Leu Gly Phe Asp Leu Asp Val Asp Val Asn Glu
                730                 735

ttcctagaag aca                                                      2334


<210> 182
<211> 737
<212> PRT
<213> Corynebacterium glutamicum

<400> 182
Met Thr Ser Ile Pro Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr
  1               5                  10                  15

Arg Ala Ser Glu Ser His Asn Val Asp Ala Gly Lys Val Trp Asn Thr
             20                  25                  30

Pro Glu Gly Ile Asp Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp
         35                  40                  45

Glu Ala Gln Ala Ala Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys
     50                  55                  60

Pro Phe Met Arg Gly Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp
 65                  70                  75                  80

Thr Ile Arg Gln Tyr Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala
                 85                  90                  95

Phe Tyr Arg Arg Asn Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala
            100                 105                 110

Phe Asp Leu Ala Thr His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val
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115 120 125

Val Gly Asp Val Gly Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp
130 135 140

Met Arg Gln Leu Phe Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser
145 150 155 160

Met Thr Met Asn Gly Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val
165 170 175

Ala Ala Glu Glu Gln Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile
180 185 190

Gln Asn Asp Ile Leu Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr
195 200 205

Pro Pro Lys Pro Ser Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr
210 215 220

Ser Leu Lys Met Pro Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His
225 230 235 240

Ile Gln Glu Ala Gly Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu
245 250 255

Ala Asp Gly Ile Glu Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp
260 265 270

Val Asp Lys Phe Ala Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met
275 280 285

Tyr Thr Phe Met Glu Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp
290 295 300

Ser Glu Leu Val Ala Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser
305 310 315 320

Leu Arg Thr His Ser Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp
325 330 335

Val Tyr Asn Asn Val Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr
340 345 350

Gln Gly His Thr Gln Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu
355 360 365

Ala Leu Pro Thr Asp Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu
370 375 380

Leu Leu Gln Gln Glu Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala
385 390 395 400

Gly Ser Tyr Tyr Val Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala
405 410 415

Arg Lys His Ile Asp Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala
420 425 430

Thr Ala Gln Gly Ile Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg
435 440 445

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Thr Gln Ala Arg Ile Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn
    450                 455                 460

Arg Tyr Val Ala Glu Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp
465                 470                 475                 480

Asn Thr Lys Val Arg Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys
                485                 490                 495

Ala Glu Arg Asn Asp Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr
            500                 505                 510

Ala Ala Ala Arg Asn Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn
        515                 520                 525

Leu Leu Lys Leu Ala Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly
    530                 535                 540

Glu Ile Ser Asp Ala Leu Glu Val Val Phe Gly Arg His Glu Ala Glu
545                 550                 555                 560

Ile Arg Thr Leu Ser Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly
                565                 570                 575

Thr Val Ser Asn Val Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu
            580                 585                 590

Ala Glu Glu Gly Arg Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln
        595                 600                 605

Asp Gly His Asp Arg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp
    610                 615                 620

Leu Gly Met Asp Val Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu
625                 630                 635                 640

Ala Ala Arg Ala Ala Val Asp Ala Asp Val His Val Val Gly Met Ser
                645                 650                 655

Ser Leu Ala Ala Gly His Leu Thr Leu Leu Pro Glu Leu Lys Lys Glu
            660                 665                 670

Leu Ala Ala Leu Gly Arg Asp Asp Ile Leu Val Thr Val Gly Gly Val
        675                 680                 685

Ile Pro Pro Gly Asp Phe Gln Asp Leu Tyr Asp Met Gly Ala Ala Ala
    690                 695                 700

Ile Tyr Pro Ser Gly Thr Val Ile Ala Glu Ser Ala Ile Asp Leu Ile
705                 710                 715                 720

Thr Arg Leu Ala Ala His Leu Gly Phe Asp Leu Asp Val Asp Val Asn
                725                 730                 735

Glu
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<210> 183
<211> 1971

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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1948)
<223> RXS00149

<400> 183
ttttcgtagg taaacacagg tgaaggcttt acaagcttgt gaactcccta cacaaaagca 60

atccaatagc tatccataag caagagaaag taagtctacg ttg act gat ctc aca   115
                                          Leu Thr Asp Leu Thr
                                          1               5

aag act gcg gtg ccc gag gaa ctt tca gag aac ctc gaa act tgg tac   163
Lys Thr Ala Val Pro Glu Glu Leu Ser Glu Asn Leu Glu Thr Trp Tyr
                10                  15                  20

aag gct gtg gcc ggt gtt ttc gcg cgc aca cag aaa aaa gac atc ggc   211
Lys Ala Val Ala Gly Val Phe Ala Arg Thr Gln Lys Lys Asp Ile Gly
            25                  30                  35

gac att gcc gta gat gtg tgg aag aaa ctc atc gtc act aca ccg gat   259
Asp Ile Ala Val Asp Val Trp Lys Lys Leu Ile Val Thr Thr Pro Asp
        40                  45                  50

ggt gtt gat atc aat ccg ctg tac acc aga gca gat gag tcc cag agg   307
Gly Val Asp Ile Asn Pro Leu Tyr Thr Arg Ala Asp Glu Ser Gln Arg
    55                  60                  65

aaa ttc act gag gtt cct ggt gag ttt ccc ttc act agg gga acc act   355
Lys Phe Thr Glu Val Pro Gly Glu Phe Pro Phe Thr Arg Gly Thr Thr
70                  75                  80                  85

gtt gat ggt gaa cgc gtt ggt tgg ggt gtt act gag act ttc gga cat   403
Val Asp Gly Glu Arg Val Gly Trp Gly Val Thr Glu Thr Phe Gly His
                90                  95                  100

gac agc ccg aag aat atc aac gct gcg gtg ctg aat gct ctg aat tct   451
Asp Ser Pro Lys Asn Ile Asn Ala Ala Val Leu Asn Ala Leu Asn Ser
            105                 110                 115

ggc acc acc aca ttg ggt ttt gag ttc tct gag gaa ttc acg gca gct   499
Gly Thr Thr Thr Leu Gly Phe Glu Phe Ser Glu Glu Phe Thr Ala Ala
        120                 125                 130

gat ctt aaa gtt gct ctc gaa ggc gtg tat ctc aac atg gct ccg ttg   547
Asp Leu Lys Val Ala Leu Glu Gly Val Tyr Leu Asn Met Ala Pro Leu
    135                 140                 145

ctg att cat gcg ggt gga tcc acg tca gag gtt gca gcg gcg ttg tat   595
Leu Ile His Ala Gly Gly Ser Thr Ser Glu Val Ala Ala Ala Leu Tyr
150                 155                 160                 165

acg ttg gcg gag gaa gcc gga acg ttt ttt gct gcg ttg acc ttg ggt   643
Thr Leu Ala Glu Glu Ala Gly Thr Phe Phe Ala Ala Leu Thr Leu Gly
                170                 175                 180

tct cgt cct ttg acg gcg cag gtt gat ggt tcg cac agt gac acc att   691
Ser Arg Pro Leu Thr Ala Gln Val Asp Gly Ser His Ser Asp Thr Ile
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185 190 195

gaa gaa gca gtt cag ttg gca gtg aat gct tcc aag cgt gcg aat gtg 739
Glu Glu Ala Val Gln Leu Ala Val Asn Ala Ser Lys Arg Ala Asn Val
200 205 210

cgc gct atc ttg gtg gat ggt tcc agt ttt tcc aac cag ggc gcg tcg 787
Arg Ala Ile Leu Val Asp Gly Ser Ser Phe Ser Asn Gln Gly Ala Ser
215 220 225

gat gct caa gaa att ggt cta agt atc gcc gcc ggt gtg gat tat gtc 835
Asp Ala Gln Glu Ile Gly Leu Ser Ile Ala Ala Gly Val Asp Tyr Val
230 235 240 245

cgt cgc ttg gtc gat gca ggc ctt tcc acg gaa gct gca ctt aag cag 883
Arg Arg Leu Val Asp Ala Gly Leu Ser Thr Glu Ala Ala Leu Lys Gln
250 255 260

gtg gcg ttc cgt ttt gcg gtc acc gat gag cag ttc gcg cag att tct 931
Val Ala Phe Arg Phe Ala Val Thr Asp Glu Gln Phe Ala Gln Ile Ser
265 270 275

aag ctg cgt gtg gct cga cgt ctg tgg gcc agg gtg tgt gag gtg ctt 979
Lys Leu Arg Val Ala Arg Arg Leu Trp Ala Arg Val Cys Glu Val Leu
280 285 290

ggt ttt cca gag ctg gcc gta gca cca cag cat gcg gtg act gca cga 1027
Gly Phe Pro Glu Leu Ala Val Ala Pro Gln His Ala Val Thr Ala Arg
295 300 305

gcg atg ttt agc cag cgt gat ccg tgg gtg aat atg ctg cgc agt act 1075
Ala Met Phe Ser Gln Arg Asp Pro Trp Val Asn Met Leu Arg Ser Thr
310 315 320 325

gtt gca gct ttc gct gca ggc gtc ggt gga gca acc gat gtg gag gtt 1123
Val Ala Ala Phe Ala Ala Gly Val Gly Gly Ala Thr Asp Val Glu Val
330 335 340

cgt act ttt gat gat gcg atc cca gat gga gtt cct gga gtg tcg agg 1171
Arg Thr Phe Asp Asp Ala Ile Pro Asp Gly Val Pro Gly Val Ser Arg
345 350 355

aat ttc gct cac cgc atc gcg cgc aat act aat ttg ttg ttg cta gaa 1219
Asn Phe Ala His Arg Ile Ala Arg Asn Thr Asn Leu Leu Leu Leu Glu
360 365 370

gag tca cat ctt ggt cac gtg gtt gat cct gct ggt gga tca tat ttc 1267
Glu Ser His Leu Gly His Val Val Asp Pro Ala Gly Gly Ser Tyr Phe
375 380 385

gtg gag agc ttc acc gat gat cta gcg gag aag gcg tgg gct gtg ttc 1315
Val Glu Ser Phe Thr Asp Asp Leu Ala Glu Lys Ala Trp Ala Val Phe
390 395 400 405

agt ggc atc gaa gct gag ggc gga tac agt gca gct tgt gca tcc ggc 1363
Ser Gly Ile Glu Ala Glu Gly Gly Tyr Ser Ala Ala Cys Ala Ser Gly
410 415 420

acg gtg act gcc atg ctt gat cag acg tgg gag cag act cgc gct gat 1411
Thr Val Thr Ala Met Leu Asp Gln Thr Trp Glu Gln Thr Arg Ala Asp
425 430 435

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gtg gcg tcg aga aag aag aag ctc act gga att aat gag ttc ccg aac    1459
Val Ala Ser Arg Lys Lys Lys Leu Thr Gly Ile Asn Glu Phe Pro Asn
        440                 445                 450

ttg gcg gag tct ccg ctg cca gct gat cgt cgg gta gaa cct gca ggt    1507
Leu Ala Glu Ser Pro Leu Pro Ala Asp Arg Arg Val Glu Pro Ala Gly
    455                 460                 465

gtg cgt cga tgg gca gcg gat ttt gaa gcg ctg cgc aat cgt tcg gat    1555
Val Arg Arg Trp Ala Ala Asp Phe Glu Ala Leu Arg Asn Arg Ser Asp
470                 475                 480                 485

gct ttc ttg gaa aag aac ggc gcg agg cca cag atc acg atg att cct    1603
Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln Ile Thr Met Ile Pro
                490                 495                 500

ctg gga ccg ttg tcc aag cac aat att cgc act ggt ttt act tcc aac    1651
Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr Gly Phe Thr Ser Asn
            505                 510                 515

ctg ttg gct tcc ggt ggc att gaa gca atc aac ccg ggt caa ctt gtt    1699
Leu Leu Ala Ser Gly Gly Ile Glu Ala Ile Asn Pro Gly Gln Leu Val
        520                 525                 530

ccc ggc act gac gct ttt gca gaa gct gca cag gcc gca ggc att gta    1747
Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln Ala Ala Gly Ile Val
    535                 540                 545

gtg gtg tgt gga acg gac caa gag tat gcc gaa acg ggg gag gga gcc    1795
Val Val Cys Gly Thr Asp Gln Glu Tyr Ala Glu Thr Gly Glu Gly Ala
550                 555                 560                 565

gtc gaa aag ctc cgc gaa gcg ggc gtt gag cgc atc ctg ctt gct ggc    1843
Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg Ile Leu Leu Ala Gly
                570                 575                 580

gcg ccg aag agc ttt gag ggc agc gcg cat gcg ccc gat ggt tat ttg    1891
Ala Pro Lys Ser Phe Glu Gly Ser Ala His Ala Pro Asp Gly Tyr Leu
            585                 590                 595

aac atg aca att gat gcc gcg gcg acg ctg gct gac ctg cta gat gct    1939
Asn Met Thr Ile Asp Ala Ala Ala Thr Leu Ala Asp Leu Leu Asp Ala
        600                 605                 610

ttg gga gct taaatcatga cgtcgatccc taa                              1971
Leu Gly Ala
    615


&lt;210&gt; 184
&lt;211&gt; 616
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 184
Leu Thr Asp Leu Thr Lys Thr Ala Val Pro Glu Glu Leu Ser Glu Asn
  1               5                  10                  15

Leu Glu Thr Trp Tyr Lys Ala Val Ala Gly Val Phe Ala Arg Thr Gln
             20                  25                  30
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Lys Lys Asp Ile Gly Asp Ile Ala Val Asp Val Trp Lys Lys Leu Ile
        35                  40                  45

Val Thr Thr Pro Asp Gly Val Asp Ile Asn Pro Leu Tyr Thr Arg Ala
    50                  55                  60

Asp Glu Ser Gln Arg Lys Phe Thr Glu Val Pro Gly Glu Phe Pro Phe
65                  70                  75                  80

Thr Arg Gly Thr Thr Val Asp Gly Glu Arg Val Gly Trp Gly Val Thr
                85                  90                  95

Glu Thr Phe Gly His Asp Ser Pro Lys Asn Ile Asn Ala Ala Val Leu
            100                 105                 110

Asn Ala Leu Asn Ser Gly Thr Thr Thr Leu Gly Phe Glu Phe Ser Glu
        115                 120                 125

Glu Phe Thr Ala Ala Asp Leu Lys Val Ala Leu Glu Gly Val Tyr Leu
    130                 135                 140

Asn Met Ala Pro Leu Leu Ile His Ala Gly Gly Ser Thr Ser Glu Val
145                 150                 155                 160

Ala Ala Ala Leu Tyr Thr Leu Ala Glu Glu Ala Gly Thr Phe Phe Ala
                165                 170                 175

Ala Leu Thr Leu Gly Ser Arg Pro Leu Thr Ala Gln Val Asp Gly Ser
            180                 185                 190

His Ser Asp Thr Ile Glu Glu Ala Val Gln Leu Ala Val Asn Ala Ser
        195                 200                 205

Lys Arg Ala Asn Val Arg Ala Ile Leu Val Asp Gly Ser Ser Phe Ser
    210                 215                 220

Asn Gln Gly Ala Ser Asp Ala Gln Glu Ile Gly Leu Ser Ile Ala Ala
225                 230                 235                 240

Gly Val Asp Tyr Val Arg Arg Leu Val Asp Ala Gly Leu Ser Thr Glu
                245                 250                 255

Ala Ala Leu Lys Gln Val Ala Phe Arg Phe Ala Val Thr Asp Glu Gln
            260                 265                 270

Phe Ala Gln Ile Ser Lys Leu Arg Val Ala Arg Arg Leu Trp Ala Arg
        275                 280                 285

Val Cys Glu Val Leu Gly Phe Pro Glu Leu Ala Val Ala Pro Gln His
    290                 295                 300

Ala Val Thr Ala Arg Ala Met Phe Ser Gln Arg Asp Pro Trp Val Asn
305                 310                 315                 320

Met Leu Arg Ser Thr Val Ala Ala Phe Ala Ala Gly Val Gly Gly Ala
                325                 330                 335

Thr Asp Val Glu Val Arg Thr Phe Asp Asp Ala Ile Pro Asp Gly Val
            340                 345                 350
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Pro Gly Val Ser Arg Asn Phe Ala His Arg Ile Ala Arg Asn Thr Asn
        355                 360                 365

Leu Leu Leu Leu Glu Glu Ser His Leu Gly His Val Val Asp Pro Ala
    370                 375                 380

Gly Gly Ser Tyr Phe Val Glu Ser Phe Thr Asp Asp Leu Ala Glu Lys
385                 390                 395                 400

Ala Trp Ala Val Phe Ser Gly Ile Glu Ala Glu Gly Gly Tyr Ser Ala
                405                 410                 415

Ala Cys Ala Ser Gly Thr Val Thr Ala Met Leu Asp Gln Thr Trp Glu
            420                 425                 430

Gln Thr Arg Ala Asp Val Ala Ser Arg Lys Lys Lys Leu Thr Gly Ile
        435                 440                 445

Asn Glu Phe Pro Asn Leu Ala Glu Ser Pro Leu Pro Ala Asp Arg Arg
    450                 455                 460

Val Glu Pro Ala Gly Val Arg Arg Trp Ala Ala Asp Phe Glu Ala Leu
465                 470                 475                 480

Arg Asn Arg Ser Asp Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln
                485                 490                 495

Ile Thr Met Ile Pro Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr
            500                 505                 510

Gly Phe Thr Ser Asn Leu Leu Ala Ser Gly Gly Ile Glu Ala Ile Asn
        515                 520                 525

Pro Gly Gln Leu Val Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln
    530                 535                 540

Ala Ala Gly Ile Val Val Val Cys Gly Thr Asp Gln Glu Tyr Ala Glu
545                 550                 555                 560

Thr Gly Glu Gly Ala Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg
                565                 570                 575

Ile Leu Leu Ala Gly Ala Pro Lys Ser Phe Glu Gly Ser Ala His Ala
            580                 585                 590

Pro Asp Gly Tyr Leu Asn Met Thr Ile Asp Ala Ala Ala Thr Leu Ala
        595                 600                 605

Asp Leu Leu Asp Ala Leu Gly Ala
    610                 615
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<210> 185
<211> 1179
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1156)
<223> RXS02106

<400> 185
ggtcgccgct tttcgacgcc cgcctgcggc gggatgactg tgatggaggg gcgcgtcgac 60

aagcaaaatc tctttagcaa attcggttac tgtggggcgc atg aat aac cat ttt 115
Met Asn Asn His Phe
1 5

gag ctc aaa gta cct ggt gga aag ctt gtc gtc gtt gat gtg acc acc 163
Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val Val Asp Val Thr Thr
10 15 20

gat ctg gat tcc att gct gac gtg aag att tcc ggc gat ttc ttc ctc 211
Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser Gly Asp Phe Phe Leu
25 30 35

gaa ccc gat gag gca ttc ttc gcc ctt ggc cgg gcg ctg cag ggg gcg 259
Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg Ala Leu Gln Gly Ala
40 45 50

tcg gtg ggt gat aac act gat cgt ttg cag gca aag ttg gat gca gcg 307
Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala Lys Leu Asp Ala Ala
55 60 65

ttg gcg gaa tat gat gac gtt gag cta cac ggc ttt agc act gcg gat 355
Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly Phe Ser Thr Ala Asp
70 75 80 85

att gct tta gct gtg cgt cgg gca gtc acc ggc gcg caa gat ttc acc 403
Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly Ala Gln Asp Phe Thr
90 95 100

gat tat gaa tgg gaa atc ctg cac cca ggg gtg ctt cct acc cca ctt 451
Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val Leu Pro Thr Pro Leu
105 110 115

aac gtt gcg ttg gat gag ctc ctt ttg gac caa gtt gcc agt ggt cag 499
Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln Val Ala Ser Gly Gln
120 125 130

cgt ggc ccg acg atg cgc att tgg gat tgg gat gat cgc gcc aca gtg 547
Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp Asp Arg Ala Thr Val
135 140 145

atc ggt agt ttc cag tca tat gtc aat gaa atc aac caa gaa ggc gtt 595
Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile Asn Gln Glu Gly Val
150 155 160 165

aat gaa cat ggt gtg acc gtg gta cga cgc atg tct ggt ggc ggt gca 643
Asn Glu His Gly Val Thr Val Val Arg Arg Met Ser Gly Gly Gly Ala
170 175 180

atg ttt atg gag ggc ggc aac tgc atc acc tat tcc ctg tat gca ccg 691
Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr Ser Leu Tyr Ala Pro
185 190 195

gaa tct ctc gtt gct ggt ttg agc tat gag cag tcc tat gaa tat ttg 739
Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln Ser Tyr Glu Tyr Leu
200 205 210

gat cgt tgg gtg att gct gcg ctg aag aca cac gat gtt gac gct tgg 787

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Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His Asp Val Asp Ala Trp
    215                 220                 225

tac gtg cct atc aat gac atc acc tcc acc ggc gga aaa atc ggt ggc    835
Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly Gly Lys Ile Gly Gly
230                 235                 240                 245

gct gca cag aaa cgt cgc agt ggc gca gtc ctc cac cac gtg acc atg    883
Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu His His Val Thr Met
                250                 255                 260

tcc tat gac atc gat gcg gac atg atg acc cag gtg ttg cgc att gga    931
Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln Val Leu Arg Ile Gly
            265                 270                 275

aag gtg aag att tcc gac aag ggt ctt cgc agc gca aag aag cgc gtt    979
Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser Ala Lys Lys Arg Val
        280                 285                 290

gat cct ctg cgc cgc caa aca ggt gca tca cgt gag caa atc atc gac    1027
Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg Glu Gln Ile Ile Asp
    295                 300                 305

acc cta aag tcc aca ttc agt gct agg tac ggc gcg caa gaa gta gag    1075
Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly Ala Gln Glu Val Glu
310                 315                 320                 325

ctc agc gat gaa gat ttc gcg gca ggc cac gac cta gta aaa acc aaa    1123
Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp Leu Val Lys Thr Lys
                330                 335                 340

tac gcc acc gag gag tgg act aag cga gtt caa tagtttctat ggatctgcac 1176
Tyr Ala Thr Glu Glu Trp Thr Lys Arg Val Gln
            345                 350

aag                                                                1179


<210> 186
<211> 352
<212> PRT
<213> Corynebacterium glutamicum

<400> 186
Met Asn Asn His Phe Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val
  1               5                  10                  15

Val Asp Val Thr Thr Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser
             20                  25                  30

Gly Asp Phe Phe Leu Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg
         35                  40                  45

Ala Leu Gln Gly Ala Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala
     50                  55                  60

Lys Leu Asp Ala Ala Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly
 65                  70                  75                  80

Phe Ser Thr Ala Asp Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly
                 85                  90                  95
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Ala Gln Asp Phe Thr Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val
            100                 105                 110

Leu Pro Thr Pro Leu Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln
        115                 120                 125

Val Ala Ser Gly Gln Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp
    130                 135                 140

Asp Arg Ala Thr Val Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile
145                 150                 155                 160

Asn Gln Glu Gly Val Asn Glu His Gly Val Thr Val Val Arg Arg Met
                165                 170                 175

Ser Gly Gly Gly Ala Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr
            180                 185                 190

Ser Leu Tyr Ala Pro Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln
        195                 200                 205

Ser Tyr Glu Tyr Leu Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His
    210                 215                 220

Asp Val Asp Ala Trp Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly
225                 230                 235                 240

Gly Lys Ile Gly Gly Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu
                245                 250                 255

His His Val Thr Met Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln
            260                 265                 270

Val Leu Arg Ile Gly Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser
        275                 280                 285

Ala Lys Lys Arg Val Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg
    290                 295                 300

Glu Gln Ile Ile Asp Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly
305                 310                 315                 320

Ala Gln Glu Val Glu Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp
                325                 330                 335

Leu Val Lys Thr Lys Tyr Ala Thr Glu Glu Trp Thr Lys Arg Val Gln
            340                 345                 350
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<210> 187
<211> 876
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(853)

<223> RXS01746

<400> 187

aaaccgccac tcccctttca ctggggagtg gcggttttgt cgtttcatgc atgcagtgtg 60

tgacttatca accttgttag ggctagggtg gatatctatc atg act gca cca aga 115
Met Thr Ala Pro Arg
1 5

gat cct ttt ttc ccc gca gat ctt tct atc cgc gcg tct gca gag ccc 163
Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg Ala Ser Ala Glu Pro
10 15 20

att gaa att cag cgg ttg ggt ttg atc gat tat caa gag gcc tgg gat 211
Ile Glu Ile Gln Arg Leu Gly Leu Ile Asp Tyr Gln Glu Ala Trp Asp
25 30 35

tat caa gca gag ctt gct acc cgt agg gct aat gat gaa atc cct gat 259
Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn Asp Glu Ile Pro Asp
40 45 50

cag ctg ctt att ttg gag cac ccg tcg gtg tat acc gca ggt aag cgc 307
Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg
55 60 65

acc cag ccg gaa gat ctt ccc acc aac gga ctg ccg gtg atc aat gct 355
Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu Pro Val Ile Asn Ala
70 75 80 85

gat cgt ggt ggt cgc atc acg tgg cat ggt cct ggc caa ttg gtg atc 403
Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro Gly Gln Leu Val Ile
90 95 100

tat ccg atc atc aaa tta gcc gat ccg atc gat gtg gtt gat tac gta 451
Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp Val Val Asp Tyr Val
105 110 115

aga cgc ctc gag gaa gcg ctc atc caa gtt gtc ggc gat atg ggt gtt 499
Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val Gly Asp Met Gly Val
120 125 130

gcc ggc gct ggg cgc att gat ggg cgt tcg ggt gtg tgg gtg cca gct 547
Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly Val Trp Val Pro Ala
135 140 145

cat gat ggt tgg gtg gac agc aag gtt gcg gcc atc ggc att cga ata 595
His Asp Gly Trp Val Asp Ser Lys Val Ala Ala Ile Gly Ile Arg Ile
150 155 160 165

act cgt ggt gtt gca atg cac ggt gtg gcc atc aac tgc aac aac acg 643
Thr Arg Gly Val Ala Met His Gly Val Ala Ile Asn Cys Asn Asn Thr
170 175 180

ttg gat ttc tat gag cac atc att ccg tgt ggc att gct gat gca ggc 691
Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly Ile Ala Asp Ala Gly
185 190 195

ttg agc aca ctc tcg agg gaa ctg aaa agg gac gtt tca gtt gag gaa 739
Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp Val Ser Val Glu Glu
200 205 210

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tta gtc gag cca tcg atc cgc gca ttg gat gat gct ttg gct ggt cgg    787
Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp Ala Leu Ala Gly Arg
    215                 220                 225

ctg gtt gtt tct gat cat tct ttc ggc agc gcg ccc gac cca act aag    835
Leu Val Val Ser Asp His Ser Phe Gly Ser Ala Pro Asp Pro Thr Lys
230                 235                 240                 245

aat ctc cct aaa cgg ggg tagtacgagg aattttgtcg gtg                  876
Asn Leu Pro Lys Arg Gly
                250


<210> 188
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

<400> 188
Met Thr Ala Pro Arg Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg
  1               5                  10                  15

Ala Ser Ala Glu Pro Ile Glu Ile Gln Arg Leu Gly Leu Ile Asp Tyr
             20                  25                  30

Gln Glu Ala Trp Asp Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn
         35                  40                  45

Asp Glu Ile Pro Asp Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr
     50                  55                  60

Thr Ala Gly Lys Arg Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu
 65                  70                  75                  80

Pro Val Ile Asn Ala Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro
                 85                  90                  95

Gly Gln Leu Val Ile Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp
            100                 105                 110

Val Val Asp Tyr Val Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val
        115                 120                 125

Gly Asp Met Gly Val Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly
    130                 135                 140

Val Trp Val Pro Ala His Asp Gly Trp Val Asp Ser Lys Val Ala Ala
145                 150                 155                 160

Ile Gly Ile Arg Ile Thr Arg Gly Val Ala Met His Gly Val Ala Ile
                165                 170                 175

Asn Cys Asn Asn Thr Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly
            180                 185                 190

Ile Ala Asp Ala Gly Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp
        195                 200                 205

Val Ser Val Glu Glu Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp
    210                 215                 220
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Ala Leu Ala Gly Arg Leu Val Val Ser Asp His Ser Phe Gly Ser Ala
225 230 235 240

Pro Asp Pro Thr Lys Asn Leu Pro Lys Arg Gly
245 250

<210> 189
<211> 1167
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1144)
<223> RXS01747

<400> 189
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ctaaaaatat cactaactcg aaagatgtaa ggttgcattt gtg act atc gca cct 115
Val Thr Ile Ala Pro
1 5

gaa gga cga cga ctg cta cgc gtc gaa gct cga aac tca gaa acc ccg 163
Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg Asn Ser Glu Thr Pro
10 15 20

att gag acg aag cct cga tgg att aga aac cag gtc aaa aac gga cct 211
Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln Val Lys Asn Gly Pro
25 30 35

gag tat cag gat atg aag gaa cgt gtc gct ggc gca tca cta cac act 259
Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly Ala Ser Leu His Thr
40 45 50

gtg tgt cag gag gct ggc tgt cct aat atc cat gag tgt tgg gaa tcc 307
Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His Glu Cys Trp Glu Ser
55 60 65

cgt gag gca acc ttc ctc att ggt ggc gcc aac tgc tct cgc cgc tgt 355
Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn Cys Ser Arg Arg Cys
70 75 80 85

gat ttc tgc atg atc aac tcg gct cgc cct gag cca ctc gac cgc ggt 403
Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu Pro Leu Asp Arg Gly
90 95 100

gag cca ctg cgt gtc gct gag tct gtt cgt gag atg cag ctg aat tac 451
Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu Met Gln Leu Asn Tyr
105 110 115

tcc acc atc acc ggt gtt acc cgt gat gat ctg gat gat gaa ggc gca 499
Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu Asp Asp Glu Gly Ala
120 125 130

tgg ctg tac tca gaa gtg gtt cgt aag atc cac gag ctg aac cca cac 547
Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His Glu Leu Asn Pro His
135 140 145

acc ggt gtg gaa aac ctg gtg cct gat ttc tcc ggc aag aag gat ctg 595

Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser Gly Lys Lys Asp Leu
150 155 160 165

ctg cag gaa gtt ttt gaa tcc cgc cca gag gtt ttc gct cac aac gtg 643
Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val Phe Ala His Asn Val
170 175 180

gaa act gtg cca cgt att ttc aag cgc att cgc cca gca ttc cgc tac 691
Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg Pro Ala Phe Arg Tyr
185 190 195

gag cgt tca ctt gat gtg atc cgt cag gct cgc gat ttc ggt ctg gtg 739
Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg Asp Phe Gly Leu Val
200 205 210

acc aag tcc aac ctg att ttg ggc atg ggt gaa acc aag gaa gaa atc 787
Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu Thr Lys Glu Glu Ile
215 220 225

acc gag gcg ctg cag gat ctg cac gac gct ggc tgt gac atc atc acc 835
Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly Cys Asp Ile Ile Thr
230 235 240 245

atc acc cag tac ctg cgt cct ggt cct ttg ttc cac ccc atc gag cgt 883
Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe His Pro Ile Glu Arg
250 255 260

tgg gtg aag cct gag gag ttc ctc gag cac gct gat gct gca aag gaa 931
Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala Asp Ala Ala Lys Glu
265 270 275

atg ggc ttc gct gct gtt atg tcc ggc cca ttg gtt cgt tcc tct tac 979
Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu Val Arg Ser Ser Tyr
280 285 290

cgt gca ggc cgt ctg tac gcg cag gcc atg gag ttc cgt ggc gag gaa 1027
Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu Phe Arg Gly Glu Glu
295 300 305

atc cca gca cac ctc gcg cac ctg aag gat act tcc gga gga tcc acc 1075
Ile Pro Ala His Leu Ala His Leu Lys Asp Thr Ser Gly Gly Ser Thr
310 315 320 325

gcc cag gaa gca tct aca ctt ctg gag cgt tac ggt gct tcc gaa gac 1123
Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr Gly Ala Ser Glu Asp
330 335 340

acc cca gtg gtg tcc ttc aac taagcccgaa gtttttaac cgc 1167
Thr Pro Val Val Ser Phe Asn
345

<210> 190
<211> 348
<212> PRT
<213> Corynebacterium glutamicum

<400> 190
Val Thr Ile Ala Pro Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg
1 5 10 15

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Asn Ser Glu Thr Pro Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln
            20                  25                  30

Val Lys Asn Gly Pro Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly
        35                  40                  45

Ala Ser Leu His Thr Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His
    50                  55                  60

Glu Cys Trp Glu Ser Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn
65                  70                  75                  80

Cys Ser Arg Arg Cys Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu
                85                  90                  95

Pro Leu Asp Arg Gly Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu
            100                 105                 110

Met Gln Leu Asn Tyr Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu
        115                 120                 125

Asp Asp Glu Gly Ala Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His
    130                 135                 140

Glu Leu Asn Pro His Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser
145                 150                 155                 160

Gly Lys Lys Asp Leu Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val
                165                 170                 175

Phe Ala His Asn Val Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg
            180                 185                 190

Pro Ala Phe Arg Tyr Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg
        195                 200                 205

Asp Phe Gly Leu Val Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu
    210                 215                 220

Thr Lys Glu Glu Ile Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly
225                 230                 235                 240

Cys Asp Ile Ile Thr Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe
                245                 250                 255

His Pro Ile Glu Arg Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala
            260                 265                 270

Asp Ala Ala Lys Glu Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu
        275                 280                 285

Val Arg Ser Ser Tyr Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu
    290                 295                 300

Phe Arg Gly Glu Glu Ile Pro Ala His Leu Ala His Leu Lys Asp Thr
305                 310                 315                 320

Ser Gly Gly Ser Thr Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr
                325                 330                 335

Gly Ala Ser Glu Asp Thr Pro Val Val Ser Phe Asn
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        340                 345


<210> 191
<211> 903
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(880)
<223> RXC01748

<400> 191
atcaccaaat gtggcggttt tgcgtcgaaa agcgtgctct ttctacacct ctttgaggtt 60

cattttcgcg gtttcctcac aatcgcctat tgttaagtac atg gca gac gcg aaa   115
                                           Met Ala Asp Ala Lys
                                            1               5

aag cag gcg gat aaa gcc gcc aag aag cag gta aga gca gcc aag aag   163
Lys Gln Ala Asp Lys Ala Ala Lys Lys Gln Val Arg Ala Ala Lys Lys
                10                  15                  20

gca cag cgc aag gag act cgc tca caa atg tgg cag gtc ttc aac atg   211
Ala Gln Arg Lys Glu Thr Arg Ser Gln Met Trp Gln Val Phe Asn Met
            25                  30                  35

caa cgc aag cag gat aag gct ctt att ccg ctt ctg ttg ctc gct att   259
Gln Arg Lys Gln Asp Lys Ala Leu Ile Pro Leu Leu Leu Leu Ala Ile
        40                  45                  50

ctt ggt atc ccg ctg gtc ctt ttc ctc atc ggt ttg att tgg ggt ggt   307
Leu Gly Ile Pro Leu Val Leu Phe Leu Ile Gly Leu Ile Trp Gly Gly
    55                  60                  65

cag tgg tgg atg ctt ccg atc ggc att gct gca ggt gtt gta gct gca   355
Gln Trp Trp Met Leu Pro Ile Gly Ile Ala Ala Gly Val Val Ala Ala
70                  75                  80                  85

atg ttt att ttc acc cgt cgc gtt gag cgt gac gtg tac aag cgc gcc   403
Met Phe Ile Phe Thr Arg Arg Val Glu Arg Asp Val Tyr Lys Arg Ala
                90                  95                  100

gaa ggt cag cag ggt gct gct ggt tgg gct gtg gag aac ctc cgc tct   451
Glu Gly Gln Gln Gly Ala Ala Gly Trp Ala Val Glu Asn Leu Arg Ser
            105                 110                 115

ggc gtg ggc atg acc tgg cgc acc aag acc gct gtt gca gtg acc act   499
Gly Val Gly Met Thr Trp Arg Thr Lys Thr Ala Val Ala Val Thr Thr
        120                 125                 130

cag atg gat gca gtg cac cgc gtc att ggt ctg tgt ggt gtt gtg ctg   547
Gln Met Asp Ala Val His Arg Val Ile Gly Leu Cys Gly Val Val Leu
    135                 140                 145

gtc ggc gag ggc tcc cct cac cgc ctg aag cca atg ctt gcg cag caa   595
Val Gly Glu Gly Ser Pro His Arg Leu Lys Pro Met Leu Ala Gln Gln
150                 155                 160                 165

aag aag cgc ctg aac cgc gtg gca cct ggt gtt cca gtg tat gaa atc   643
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Lys Lys Arg Leu Asn Arg Val Ala Pro Gly Val Pro Val Tyr Glu Ile
170 175 180

atc acg ggc aac ggc gaa ggc cag acc cct atc gcg aag ctg cag cgt 691
Ile Thr Gly Asn Gly Glu Gly Gln Thr Pro Ile Ala Lys Leu Gln Arg
185 190 195

gaa ctg gtc aag ctg cct cgc aac tac aag aag aac gac gtc gct gcc 739
Glu Leu Val Lys Leu Pro Arg Asn Tyr Lys Lys Asn Asp Val Ala Ala
200 205 210

ctg gcc gct cgc att gag gct atg gac aat gtc gga aac gct cct ggc 787
Leu Ala Ala Arg Ile Glu Ala Met Asp Asn Val Gly Asn Ala Pro Gly
215 220 225

gga tct ttg cct aag ggt cca ttg cca aag ggc gca agc atg tcc ggt 835
Gly Ser Leu Pro Lys Gly Pro Leu Pro Lys Gly Ala Ser Met Ser Gly
230 235 240 245

atg aac cgc cgc gct cgc cga cag gct gaa cgc aag ggc gag gct 880
Met Asn Arg Arg Ala Arg Arg Gln Ala Glu Arg Lys Gly Glu Ala
250 255 260

taaagccttt tcgctttcgc gtc 903

<210> 192
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

<400> 192
Met Ala Asp Ala Lys Lys Gln Ala Asp Lys Ala Ala Lys Lys Gln Val
1 5 10 15

Arg Ala Ala Lys Lys Ala Gln Arg Lys Glu Thr Arg Ser Gln Met Trp
20 25 30

Gln Val Phe Asn Met Gln Arg Lys Gln Asp Lys Ala Leu Ile Pro Leu
35 40 45

Leu Leu Leu Ala Ile Leu Gly Ile Pro Leu Val Leu Phe Leu Ile Gly
50 55 60

Leu Ile Trp Gly Gly Gln Trp Trp Met Leu Pro Ile Gly Ile Ala Ala
65 70 75 80

Gly Val Val Ala Ala Met Phe Ile Phe Thr Arg Arg Val Glu Arg Asp
85 90 95

Val Tyr Lys Arg Ala Glu Gly Gln Gln Gly Ala Ala Gly Trp Ala Val
100 105 110

Glu Asn Leu Arg Ser Gly Val Gly Met Thr Trp Arg Thr Lys Thr Ala
115 120 125

Val Ala Val Thr Thr Gln Met Asp Ala Val His Arg Val Ile Gly Leu
130 135 140

Cys Gly Val Val Leu Val Gly Glu Gly Ser Pro His Arg Leu Lys Pro
145 150 155 160

```
Met Leu Ala Gln Gln Lys Lys Arg Leu Asn Arg Val Ala Pro Gly Val
                165                 170                 175

Pro Val Tyr Glu Ile Ile Thr Gly Asn Gly Glu Gly Gln Thr Pro Ile
            180                 185                 190

Ala Lys Leu Gln Arg Glu Leu Val Lys Leu Pro Arg Asn Tyr Lys Lys
        195                 200                 205

Asn Asp Val Ala Ala Leu Ala Ala Arg Ile Glu Ala Met Asp Asn Val
    210                 215                 220

Gly Asn Ala Pro Gly Gly Ser Leu Pro Lys Gly Pro Leu Pro Lys Gly
225                 230                 235                 240

Ala Ser Met Ser Gly Met Asn Arg Arg Ala Arg Arg Gln Ala Glu Arg
                245                 250                 255

Lys Gly Glu Ala
            260


<210> 193
<211> 936
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(913)
<223> RXC00354

<400> 193
ggcttgtcgg taaggctgca gggtagcggg agtttccttc agattggaag ttctttaatt 60

ttctcgatta tgtacctcat ttacgcgtaa agtttggggc atg gga aag tta ctt   115
                                            Met Gly Lys Leu Leu
                                             1               5

ttc gta gac atc ggt ggc aca ctg ctg gat tac tca aat gaa gtt ccg   163
Phe Val Asp Ile Gly Gly Thr Leu Leu Asp Tyr Ser Asn Glu Val Pro
                10                  15                  20

cgt tcg gcc gtt gac gcg atc cgt aag gca cgc gcc aaa gga cac cgc   211
Arg Ser Ala Val Asp Ala Ile Arg Lys Ala Arg Ala Lys Gly His Arg
            25                  30                  35

gtg tac ttg agc tct ggt cga agc agc gct gag gtg act tct cag ttg   259
Val Tyr Leu Ser Ser Gly Arg Ser Ser Ala Glu Val Thr Ser Gln Leu
        40                  45                  50

tgg gat atc gga gtg gat ggc ctc att ggc gca aat ggt gga tat gtg   307
Trp Asp Ile Gly Val Asp Gly Leu Ile Gly Ala Asn Gly Gly Tyr Val
    55                  60                  65

gaa agc gca cag gag tct gtg ttc cac cgc cgt ttg tcg ggt gag gag   355
Glu Ser Ala Gln Glu Ser Val Phe His Arg Arg Leu Ser Gly Glu Glu
70                  75                  80                  85

acc cgc cac att gtg gag tgg ctc tac aac cgt ggt ttg gag ttt tat   403
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Thr Arg His Ile Val Glu Trp Leu Tyr Asn Arg Gly Leu Glu Phe Tyr
90 95 100

ctc gag tcc aac aac ggt ttg tat gca agc cgt ggt ttc cgt gag gct 451
Leu Glu Ser Asn Asn Gly Leu Tyr Ala Ser Arg Gly Phe Arg Glu Ala
105 110 115

tct aag cca gtg ctg tct cgc ctt tcg gag aag acc gac gtg aca gtc 499
Ser Lys Pro Val Leu Ser Arg Leu Ser Glu Lys Thr Asp Val Thr Val
120 125 130

gat agc atg tac ccg gat atg ttc tgg ggc gcg agc ctt gat cgt gac 547
Asp Ser Met Tyr Pro Asp Met Phe Trp Gly Ala Ser Leu Asp Arg Asp
135 140 145

gat gtg aac aag atc agt tac atc ttc aat tct cag gaa gat ttg gac 595
Asp Val Asn Lys Ile Ser Tyr Ile Phe Asn Ser Gln Glu Asp Leu Asp
150 155 160 165

gca gcg cgt gag gcg ttc cct aac ctg gag cac acc acg tgg ggt ggt 643
Ala Ala Arg Glu Ala Phe Pro Asn Leu Glu His Thr Thr Trp Gly Gly
170 175 180

cag acg ggt gcg ttg ttc ggc acg atc ggt gtg tct gtc aac aag aag 691
Gln Thr Gly Ala Leu Phe Gly Thr Ile Gly Val Ser Val Asn Lys Lys
185 190 195

atc ggc gtg gat cgc ctg ctg aag tac ctg aac gca gat cgc gca aac 739
Ile Gly Val Asp Arg Leu Leu Lys Tyr Leu Asn Ala Asp Arg Ala Asn
200 205 210

acc att gcg ttc ggc gac agc gat gag gat ctc tcc cta ttt gag gcg 787
Thr Ile Ala Phe Gly Asp Ser Asp Glu Asp Leu Ser Leu Phe Glu Ala
215 220 225

agc gct tac ggc gtc gcg atg ggc gag gcc acc gaa tcg ctc aag gct 835
Ser Ala Tyr Gly Val Ala Met Gly Glu Ala Thr Glu Ser Leu Lys Ala
230 235 240 245

gct gct gac ctg gtc acg gat gct gtt ggg cag gac ggc ttg cgc aat 883
Ala Ala Asp Leu Val Thr Asp Ala Val Gly Gln Asp Gly Leu Arg Asn
250 255 260

gcg ttt tta aag ctt gag ctt atc gac gcc tgaccccatc aaagaacttc 933
Ala Phe Leu Lys Leu Glu Leu Ile Asp Ala
265 270

cca 936

<210> 194
<211> 271
<212> PRT
<213> Corynebacterium glutamicum

<400> 194
Met Gly Lys Leu Leu Phe Val Asp Ile Gly Gly Thr Leu Leu Asp Tyr
1 5 10 15

Ser Asn Glu Val Pro Arg Ser Ala Val Asp Ala Ile Arg Lys Ala Arg
20 25 30

Ala Lys Gly His Arg Val Tyr Leu Ser Ser Gly Arg Ser Ser Ala Glu
35 40 45

Val Thr Ser Gln Leu Trp Asp Ile Gly Val Asp Gly Leu Ile Gly Ala
50 55 60

Asn Gly Gly Tyr Val Glu Ser Ala Gln Glu Ser Val Phe His Arg Arg
65 70 75 80

Leu Ser Gly Glu Glu Thr Arg His Ile Val Glu Trp Leu Tyr Asn Arg
85 90 95

Gly Leu Glu Phe Tyr Leu Glu Ser Asn Asn Gly Leu Tyr Ala Ser Arg
100 105 110

Gly Phe Arg Glu Ala Ser Lys Pro Val Leu Ser Arg Leu Ser Glu Lys
115 120 125

Thr Asp Val Thr Val Asp Ser Met Tyr Pro Asp Met Phe Trp Gly Ala
130 135 140

Ser Leu Asp Arg Asp Asp Val Asn Lys Ile Ser Tyr Ile Phe Asn Ser
145 150 155 160

Gln Glu Asp Leu Asp Ala Ala Arg Glu Ala Phe Pro Asn Leu Glu His
165 170 175

Thr Thr Trp Gly Gly Gln Thr Gly Ala Leu Phe Gly Thr Ile Gly Val
180 185 190

Ser Val Asn Lys Lys Ile Gly Val Asp Arg Leu Leu Lys Tyr Leu Asn
195 200 205

Ala Asp Arg Ala Asn Thr Ile Ala Phe Gly Asp Ser Asp Glu Asp Leu
210 215 220

Ser Leu Phe Glu Ala Ser Ala Tyr Gly Val Ala Met Gly Glu Ala Thr
225 230 235 240

Glu Ser Leu Lys Ala Ala Ala Asp Leu Val Thr Asp Ala Val Gly Gln
245 250 255

Asp Gly Leu Arg Asn Ala Phe Leu Lys Leu Glu Leu Ile Asp Ala
260 265 270

<210> 195
<211> 1740
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1717)
<223> RXC01749

<400> 195
ggtttttgcg tgctctggtt tagggactgg ttttgggaac gtgcccagtt ccacatcaaa 60

taacgctgag gtcgtactta atccatgaga tcatgaatgg gtg agc ttc ctt gta 115

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                                                    Val Ser Phe Leu Val
                                                     1               5

gaa aat caa tta ctc gcg ttg gtt gtc atc atg acg gtc gga cta ttg    163
Glu Asn Gln Leu Leu Ala Leu Val Val Ile Met Thr Val Gly Leu Leu
                 10                  15                  20

ctc ggc cgc atc aaa att ttc ggg ttc cgt ctc ggc gtc gcc gct gta    211
Leu Gly Arg Ile Lys Ile Phe Gly Phe Arg Leu Gly Val Ala Ala Val
             25                  30                  35

ctg ttt gta ggt cta gcg cta tcc acc att gag ccg gat att tcc gtc    259
Leu Phe Val Gly Leu Ala Leu Ser Thr Ile Glu Pro Asp Ile Ser Val
         40                  45                  50

cca tcc ctc att tac gtg gtt gga ctg tcg ctt ttt gtc tac acg atc    307
Pro Ser Leu Ile Tyr Val Val Gly Leu Ser Leu Phe Val Tyr Thr Ile
     55                  60                  65

ggt ctg gaa gcc ggc cct gga ttc ttc acc tcc atg aaa acc act ggt    355
Gly Leu Glu Ala Gly Pro Gly Phe Phe Thr Ser Met Lys Thr Thr Gly
 70                  75                  80                  85

ctg cgc aac aac gca ctg acc ttg ggc gcc atc atc gcc acc acg gca    403
Leu Arg Asn Asn Ala Leu Thr Leu Gly Ala Ile Ile Ala Thr Thr Ala
                 90                  95                 100

ctc gca tgg gca ctc atc aca gtt ttg aac atc gat gcc gcc tcc ggc    451
Leu Ala Trp Ala Leu Ile Thr Val Leu Asn Ile Asp Ala Ala Ser Gly
            105                 110                 115

gcc ggc atg ctc acc ggc gcg ctc acc aac acc cca gcc atg gcc gca    499
Ala Gly Met Leu Thr Gly Ala Leu Thr Asn Thr Pro Ala Met Ala Ala
        120                 125                 130

gtt gtt gac gca ctt cct tcg ctt atc gac gac acc ggc cag ctt cac    547
Val Val Asp Ala Leu Pro Ser Leu Ile Asp Asp Thr Gly Gln Leu His
    135                 140                 145

ctc atc gcc gag ctg ccc gtc gtc gca tat tcc ttg gca tac ccc ctc    595
Leu Ile Ala Glu Leu Pro Val Val Ala Tyr Ser Leu Ala Tyr Pro Leu
150                 155                 160                 165

ggt gtg ctc atc gtt att ctc tcc atc gcc atc ttc agc tct gtg ttc    643
Gly Val Leu Ile Val Ile Leu Ser Ile Ala Ile Phe Ser Ser Val Phe
                170                 175                 180

aaa gtc gac cac aac aaa gaa gcc gaa gaa gcg ggc gtt gcg gtc cag    691
Lys Val Asp His Asn Lys Glu Ala Glu Glu Ala Gly Val Ala Val Gln
            185                 190                 195

gaa ctc aaa ggc cgt cgc atc cgc gtc acc gtc gct gat ctt cca gcc    739
Glu Leu Lys Gly Arg Arg Ile Arg Val Thr Val Ala Asp Leu Pro Ala
        200                 205                 210

ctg gag aac atc cca gag ctg ctc aac ctc cac gtc att gtg tcc cga    787
Leu Glu Asn Ile Pro Glu Leu Leu Asn Leu His Val Ile Val Ser Arg
    215                 220                 225

gtg gaa cga gac ggt gag caa ttc atc ccg ctt tat ggc gaa cac gca    835
Val Glu Arg Asp Gly Glu Gln Phe Ile Pro Leu Tyr Gly Glu His Ala
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230 235 240 245

cgc atc ggc gat gtc tta aca gtg gtg ggt gcc gat gaa gaa ctc aac 883
Arg Ile Gly Asp Val Leu Thr Val Val Gly Ala Asp Glu Glu Leu Asn
250 255 260

cgc gcg gaa aaa gcc atc ggt gaa ctc att gac ggc gac ccc tac agc 931
Arg Ala Glu Lys Ala Ile Gly Glu Leu Ile Asp Gly Asp Pro Tyr Ser
265 270 275

aat gtg gaa ctt gat tac cga cgc atc ttc gtc tca aac aca gca gtc 979
Asn Val Glu Leu Asp Tyr Arg Arg Ile Phe Val Ser Asn Thr Ala Val
280 285 290

gtg ggc act ccc cta tcc aag ctc cag cca ctg ttt aaa gac atg ctg 1027
Val Gly Thr Pro Leu Ser Lys Leu Gln Pro Leu Phe Lys Asp Met Leu
295 300 305

atc acc cgc atc agg cgc ggc gac aca gat ttg gtg gcc tcc tcc gac 1075
Ile Thr Arg Ile Arg Arg Gly Asp Thr Asp Leu Val Ala Ser Ser Asp
310 315 320 325

atg act ttg cag ctc ggt gac cgt gtc cgc gtt gtc gca cca gca gaa 1123
Met Thr Leu Gln Leu Gly Asp Arg Val Arg Val Val Ala Pro Ala Glu
330 335 340

aaa ctc cgc gaa gca acc caa ttg ctc ggc gat tcc tac aag aaa ctc 1171
Lys Leu Arg Glu Ala Thr Gln Leu Leu Gly Asp Ser Tyr Lys Lys Leu
345 350 355

tcc gat ttc aac ctg ctc cca ctc gct gcc ggc ctc atg atc ggt gtg 1219
Ser Asp Phe Asn Leu Leu Pro Leu Ala Ala Gly Leu Met Ile Gly Val
360 365 370

ctt gtc ggc atg gtg gag ttc cca cta cca ggt gga agc tcc ctg aaa 1267
Leu Val Gly Met Val Glu Phe Pro Leu Pro Gly Gly Ser Ser Leu Lys
375 380 385

ctg ggt aac gca ggt gga ccg cta gtt gtt gcg ctg ctg ctc ggc atg 1315
Leu Gly Asn Ala Gly Gly Pro Leu Val Val Ala Leu Leu Leu Gly Met
390 395 400 405

atc aat cgc aca ggc aag ttc gtc tgg caa atc ccc tac gga gca aac 1363
Ile Asn Arg Thr Gly Lys Phe Val Trp Gln Ile Pro Tyr Gly Ala Asn
410 415 420

ctt gcc ctt cgc caa ctg ggc atc aca cta ttt ttg gct gcc atc ggt 1411
Leu Ala Leu Arg Gln Leu Gly Ile Thr Leu Phe Leu Ala Ala Ile Gly
425 430 435

acc tca gcg ggc gca gga ttt cga tca gcg atc agc gac ccc caa tca 1459
Thr Ser Ala Gly Ala Gly Phe Arg Ser Ala Ile Ser Asp Pro Gln Ser
440 445 450

ctc acc atc atc ggc ttc ggt gcg ctg ctc act ttg ttc atc tcc atc 1507
Leu Thr Ile Ile Gly Phe Gly Ala Leu Leu Thr Leu Phe Ile Ser Ile
455 460 465

acg gtg ctg ttc gtt ggc cac aaa ctg atg aaa atc ccc ttc ggt gaa 1555
Thr Val Leu Phe Val Gly His Lys Leu Met Lys Ile Pro Phe Gly Glu
470 475 480 485

acc gct ggc atc ctc gcc ggt acg caa acc cac cct gct gtg ctg agt 1603
Thr Ala Gly Ile Leu Ala Gly Thr Gln Thr His Pro Ala Val Leu Ser
490 495 500

tat gtg tca gat gcc tcc cgc aac gag ctc cct gcc atg ggt tat acc 1651
Tyr Val Ser Asp Ala Ser Arg Asn Glu Leu Pro Ala Met Gly Tyr Thr
505 510 515

tct gtg tat ccg ctg gcg atg atc gca aag atc ctg gcc gcc caa acg 1699
Ser Val Tyr Pro Leu Ala Met Ile Ala Lys Ile Leu Ala Ala Gln Thr
520 525 530

ttg ttg ttc cta ctt atc tagcattgac cccttaagcg cag 1740
Leu Leu Phe Leu Leu Ile
535

<210> 196
<211> 539
<212> PRT
<213> Corynebacterium glutamicum

<400> 196
Val Ser Phe Leu Val Glu Asn Gln Leu Leu Ala Leu Val Val Ile Met
1 5 10 15

Thr Val Gly Leu Leu Leu Gly Arg Ile Lys Ile Phe Gly Phe Arg Leu
20 25 30

Gly Val Ala Ala Val Leu Phe Val Gly Leu Ala Leu Ser Thr Ile Glu
35 40 45

Pro Asp Ile Ser Val Pro Ser Leu Ile Tyr Val Val Gly Leu Ser Leu
50 55 60

Phe Val Tyr Thr Ile Gly Leu Glu Ala Gly Pro Gly Phe Phe Thr Ser
65 70 75 80

Met Lys Thr Thr Gly Leu Arg Asn Asn Ala Leu Thr Leu Gly Ala Ile
85 90 95

Ile Ala Thr Thr Ala Leu Ala Trp Ala Leu Ile Thr Val Leu Asn Ile
100 105 110

Asp Ala Ala Ser Gly Ala Gly Met Leu Thr Gly Ala Leu Thr Asn Thr
115 120 125

Pro Ala Met Ala Ala Val Val Asp Ala Leu Pro Ser Leu Ile Asp Asp
130 135 140

Thr Gly Gln Leu His Leu Ile Ala Glu Leu Pro Val Val Ala Tyr Ser
145 150 155 160

Leu Ala Tyr Pro Leu Gly Val Leu Ile Val Ile Leu Ser Ile Ala Ile
165 170 175

Phe Ser Ser Val Phe Lys Val Asp His Asn Lys Glu Ala Glu Glu Ala
180 185 190

Gly Val Ala Val Gln Glu Leu Lys Gly Arg Arg Ile Arg Val Thr Val

195 200 205

Ala Asp Leu Pro Ala Leu Glu Asn Ile Pro Glu Leu Leu Asn Leu His
210 215 220

Val Ile Val Ser Arg Val Glu Arg Asp Gly Glu Gln Phe Ile Pro Leu
225 230 235 240

Tyr Gly Glu His Ala Arg Ile Gly Asp Val Leu Thr Val Val Gly Ala
245 250 255

Asp Glu Glu Leu Asn Arg Ala Glu Lys Ala Ile Gly Glu Leu Ile Asp
260 265 270

Gly Asp Pro Tyr Ser Asn Val Glu Leu Asp Tyr Arg Arg Ile Phe Val
275 280 285

Ser Asn Thr Ala Val Val Gly Thr Pro Leu Ser Lys Leu Gln Pro Leu
290 295 300

Phe Lys Asp Met Leu Ile Thr Arg Ile Arg Arg Gly Asp Thr Asp Leu
305 310 315 320

Val Ala Ser Ser Asp Met Thr Leu Gln Leu Gly Asp Arg Val Arg Val
325 330 335

Val Ala Pro Ala Glu Lys Leu Arg Glu Ala Thr Gln Leu Leu Gly Asp
340 345 350

Ser Tyr Lys Lys Leu Ser Asp Phe Asn Leu Leu Pro Leu Ala Ala Gly
355 360 365

Leu Met Ile Gly Val Leu Val Gly Met Val Glu Phe Pro Leu Pro Gly
370 375 380

Gly Ser Ser Leu Lys Leu Gly Asn Ala Gly Gly Pro Leu Val Val Ala
385 390 395 400

Leu Leu Leu Gly Met Ile Asn Arg Thr Gly Lys Phe Val Trp Gln Ile
405 410 415

Pro Tyr Gly Ala Asn Leu Ala Leu Arg Gln Leu Gly Ile Thr Leu Phe
420 425 430

Leu Ala Ala Ile Gly Thr Ser Ala Gly Ala Gly Phe Arg Ser Ala Ile
435 440 445

Ser Asp Pro Gln Ser Leu Thr Ile Ile Gly Phe Gly Ala Leu Leu Thr
450 455 460

Leu Phe Ile Ser Ile Thr Val Leu Phe Val Gly His Lys Leu Met Lys
465 470 475 480

Ile Pro Phe Gly Glu Thr Ala Gly Ile Leu Ala Gly Thr Gln Thr His
485 490 495

Pro Ala Val Leu Ser Tyr Val Ser Asp Ala Ser Arg Asn Glu Leu Pro
500 505 510

Ala Met Gly Tyr Thr Ser Val Tyr Pro Leu Ala Met Ile Ala Lys Ile
515 520 525

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Leu Ala Ala Gln Thr Leu Leu Phe Leu Leu Ile
    530                 535


<210> 197
<211> 1023
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1000)
<223> RXA02268

<400> 197
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ttgccgagcg caagccggcc tacggcgcta gtgtgagcac atg tcc cag gaa aat   115
                                          Met Ser Gln Glu Asn
                                          1               5

tct ggt ttg ttc aag cgc gcg att aca cgt ggg gtg gct aag gtg cgc   163
Ser Gly Leu Phe Lys Arg Ala Ile Thr Arg Gly Val Ala Lys Val Arg
                10                  15                  20

cgg aat ccg cgc gag gat ttt gcg gag gaa ttc acc caa gaa ctc tac   211
Arg Asn Pro Arg Glu Asp Phe Ala Glu Glu Phe Thr Gln Glu Leu Tyr
            25                  30                  35

gat cac gca aca aat atc acc ctg ccc ctg acg gcg cgg ctg aag ccg   259
Asp His Ala Thr Asn Ile Thr Leu Pro Leu Thr Ala Arg Leu Lys Pro
        40                  45                  50

aat ggg ttt ttc cag gat gat tgg cgg gcg cga cca agt ggt gcg cga   307
Asn Gly Phe Phe Gln Asp Asp Trp Arg Ala Arg Pro Ser Gly Ala Arg
    55                  60                  65

ccg tgg ccg atc gtg cta att cac gga tcc ggg gcc agc aag ggt tca   355
Pro Trp Pro Ile Val Leu Ile His Gly Ser Gly Ala Ser Lys Gly Ser
70                  75                  80                  85

tgg gag gaa atg ggc gct gag ctg cgc agc aaa ggt tgg gcc gtg ttt   403
Trp Glu Glu Met Gly Ala Glu Leu Arg Ser Lys Gly Trp Ala Val Phe
                90                  95                  100

gcc cct gac ttt gga acg cgt gcc acc gag cca att gcg gcg tcg gct   451
Ala Pro Asp Phe Gly Thr Arg Ala Thr Glu Pro Ile Ala Ala Ser Ala
            105                 110                 115

gcc caa att ggt gcg tat att gat gcc gtt ttg ttg gtg acg ggc gct   499
Ala Gln Ile Gly Ala Tyr Ile Asp Ala Val Leu Leu Val Thr Gly Ala
        120                 125                 130

gcg cag att gtg ctg gtt ggg cat tcg caa ggc ggt gtc gtg gcg cgg   547
Ala Gln Ile Val Leu Val Gly His Ser Gln Gly Gly Val Val Ala Arg
    135                 140                 145

tat tgg atg cgc acc tac ggc gga tac atg aag gtc agg cac atg att   595
Tyr Trp Met Arg Thr Tyr Gly Gly Tyr Met Lys Val Arg His Met Ile
150                 155                 160                 165
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tcc atc tct acg cca aat cac gga acg ctc atg gga ggc att tta aac 643
Ser Ile Ser Thr Pro Asn His Gly Thr Leu Met Gly Gly Ile Leu Asn
170 175 180

ccg atg acg aag gtg aaa tcg gga gag gga acg atc gaa aag ctg atg 691
Pro Met Thr Lys Val Lys Ser Gly Glu Gly Thr Ile Glu Lys Leu Met
185 190 195

cac aga cta ttc ggg ccc act ggt ttt gaa cag ctg cgc gga cac gac 739
His Arg Leu Phe Gly Pro Thr Gly Phe Glu Gln Leu Arg Gly His Asp
200 205 210

atc atc gag ttt ttg gcc gac ggt ggg gac ctc gat cca ggc gtc acc 787
Ile Ile Glu Phe Leu Ala Asp Gly Gly Asp Leu Asp Pro Gly Val Thr
215 220 225

tac acc tgc att ggt acc cat ttt gat cct ttc atc caa cct ccg gag 835
Tyr Thr Cys Ile Gly Thr His Phe Asp Pro Phe Ile Gln Pro Pro Glu
230 235 240 245

gtg gcc ttt ttg gag gtc aac gag gac gat gat cca aat cga gtc cac 883
Val Ala Phe Leu Glu Val Asn Glu Asp Asp Asp Pro Asn Arg Val His
250 255 260

aat att tgg gtc gaa gat gaa cac ccg cgc gca atg att gcc cac aac 931
Asn Ile Trp Val Glu Asp Glu His Pro Arg Ala Met Ile Ala His Asn
265 270 275

gat atg gtg cgc gat ccc agg gtg atc gaa atc gta cgc gca gag ctc 979
Asp Met Val Arg Asp Pro Arg Val Ile Glu Ile Val Arg Ala Glu Leu
280 285 290

gac cgg gtg gca cgc ctc ggc taagttgggg acatggttga cgc 1023
Asp Arg Val Ala Arg Leu Gly
295 300

<210> 198
<211> 300
<212> PRT
<213> Corynebacterium glutamicum

<400> 198
Met Ser Gln Glu Asn Ser Gly Leu Phe Lys Arg Ala Ile Thr Arg Gly
1 5 10 15

Val Ala Lys Val Arg Arg Asn Pro Arg Glu Asp Phe Ala Glu Glu Phe
20 25 30

Thr Gln Glu Leu Tyr Asp His Ala Thr Asn Ile Thr Leu Pro Leu Thr
35 40 45

Ala Arg Leu Lys Pro Asn Gly Phe Phe Gln Asp Asp Trp Arg Ala Arg
50 55 60

Pro Ser Gly Ala Arg Pro Trp Pro Ile Val Leu Ile His Gly Ser Gly
65 70 75 80

Ala Ser Lys Gly Ser Trp Glu Glu Met Gly Ala Glu Leu Arg Ser Lys
85 90 95

```
Gly Trp Ala Val Phe Ala Pro Asp Phe Gly Thr Arg Ala Thr Glu Pro
            100                 105                 110

Ile Ala Ala Ser Ala Ala Gln Ile Gly Ala Tyr Ile Asp Ala Val Leu
        115                 120                 125

Leu Val Thr Gly Ala Ala Gln Ile Val Leu Val Gly His Ser Gln Gly
    130                 135                 140

Gly Val Val Ala Arg Tyr Trp Met Arg Thr Tyr Gly Gly Tyr Met Lys
145                 150                 155                 160

Val Arg His Met Ile Ser Ile Ser Thr Pro Asn His Gly Thr Leu Met
                165                 170                 175

Gly Gly Ile Leu Asn Pro Met Thr Lys Val Lys Ser Gly Glu Gly Thr
            180                 185                 190

Ile Glu Lys Leu Met His Arg Leu Phe Gly Pro Thr Gly Phe Glu Gln
        195                 200                 205

Leu Arg Gly His Asp Ile Ile Glu Phe Leu Ala Asp Gly Gly Asp Leu
    210                 215                 220

Asp Pro Gly Val Thr Tyr Thr Cys Ile Gly Thr His Phe Asp Pro Phe
225                 230                 235                 240

Ile Gln Pro Pro Glu Val Ala Phe Leu Glu Val Asn Glu Asp Asp Asp
                245                 250                 255

Pro Asn Arg Val His Asn Ile Trp Val Glu Asp Glu His Pro Arg Ala
            260                 265                 270

Met Ile Ala His Asn Asp Met Val Arg Asp Pro Arg Val Ile Glu Ile
        275                 280                 285

Val Arg Ala Glu Leu Asp Arg Val Ala Arg Leu Gly
    290                 295                 300


<210> 199
<211> 1095
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1072)
<223> RXA02269

<400> 199
cgcaatgatt gcccacaacg atatggtgcg cgatcccagg gtgatcgaaa tcgtacgcgc 60

agagctcgac cgggtggcac gcctcggcta agttggggac atg gtt gac gcc ctc    115
                                          Met Val Asp Ala Leu
                                          1               5

aat gat ctc cgc cga gaa ctc aca aac gcg tta agg tcc gtg tgg aaa    163
Asn Asp Leu Arg Arg Glu Leu Thr Asn Ala Leu Arg Ser Val Trp Lys
                10                  15                  20
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aac ctc ccc act gat aac gcc ccg cag gcc gat gcc ttg cca gac gat    211
Asn Leu Pro Thr Asp Asn Ala Pro Gln Ala Asp Ala Leu Pro Asp Asp
            25                  30                  35

gta gtg gaa gag att gcg ata aat ttc tac cgt gat ccc aaa aac cgc    259
Val Val Glu Glu Ile Ala Ile Asn Phe Tyr Arg Asp Pro Lys Asn Arg
        40                  45                  50

ggc aaa ctc aac gaa gac aaa aca gat tcc ttg ccg atg ctc gcg cgc    307
Gly Lys Leu Asn Glu Asp Lys Thr Asp Ser Leu Pro Met Leu Ala Arg
    55                  60                  65

ata cgt tca cgt gga ctt ttt gaa gac gat tgg cgc gcc cgc ccc acc    355
Ile Arg Ser Arg Gly Leu Phe Glu Asp Asp Trp Arg Ala Arg Pro Thr
70                  75                  80                  85

gaa gac cgc ccc tgg cca gtg gta tta gtc cac gga act gga tca aca    403
Glu Asp Arg Pro Trp Pro Val Val Leu Val His Gly Thr Gly Ser Thr
                90                  95                  100

aaa ggt gat tgg caa gac ttg gga gcc gat cta cgc cgc gac ggc tgg    451
Lys Gly Asp Trp Gln Asp Leu Gly Ala Asp Leu Arg Arg Asp Gly Trp
            105                 110                 115

gca gtg ttt gca ccc gaa ttt ggc caa cgc gcc acc ggt tca gtc gca    499
Ala Val Phe Ala Pro Glu Phe Gly Gln Arg Ala Thr Gly Ser Val Ala
        120                 125                 130

gaa tca tcc gca caa att ggc gcc tat ata gat aca gta ttg ctt gct    547
Glu Ser Ser Ala Gln Ile Gly Ala Tyr Ile Asp Thr Val Leu Leu Ala
    135                 140                 145

aca gga gcc tca aaa gtc att gtc gtt ggc cac tcc caa ggc ggc gtg    595
Thr Gly Ala Ser Lys Val Ile Val Val Gly His Ser Gln Gly Gly Val
150                 155                 160                 165

ttg ctg aga tac tgg atg cgt gtt ttg ggt ggt gca tcc aaa gtc aaa    643
Leu Leu Arg Tyr Trp Met Arg Val Leu Gly Gly Ala Ser Lys Val Lys
                170                 175                 180

cac atg gtc tcc ctc gct gtc ccc aat cac ggc acc acc atg ggc gga    691
His Met Val Ser Leu Ala Val Pro Asn His Gly Thr Thr Met Gly Gly
            185                 190                 195

atc gtc agc ccg cta atc cgt aac aat cgt ggc gaa agt gtg gtt aat    739
Ile Val Ser Pro Leu Ile Arg Asn Asn Arg Gly Glu Ser Val Val Asn
        200                 205                 210

tct gtc gtt caa tca tgg ttc ggc gaa gct gga ttt gaa atg atc cgc    787
Ser Val Val Gln Ser Trp Phe Gly Glu Ala Gly Phe Glu Met Ile Arg
    215                 220                 225

gga cac gac acc atc aac gcc atc aat gaa ggc ggc gat ttg gat cca    835
Gly His Asp Thr Ile Asn Ala Ile Asn Glu Gly Gly Asp Leu Asp Pro
230                 235                 240                 245

gac gtg aca tat ctg tgc atc gcc acc cac ttt gac acc gtg att cag    883
Asp Val Thr Tyr Leu Cys Ile Ala Thr His Phe Asp Thr Val Ile Gln
                250                 255                 260
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ccc cct gaa acc tgc ttc cta gag gcc cgg aac ccc gaa gaa ctc aag 931
Pro Pro Glu Thr Cys Phe Leu Glu Ala Arg Asn Pro Glu Glu Leu Lys
265 270 275

cgg gtc caa aac atc tgg gtg gaa aac ctc gac ccc aat tca gtc gtg 979
Arg Val Gln Asn Ile Trp Val Glu Asn Leu Asp Pro Asn Ser Val Val
280 285 290

ctc cac gaa gca atg cct tac gat ccc cgc gta cgc gca ctg gtc agg 1027
Leu His Glu Ala Met Pro Tyr Asp Pro Arg Val Arg Ala Leu Val Arg
295 300 305

gcg gat ttg agc aaa ttg gtg gag att tcc gag act gcg gag aac 1072
Ala Asp Leu Ser Lys Leu Val Glu Ile Ser Glu Thr Ala Glu Asn
310 315 320

taggggtttt ggtggttgtc taa 1095

<210> 200
<211> 324
<212> PRT
<213> Corynebacterium glutamicum

<400> 200
Met Val Asp Ala Leu Asn Asp Leu Arg Arg Glu Leu Thr Asn Ala Leu
1 5 10 15

Arg Ser Val Trp Lys Asn Leu Pro Thr Asp Asn Ala Pro Gln Ala Asp
20 25 30

Ala Leu Pro Asp Asp Val Val Glu Glu Ile Ala Ile Asn Phe Tyr Arg
35 40 45

Asp Pro Lys Asn Arg Gly Lys Leu Asn Glu Asp Lys Thr Asp Ser Leu
50 55 60

Pro Met Leu Ala Arg Ile Arg Ser Arg Gly Leu Phe Glu Asp Asp Trp
65 70 75 80

Arg Ala Arg Pro Thr Glu Asp Arg Pro Trp Pro Val Val Leu Val His
85 90 95

Gly Thr Gly Ser Thr Lys Gly Asp Trp Gln Asp Leu Gly Ala Asp Leu
100 105 110

Arg Arg Asp Gly Trp Ala Val Phe Ala Pro Glu Phe Gly Gln Arg Ala
115 120 125

Thr Gly Ser Val Ala Glu Ser Ser Ala Gln Ile Gly Ala Tyr Ile Asp
130 135 140

Thr Val Leu Leu Ala Thr Gly Ala Ser Lys Val Ile Val Val Gly His
145 150 155 160

Ser Gln Gly Gly Val Leu Leu Arg Tyr Trp Met Arg Val Leu Gly Gly
165 170 175

Ala Ser Lys Val Lys His Met Val Ser Leu Ala Val Pro Asn His Gly
180 185 190

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Thr Thr Met Gly Gly Ile Val Ser Pro Leu Ile Arg Asn Asn Arg Gly
        195                 200                 205

Glu Ser Val Val Asn Ser Val Val Gln Ser Trp Phe Gly Glu Ala Gly
    210                 215                 220

Phe Glu Met Ile Arg Gly His Asp Thr Ile Asn Ala Ile Asn Glu Gly
225                 230                 235                 240

Gly Asp Leu Asp Pro Asp Val Thr Tyr Leu Cys Ile Ala Thr His Phe
                245                 250                 255

Asp Thr Val Ile Gln Pro Pro Glu Thr Cys Phe Leu Glu Ala Arg Asn
            260                 265                 270

Pro Glu Glu Leu Lys Arg Val Gln Asn Ile Trp Val Glu Asn Leu Asp
        275                 280                 285

Pro Asn Ser Val Val Leu His Glu Ala Met Pro Tyr Asp Pro Arg Val
    290                 295                 300

Arg Ala Leu Val Arg Ala Asp Leu Ser Lys Leu Val Glu Ile Ser Glu
305                 310                 315                 320

Thr Ala Glu Asn



<210> 201
<211> 1146
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1123)
<223> RXA01614

<400> 201
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tcgcgcacac cacaccaaca atcgacctat cgttatacgt atg aat cag atg cag   115
                                           Met Asn Gln Met Gln
                                            1               5

cag tgg aaa cca gac ttc ctg gga gag ggc tac caa aac ctc acc atc   163
Gln Trp Lys Pro Asp Phe Leu Gly Glu Gly Tyr Gln Asn Leu Thr Ile
                10                  15                  20

gag ctc ggc gac gac ccg gat aat gaa aca gat gtt gtg aca acg gtt   211
Glu Leu Gly Asp Asp Pro Asp Asn Glu Thr Asp Val Val Thr Thr Val
            25                  30                  35

gtg cgc tac aac cca gac aat cac gcg gac gag tct ttt gct gcc cgc   259
Val Arg Tyr Asn Pro Asp Asn His Ala Asp Glu Ser Phe Ala Ala Arg
        40                  45                  50

cca gcg ttg ctg tgg gtt cac ggc atg acg gac tac ttc ttc cac act   307
Pro Ala Leu Leu Trp Val His Gly Met Thr Asp Tyr Phe Phe His Thr
    55                  60                  65
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gaa ttc gcg gag ttt ttc cac aat gcc ggt ttt gct gtg tac ggc att     355
Glu Phe Ala Glu Phe Phe His Asn Ala Gly Phe Ala Val Tyr Gly Ile
 70                 75                  80                  85

gat ctt aga aaa tgt gga cgc tcc tac cgt cca gga cag cag tgg cac     403
Asp Leu Arg Lys Cys Gly Arg Ser Tyr Arg Pro Gly Gln Gln Trp His
                 90                  95                 100

tac acc tct gat ctt gcc cat tac ttc cct gac tta aca gct gct gcc     451
Tyr Thr Ser Asp Leu Ala His Tyr Phe Pro Asp Leu Thr Ala Ala Ala
            105                 110                 115

gag gtc atc tct tcc acc cac cct gag cta gtc ccc gtc gcc cat tcc     499
Glu Val Ile Ser Ser Thr His Pro Glu Leu Val Pro Val Ala His Ser
        120                 125                 130

act ggt gga ctc atc gtt cct ctg tgg atg tcc cag atg cgc aca agc     547
Thr Gly Gly Leu Ile Val Pro Leu Trp Met Ser Gln Met Arg Thr Ser
    135                 140                 145

aat cca gct gcc att gag aag att cca gcg ctg gtc ctc aac agt ccg     595
Asn Pro Ala Ala Ile Glu Lys Ile Pro Ala Leu Val Leu Asn Ser Pro
150                 155                 160                 165

tgg ctg gac atg atg tat cca cca ctg ttc atc aag ctg atc acc cct     643
Trp Leu Asp Met Met Tyr Pro Pro Leu Phe Ile Lys Leu Ile Thr Pro
                170                 175                 180

atg gtg agg gtg ttg ggc aaa cgc tcc ccc aca acc atc atc cca ggc     691
Met Val Arg Val Leu Gly Lys Arg Ser Pro Thr Thr Ile Ile Pro Gly
            185                 190                 195

gga ggt ttg gga gca tac gga aaa tcg atc cat aag aac ttt tac ggc     739
Gly Gly Leu Gly Ala Tyr Gly Lys Ser Ile His Lys Asn Phe Tyr Gly
        200                 205                 210

gaa tgg gac ttt gac acc acc atc aag cct gta gaa gga cat aaa aag     787
Glu Trp Asp Phe Asp Thr Thr Ile Lys Pro Val Glu Gly His Lys Lys
    215                 220                 225

agc atc gga tgg ctt cgg gca gtc atg gct ggc caa gca gaa atc cat     835
Ser Ile Gly Trp Leu Arg Ala Val Met Ala Gly Gln Ala Glu Ile His
230                 235                 240                 245

cac gac cac gtg aat gtc gga gtg gac gtg ctc acg ctg tgt tca aat     883
His Asp His Val Asn Val Gly Val Asp Val Leu Thr Leu Cys Ser Asn
                250                 255                 260

aag tcc tgg ttg aag tct gaa tac aca gag gac acc aac act tca gac     931
Lys Ser Trp Leu Lys Ser Glu Tyr Thr Glu Asp Thr Asn Thr Ser Asp
            265                 270                 275

gcg gtt ttg gat gtg aaa cac att caa aag tgg gct cct cat ttg agc     979
Ala Val Leu Asp Val Lys His Ile Gln Lys Trp Ala Pro His Leu Ser
        280                 285                 290

tcg cca tcg tcc agg gtt gat gtt gag atc atc gac aac gct cgc cac     1027
Ser Pro Ser Ser Arg Val Asp Val Glu Ile Ile Asp Asn Ala Arg His
    295                 300                 305

gat att ttc ctc tca agg aaa ccc gcc aga gat cac gcc tct gaa gta     1075
```

```
Asp Ile Phe Leu Ser Arg Lys Pro Ala Arg Asp His Ala Ser Glu Val
310                 315                 320                 325

ctc aac aac tgg ctg caa tcg aag ctt tcc agc ctc aaa cca tct caa    1123
Leu Asn Asn Trp Leu Gln Ser Lys Leu Ser Ser Leu Lys Pro Ser Gln
                330                 335                 340

taacaccgcg aattatagac tga                                          1146


<210> 202
<211> 341
<212> PRT
<213> Corynebacterium glutamicum

<400> 202
Met Asn Gln Met Gln Gln Trp Lys Pro Asp Phe Leu Gly Glu Gly Tyr
  1               5                  10                  15

Gln Asn Leu Thr Ile Glu Leu Gly Asp Asp Pro Asp Asn Glu Thr Asp
             20                  25                  30

Val Val Thr Thr Val Val Arg Tyr Asn Pro Asp Asn His Ala Asp Glu
         35                  40                  45

Ser Phe Ala Ala Arg Pro Ala Leu Leu Trp Val His Gly Met Thr Asp
     50                  55                  60

Tyr Phe Phe His Thr Glu Phe Ala Glu Phe Phe His Asn Ala Gly Phe
 65                  70                  75                  80

Ala Val Tyr Gly Ile Asp Leu Arg Lys Cys Gly Arg Ser Tyr Arg Pro
                 85                  90                  95

Gly Gln Gln Trp His Tyr Thr Ser Asp Leu Ala His Tyr Phe Pro Asp
            100                 105                 110

Leu Thr Ala Ala Ala Glu Val Ile Ser Ser Thr His Pro Glu Leu Val
        115                 120                 125

Pro Val Ala His Ser Thr Gly Gly Leu Ile Val Pro Leu Trp Met Ser
    130                 135                 140

Gln Met Arg Thr Ser Asn Pro Ala Ala Ile Glu Lys Ile Pro Ala Leu
145                 150                 155                 160

Val Leu Asn Ser Pro Trp Leu Asp Met Met Tyr Pro Pro Leu Phe Ile
                165                 170                 175

Lys Leu Ile Thr Pro Met Val Arg Val Leu Gly Lys Arg Ser Pro Thr
            180                 185                 190

Thr Ile Ile Pro Gly Gly Gly Leu Gly Ala Tyr Gly Lys Ser Ile His
        195                 200                 205

Lys Asn Phe Tyr Gly Glu Trp Asp Phe Asp Thr Thr Ile Lys Pro Val
    210                 215                 220

Glu Gly His Lys Lys Ser Ile Gly Trp Leu Arg Ala Val Met Ala Gly
225                 230                 235                 240
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```
Gln Ala Glu Ile His His Asp His Val Asn Val Gly Val Asp Val Leu
                245                 250                 255

Thr Leu Cys Ser Asn Lys Ser Trp Leu Lys Ser Glu Tyr Thr Glu Asp
            260                 265                 270

Thr Asn Thr Ser Asp Ala Val Leu Asp Val Lys His Ile Gln Lys Trp
        275                 280                 285

Ala Pro His Leu Ser Ser Pro Ser Ser Arg Val Asp Val Glu Ile Ile
    290                 295                 300

Asp Asn Ala Arg His Asp Ile Phe Leu Ser Arg Lys Pro Ala Arg Asp
305                 310                 315                 320

His Ala Ser Glu Val Leu Asn Asn Trp Leu Gln Ser Lys Leu Ser Ser
                325                 330                 335

Leu Lys Pro Ser Gln
            340


<210> 203
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(607)
<223> RXA01983

<400> 203
atatcgctgc catggcagcc ttgctgggca acctcaagca cactgaccta gaagagctcc 60

ccaccgatta ccaggggtgt cctcccatgt ccgctgcgtt atg gaa ggc tac gga   115
                                          Met Glu Gly Tyr Gly
                                          1               5

cct acc cag atc gaa aag ctc tta cct gca tac aca cag gtc aac aca   163
Pro Thr Gln Ile Glu Lys Leu Leu Pro Ala Tyr Thr Gln Val Asn Thr
                10                  15                  20

gcc ggg aat aat cca gcg acg acg cct gag caa gat ctc ctc ggc gga   211
Ala Gly Asn Asn Pro Ala Thr Thr Pro Glu Gln Asp Leu Leu Gly Gly
            25                  30                  35

gct gca acc tcg ccg gaa aac tac gac cac cag ctg cag tac gca gtc   259
Ala Ala Thr Ser Pro Glu Asn Tyr Asp His Gln Leu Gln Tyr Ala Val
        40                  45                  50

gac gcc agt ccg gtg cat cag aat gcg gca cag gca ccg ccc ttc ctg   307
Asp Ala Ser Pro Val His Gln Asn Ala Ala Gln Ala Pro Pro Phe Leu
    55                  60                  65

atc atg cac ggc act ggt gac cgg atg gtc cct ccg gag caa tcg gct   355
Ile Met His Gly Thr Gly Asp Arg Met Val Pro Pro Glu Gln Ser Ala
70                  75                  80                  85

gcg ctg cac acc cat ctt gtg cag gct ggt cgg cag tcc acc ctg gta   403
Ala Leu His Thr His Leu Val Gln Ala Gly Arg Gln Ser Thr Leu Val
```

```
                 90                   95                  100

ctc att gag ggc ttt ggc cac ggt ttc ctc aat ccc ggg gaa gtc gcg    451
Leu Ile Glu Gly Phe Gly His Gly Phe Leu Asn Pro Gly Glu Val Ala
            105                 110                 115

gag ctg ggg cca aac gtt cga cta gac aat ggt cgg ctc gag cgg gag    499
Glu Leu Gly Pro Asn Val Arg Leu Asp Asn Gly Arg Leu Glu Arg Glu
        120                 125                 130

cct cag aca aat ttc agc gcg cag cag agt ccg gga aac ccc ttt gaa    547
Pro Gln Thr Asn Phe Ser Ala Gln Gln Ser Pro Gly Asn Pro Phe Glu
    135                 140                 145

cta cag gga ctt gcc gcc gac cat gag atg atc aag cgc ttt ttc acc    595
Leu Gln Gly Leu Ala Ala Asp His Glu Met Ile Lys Arg Phe Phe Thr
150                 155                 160                 165

ctg cac ctt cgc taagactcta ccttcaccca act                          630
Leu His Leu Arg
```

<210> 204
<211> 169
<212> PRT
<213> Corynebacterium glutamicum

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<400> 204
Met Glu Gly Tyr Gly Pro Thr Gln Ile Glu Lys Leu Leu Pro Ala Tyr
  1               5                  10                  15

Thr Gln Val Asn Thr Ala Gly Asn Asn Pro Ala Thr Thr Pro Glu Gln
             20                  25                  30

Asp Leu Leu Gly Gly Ala Ala Thr Ser Pro Glu Asn Tyr Asp His Gln
         35                  40                  45

Leu Gln Tyr Ala Val Asp Ala Ser Pro Val His Gln Asn Ala Ala Gln
     50                  55                  60

Ala Pro Pro Phe Leu Ile Met His Gly Thr Gly Asp Arg Met Val Pro
 65                  70                  75                  80

Pro Glu Gln Ser Ala Ala Leu His Thr His Leu Val Gln Ala Gly Arg
                 85                  90                  95

Gln Ser Thr Leu Val Leu Ile Glu Gly Phe Gly His Gly Phe Leu Asn
            100                 105                 110

Pro Gly Glu Val Ala Glu Leu Gly Pro Asn Val Arg Leu Asp Asn Gly
        115                 120                 125

Arg Leu Glu Arg Glu Pro Gln Thr Asn Phe Ser Ala Gln Gln Ser Pro
    130                 135                 140

Gly Asn Pro Phe Glu Leu Gln Gly Leu Ala Ala Asp His Glu Met Ile
145                 150                 155                 160

Lys Arg Phe Phe Thr Leu His Leu Arg
                165
```

<210> 205
<211> 1414
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1414)
<223> RXN02947

<400> 205
gtatgttcac acaagaaccc tgcacaacgc cttcaaagta cgtcgaccac gaccaagcgc 60

attattcact ctcacccttc aggatttaga ctaagaaacc atg act gca gca cag 115
Met Thr Ala Ala Gln
1 5

acc aaa cct gac ctc acc acc acg gct gga aag ctg tcc gat ctt cgc 163
Thr Lys Pro Asp Leu Thr Thr Thr Ala Gly Lys Leu Ser Asp Leu Arg
10 15 20

tcc cgt ctt gca gaa gct caa gct cca atg ggc gaa gca act gta gaa 211
Ser Arg Leu Ala Glu Ala Gln Ala Pro Met Gly Glu Ala Thr Val Glu
25 30 35

aaa gtg cac gct gct ggc agg aag act gcc cgc gaa cgt atc gag tat 259
Lys Val His Ala Ala Gly Arg Lys Thr Ala Arg Glu Arg Ile Glu Tyr
40 45 50

ttg ctc gat gag ggc tct ttc gta gag atc gat gct ctt gct cgt cac 307
Leu Leu Asp Glu Gly Ser Phe Val Glu Ile Asp Ala Leu Ala Arg His
55 60 65

cgt tcc aag aac ttc ggc ctg gat gcc aag cgt cca gtt act gac ggt 355
Arg Ser Lys Asn Phe Gly Leu Asp Ala Lys Arg Pro Val Thr Asp Gly
70 75 80 85

gtt gtg act ggt tac ggc acc atc gat ggc cgt aag gtc tgt gtg ttc 403
Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg Lys Val Cys Val Phe
90 95 100

tcc cag gac ggc gct gta ttc ggt ggc gct ttg ggt gaa gtt tat ggt 451
Ser Gln Asp Gly Ala Val Phe Gly Gly Ala Leu Gly Glu Val Tyr Gly
105 110 115

gaa aag atc gtt aag gtt atg gat ctt gcg atc aag acc ggt gtg cct 499
Glu Lys Ile Val Lys Val Met Asp Leu Ala Ile Lys Thr Gly Val Pro
120 125 130

ttg atc gga atc aat gag ggt gct ggt gcg cgt atc cag gaa ggt gtt 547
Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg Ile Gln Glu Gly Val
135 140 145

gtg tct ctg ggt ctg tac tca cag atc ttc tac cgc aac acc cag gcg 595
Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr Arg Asn Thr Gln Ala
150 155 160 165

tct ggc gtt atc cca cag atc tct ttg atc atg ggt gcc tgc gct ggt 643
Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met Gly Ala Cys Ala Gly

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                170                 175                 180

ggt cac gtg tac tcc cct gct ctg act gac ttc atc gtc atg gtg gat    691
Gly His Val Tyr Ser Pro Ala Leu Thr Asp Phe Ile Val Met Val Asp
            185                 190                 195

cag act tcc aag atg ttt atc acc ggc cct gat gtc atc aag act gtc    739
Gln Thr Ser Lys Met Phe Ile Thr Gly Pro Asp Val Ile Lys Thr Val
        200                 205                 210

acc ggt gaa gat gtc acc cag gag gag ctc ggt ggc gct cac acc cac    787
Thr Gly Glu Asp Val Thr Gln Glu Glu Leu Gly Gly Ala His Thr His
    215                 220                 225

atg gct acc tcc ggt acc tcc cat tac tct gct tct gat gat tca gat    835
Met Ala Thr Ser Gly Thr Ser His Tyr Ser Ala Ser Asp Asp Ser Asp
230                 235                 240                 245

gct ttg gat tgg gtt cgc gag ctg acc tct tat ctt cca tcc aac aac    883
Ala Leu Asp Trp Val Arg Glu Leu Thr Ser Tyr Leu Pro Ser Asn Asn
                250                 255                 260

cgt gcg gaa act cct cgc cag gag gcc gac atc atg atc ggt tcc atc    931
Arg Ala Glu Thr Pro Arg Gln Glu Ala Asp Ile Met Ile Gly Ser Ile
            265                 270                 275

cag gaa aac atc aac gat gtg gat ctg gaa ttg gac acc atc atc ccg    979
Gln Glu Asn Ile Asn Asp Val Asp Leu Glu Leu Asp Thr Ile Ile Pro
        280                 285                 290

gat tcc ccg aac cag cct tat gac atg aag gaa gtt att tcc cgc atc    1027
Asp Ser Pro Asn Gln Pro Tyr Asp Met Lys Glu Val Ile Ser Arg Ile
    295                 300                 305

gtc gac gac gcc gag ttc ttc gag atc cag gaa gac tac gca gag aac    1075
Val Asp Asp Ala Glu Phe Phe Glu Ile Gln Glu Asp Tyr Ala Glu Asn
310                 315                 320                 325

atc ctg tgt ggc ttc gct cgc gtt gag gtc cgt tct gtt ggc atc gtg    1123
Ile Leu Cys Gly Phe Ala Arg Val Glu Val Arg Ser Val Gly Ile Val
                330                 335                 340

gct aac cag cca acc cag ttc gct ggc tgc ttg gat att aag gca tct    1171
Ala Asn Gln Pro Thr Gln Phe Ala Gly Cys Leu Asp Ile Lys Ala Ser
            345                 350                 355

gag aag gct gcc cgt ttc atc cgc acc tgc gat gcc ttc aac atc cca    1219
Glu Lys Ala Ala Arg Phe Ile Arg Thr Cys Asp Ala Phe Asn Ile Pro
        360                 365                 370

atc ctt gag ttc gtg gac gtt cca ggc ttc ctg cct ggc acc aac cag    1267
Ile Leu Glu Phe Val Asp Val Pro Gly Phe Leu Pro Gly Thr Asn Gln
    375                 380                 385

gaa ttc gac ggc atc atc cgc cgc ggc gca aag ctg ctt tac gct tac    1315
Glu Phe Asp Gly Ile Ile Arg Arg Gly Ala Lys Leu Leu Tyr Ala Tyr
390                 395                 400                 405

gct gaa gca acc gtc ggc aag atc acc gtc atc acc cgc aag tcc tac    1363
Ala Glu Ala Thr Val Gly Lys Ile Thr Val Ile Thr Arg Lys Ser Tyr
                410                 415                 420
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ggc gga gcg tac tgc gtg atg ggt tcc aag gat atg ggc gct ggc ctg    1411
Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Asp Met Gly Ala Gly Leu
            425                 430                 435

gta                                                                1414
Val



<210> 206
<211> 438
<212> PRT
<213> Corynebacterium glutamicum

<400> 206
Met Thr Ala Ala Gln Thr Lys Pro Asp Leu Thr Thr Thr Ala Gly Lys
  1               5                  10                  15

Leu Ser Asp Leu Arg Ser Arg Leu Ala Glu Ala Gln Ala Pro Met Gly
            20                  25                  30

Glu Ala Thr Val Glu Lys Val His Ala Ala Gly Arg Lys Thr Ala Arg
        35                  40                  45

Glu Arg Ile Glu Tyr Leu Leu Asp Glu Gly Ser Phe Val Glu Ile Asp
    50                  55                  60

Ala Leu Ala Arg His Arg Ser Lys Asn Phe Gly Leu Asp Ala Lys Arg
65                  70                  75                  80

Pro Val Thr Asp Gly Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg
                85                  90                  95

Lys Val Cys Val Phe Ser Gln Asp Gly Ala Val Phe Gly Gly Ala Leu
            100                 105                 110

Gly Glu Val Tyr Gly Glu Lys Ile Val Lys Val Met Asp Leu Ala Ile
        115                 120                 125

Lys Thr Gly Val Pro Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg
    130                 135                 140

Ile Gln Glu Gly Val Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr
145                 150                 155                 160

Arg Asn Thr Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met
                165                 170                 175

Gly Ala Cys Ala Gly Gly His Val Tyr Ser Pro Ala Leu Thr Asp Phe
            180                 185                 190

Ile Val Met Val Asp Gln Thr Ser Lys Met Phe Ile Thr Gly Pro Asp
        195                 200                 205

Val Ile Lys Thr Val Thr Gly Glu Asp Val Thr Gln Glu Glu Leu Gly
    210                 215                 220

Gly Ala His Thr His Met Ala Thr Ser Gly Thr Ser His Tyr Ser Ala
225                 230                 235                 240
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Ser Asp Asp Ser Asp Ala Leu Asp Trp Val Arg Glu Leu Thr Ser Tyr
                245                 250                 255

Leu Pro Ser Asn Asn Arg Ala Glu Thr Pro Arg Gln Glu Ala Asp Ile
            260                 265                 270

Met Ile Gly Ser Ile Gln Glu Asn Ile Asn Asp Val Asp Leu Glu Leu
        275                 280                 285

Asp Thr Ile Ile Pro Asp Ser Pro Asn Gln Pro Tyr Asp Met Lys Glu
    290                 295                 300

Val Ile Ser Arg Ile Val Asp Asp Ala Glu Phe Phe Glu Ile Gln Glu
305                 310                 315                 320

Asp Tyr Ala Glu Asn Ile Leu Cys Gly Phe Ala Arg Val Glu Val Arg
                325                 330                 335

Ser Val Gly Ile Val Ala Asn Gln Pro Thr Gln Phe Ala Gly Cys Leu
            340                 345                 350

Asp Ile Lys Ala Ser Glu Lys Ala Ala Arg Phe Ile Arg Thr Cys Asp
        355                 360                 365

Ala Phe Asn Ile Pro Ile Leu Glu Phe Val Asp Val Pro Gly Phe Leu
    370                 375                 380

Pro Gly Thr Asn Gln Glu Phe Asp Gly Ile Ile Arg Arg Gly Ala Lys
385                 390                 395                 400

Leu Leu Tyr Ala Tyr Ala Glu Ala Thr Val Gly Lys Ile Thr Val Ile
                405                 410                 415

Thr Arg Lys Ser Tyr Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Asp
            420                 425                 430

Met Gly Ala Gly Leu Val
        435


<210> 207
<211> 688
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(688)
<223> FRXA02320

<400> 207
gtatgttcac acaagaaccc tgcacaacgc cttcaaagta cgtcgaccac gaccaagcgc 60

attattcact ctcacccttc aggatttaga ctaagaaacc atg act gca gca cag   115
                                            Met Thr Ala Ala Gln
                                            1               5

acc aaa cct gac ctc acc acc acg gct gga aag ctg tcc gat ctt cgc   163
Thr Lys Pro Asp Leu Thr Thr Thr Ala Gly Lys Leu Ser Asp Leu Arg
                10                  15                  20
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tcc cgt ctt gca gaa gct caa gct cca atg ggc gaa gca act gta gaa 211
Ser Arg Leu Ala Glu Ala Gln Ala Pro Met Gly Glu Ala Thr Val Glu
25 30 35

aaa gtg cac gct gct ggc agg aag act gcc cgc gaa cgt atc gag tat 259
Lys Val His Ala Ala Gly Arg Lys Thr Ala Arg Glu Arg Ile Glu Tyr
40 45 50

ttg ctc gat gag ggc tct ttc gta gag atc gat gct ctt gct cgt cac 307
Leu Leu Asp Glu Gly Ser Phe Val Glu Ile Asp Ala Leu Ala Arg His
55 60 65

cgt tcc aag aac ttc ggc ctg gat gcc aag cgt cca gtt act gac ggt 355
Arg Ser Lys Asn Phe Gly Leu Asp Ala Lys Arg Pro Val Thr Asp Gly
70 75 80 85

gtt gtg act ggt tac ggc acc atc gat ggc cgt aag gtc tgt gtg ttc 403
Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg Lys Val Cys Val Phe
90 95 100

tcc cag gac ggc gct gta ttc ggt ggc gct ttg ggt gaa gtt tat ggt 451
Ser Gln Asp Gly Ala Val Phe Gly Gly Ala Leu Gly Glu Val Tyr Gly
105 110 115

gaa aag atc gtt aag gtt atg gat ctt gcg atc aag acc ggt gtg cct 499
Glu Lys Ile Val Lys Val Met Asp Leu Ala Ile Lys Thr Gly Val Pro
120 125 130

ttg atc gga atc aat gag ggt gct ggt gcg cgt atc cag gaa ggt gtt 547
Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg Ile Gln Glu Gly Val
135 140 145

gtg tct ctg ggt ctg tac tca cag atc ttc tac cgc aac acc cag gcg 595
Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr Arg Asn Thr Gln Ala
150 155 160 165

tct ggc gtt atc cca cag atc tct ttg atc atg ggt gcc tgc gct ggt 643
Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met Gly Ala Cys Ala Gly
170 175 180

ggt cac gtg tac tcc cct gct ctg act gac ttc atc gtc atg gtg 688
Gly His Val Tyr Ser Pro Ala Leu Thr Asp Phe Ile Val Met Val
185 190 195

<210> 208
<211> 196
<212> PRT
<213> Corynebacterium glutamicum

<400> 208
Met Thr Ala Ala Gln Thr Lys Pro Asp Leu Thr Thr Thr Ala Gly Lys
1 5 10 15

Leu Ser Asp Leu Arg Ser Arg Leu Ala Glu Ala Gln Ala Pro Met Gly
20 25 30

Glu Ala Thr Val Glu Lys Val His Ala Ala Gly Arg Lys Thr Ala Arg
35 40 45

Glu Arg Ile Glu Tyr Leu Leu Asp Glu Gly Ser Phe Val Glu Ile Asp

50 55 60

Ala Leu Ala Arg His Arg Ser Lys Asn Phe Gly Leu Asp Ala Lys Arg
65 70 75 80

Pro Val Thr Asp Gly Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg
85 90 95

Lys Val Cys Val Phe Ser Gln Asp Gly Ala Val Phe Gly Gly Ala Leu
100 105 110

Gly Glu Val Tyr Gly Glu Lys Ile Val Lys Val Met Asp Leu Ala Ile
115 120 125

Lys Thr Gly Val Pro Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg
130 135 140

Ile Gln Glu Gly Val Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr
145 150 155 160

Arg Asn Thr Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met
165 170 175

Gly Ala Cys Ala Gly Gly His Val Tyr Ser Pro Ala Leu Thr Asp Phe
180 185 190

Ile Val Met Val
195

<210> 209
<211> 519
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(519)
<223> FRXA02851

<400> 209
cct cgc cag aag gcc gac atc atg atc ggt tcc atc cag gaa aac atc 48
Pro Arg Gln Lys Ala Asp Ile Met Ile Gly Ser Ile Gln Glu Asn Ile
1 5 10 15

aac gat gtg gat ctg gaa ttg gac acc atc atc ccg gat tcc ccg aac 96
Asn Asp Val Asp Leu Glu Leu Asp Thr Ile Ile Pro Asp Ser Pro Asn
20 25 30

cag cct tat gac atg aag gaa gtt att tcc cgc atc gtn gac gac gcc 144
Gln Pro Tyr Asp Met Lys Glu Val Ile Ser Arg Ile Val Asp Asp Ala
35 40 45

gag ttc ttc gag atc cag gaa gac tac gca gag aac atc ctg tgt ggc 192
Glu Phe Phe Glu Ile Gln Glu Asp Tyr Ala Glu Asn Ile Leu Cys Gly
50 55 60

ttc gct cgc gtt gag gnc cgt tnt gtt ggc atc gtg gct aac cag cca 240
Phe Ala Arg Val Glu Xaa Arg Xaa Val Gly Ile Val Ala Asn Gln Pro
65 70 75 80

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acc cag ttc gct ggc tgn ttg gat att aag gca tct gag aag gct gcc     288
Thr Gln Phe Ala Gly Xaa Leu Asp Ile Lys Ala Ser Glu Lys Ala Ala
                85                  90                  95

cgt ttc atc cgc acc tgc gat gcc ttc aac atc cca atc ctt gag ttc     336
Arg Phe Ile Arg Thr Cys Asp Ala Phe Asn Ile Pro Ile Leu Glu Phe
            100                 105                 110

gtg gac gtt cca ggc ttc ctg cct ggc acc aac cag gaa ttc gac ggc     384
Val Asp Val Pro Gly Phe Leu Pro Gly Thr Asn Gln Glu Phe Asp Gly
        115                 120                 125

atc atc cgc cgc ggc gca aag ctg ctt tac gct tac gct gaa gca acc     432
Ile Ile Arg Arg Gly Ala Lys Leu Leu Tyr Ala Tyr Ala Glu Ala Thr
    130                 135                 140

gtc ggc aag atc acc gtc atc acc cgc aag tcc tac ggc gga gcg tac     480
Val Gly Lys Ile Thr Val Ile Thr Arg Lys Ser Tyr Gly Gly Ala Tyr
145                 150                 155                 160

tgc gtg atg ggt tcc aag gat atg ggc gct ggc ctg gta                 519
Cys Val Met Gly Ser Lys Asp Met Gly Ala Gly Leu Val
                165                 170


<210> 210
<211> 173
<212> PRT
<213> Corynebacterium glutamicum

<400> 210
Pro Arg Gln Lys Ala Asp Ile Met Ile Gly Ser Ile Gln Glu Asn Ile
  1               5                  10                  15

Asn Asp Val Asp Leu Glu Leu Asp Thr Ile Ile Pro Asp Ser Pro Asn
            20                  25                  30

Gln Pro Tyr Asp Met Lys Glu Val Ile Ser Arg Ile Val Asp Asp Ala
        35                  40                  45

Glu Phe Phe Glu Ile Gln Glu Asp Tyr Ala Glu Asn Ile Leu Cys Gly
    50                  55                  60

Phe Ala Arg Val Glu Xaa Arg Xaa Val Gly Ile Val Ala Asn Gln Pro
65                  70                  75                  80

Thr Gln Phe Ala Gly Xaa Leu Asp Ile Lys Ala Ser Glu Lys Ala Ala
                85                  90                  95

Arg Phe Ile Arg Thr Cys Asp Ala Phe Asn Ile Pro Ile Leu Glu Phe
            100                 105                 110

Val Asp Val Pro Gly Phe Leu Pro Gly Thr Asn Gln Glu Phe Asp Gly
        115                 120                 125

Ile Ile Arg Arg Gly Ala Lys Leu Leu Tyr Ala Tyr Ala Glu Ala Thr
    130                 135                 140

Val Gly Lys Ile Thr Val Ile Thr Arg Lys Ser Tyr Gly Gly Ala Tyr
145                 150                 155                 160
```

```
Cys Val Met Gly Ser Lys Asp Met Gly Ala Gly Leu Val
                165                 170


<210> 211
<211> 1752
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1729)
<223> RXN02321

<400> 211
tttaaaaact acccgcacgc agcacgaacc tgttcagtga tgtaaatcac cgcggaaata 60

ttgtggacgt taccccgcc taccgctacg atttcaaaac atg acc att tcc tca    115
                                           Met Thr Ile Ser Ser
                                           1               5

cct ttg att gac gtc gcc aac ctt cca gac atc aac acc act gcc ggc   163
Pro Leu Ile Asp Val Ala Asn Leu Pro Asp Ile Asn Thr Thr Ala Gly
                10                  15                  20

aag atc gcc gac ctt aag gct cgc cgc gcg gaa gcc cat ttc ccc atg   211
Lys Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu Ala His Phe Pro Met
            25                  30                  35

ggt gaa aag gca gta gag aag gtc cac gct gct gga cgc ctc act gcc   259
Gly Glu Lys Ala Val Glu Lys Val His Ala Ala Gly Arg Leu Thr Ala
        40                  45                  50

cgt gag cgc ttg gat tac tta ctc gat gag ggc tcc ttc atc gag acc   307
Arg Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly Ser Phe Ile Glu Thr
    55                  60                  65

gat cag ctg gct cgc cac cgc acc acc gct ttc tgc ctg ggc gct aag   355
Asp Gln Leu Ala Arg His Arg Thr Thr Ala Phe Cys Leu Gly Ala Lys
70                  75                  80                  85

cgt cct gca acc gac ggt atc gtg acc ggc tgg ggc acc att gat gga   403
Arg Pro Ala Thr Asp Gly Ile Val Thr Gly Trp Gly Thr Ile Asp Gly
                90                  95                  100

cgc gaa gtc tgc atc ttc tcg cag gac ggc acc gta ttc ggt ggc gcg   451
Arg Glu Val Cys Ile Phe Ser Gln Asp Gly Thr Val Phe Gly Gly Ala
            105                 110                 115

ctt ggt gag gtg tac ggc gaa aag atg atc aag atc atg gag ctg gca   499
Leu Gly Glu Val Tyr Gly Glu Lys Met Ile Lys Ile Met Glu Leu Ala
        120                 125                 130

atc gac acc ggc cgc cca ttg atc ggt ctt tac gaa ggc gct ggc gct   547
Ile Asp Thr Gly Arg Pro Leu Ile Gly Leu Tyr Glu Gly Ala Gly Ala
    135                 140                 145

cgt att cag gac ggc gct gtc tcc ctg gac ttc att tcc cag acc ttc   595
Arg Ile Gln Asp Gly Ala Val Ser Leu Asp Phe Ile Ser Gln Thr Phe
150                 155                 160                 165
```

tac caa aac att cag gct tct ggc gtt atc cca cag atc tcc gtc atc 643
Tyr Gln Asn Ile Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Val Ile
170 175 180

atg ggc gca tgt gca ggt ggc aac gct tac ggc cca gct ctg acc gac 691
Met Gly Ala Cys Ala Gly Gly Asn Ala Tyr Gly Pro Ala Leu Thr Asp
185 190 195

ttc gtg gtc atg gtg gac aag acc tcc aag atg ttc gtt acc ggc cca 739
Phe Val Val Met Val Asp Lys Thr Ser Lys Met Phe Val Thr Gly Pro
200 205 210

gac gtg atc aag acc gtc acc ggc gag gaa atc acc cag gaa gag ctt 787
Asp Val Ile Lys Thr Val Thr Gly Glu Glu Ile Thr Gln Glu Glu Leu
215 220 225

ggc gga gca acc acc cac atg gtg acc gct ggt aac tcc cac tac acc 835
Gly Gly Ala Thr Thr His Met Val Thr Ala Gly Asn Ser His Tyr Thr
230 235 240 245

gct gcg acc gat gag gaa gca ctg gat tgg gta cag gac ctg gtg tcc 883
Ala Ala Thr Asp Glu Glu Ala Leu Asp Trp Val Gln Asp Leu Val Ser
250 255 260

ttc ctc cca tcc aac aat cgc tcc tac gca ccg atg gaa gac ttc gac 931
Phe Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro Met Glu Asp Phe Asp
265 270 275

gag gaa gaa ggc ggc gtt gaa gaa aac atc acc gct gac gat ctg aag 979
Glu Glu Glu Gly Gly Val Glu Glu Asn Ile Thr Ala Asp Asp Leu Lys
280 285 290

ctc gac gag atc atc cca gat tcc gcg acc gtt cct tac gac gtc cgc 1027
Leu Asp Glu Ile Ile Pro Asp Ser Ala Thr Val Pro Tyr Asp Val Arg
295 300 305

gat gtc atc gaa tgc ctc acc gac gat ggc gaa tac ctg gaa atc cag 1075
Asp Val Ile Glu Cys Leu Thr Asp Asp Gly Glu Tyr Leu Glu Ile Gln
310 315 320 325

gca gac cgc gca gaa aac gtt gtt att gca ttc ggc cgc atc gaa ggc 1123
Ala Asp Arg Ala Glu Asn Val Val Ile Ala Phe Gly Arg Ile Glu Gly
330 335 340

cag tcc gtt ggc ttt gtt gcc aac cag cca acc cag ttc gct ggc tgc 1171
Gln Ser Val Gly Phe Val Ala Asn Gln Pro Thr Gln Phe Ala Gly Cys
345 350 355

ctg gac atc gac tcc tct gag aag gca gct cgc ttc gtc cgc acc tgc 1219
Leu Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg Phe Val Arg Thr Cys
360 365 370

gac gcg ttc aac atc cca atc gtc atg ctt gtc gac gtc ccc ggc ttc 1267
Asp Ala Phe Asn Ile Pro Ile Val Met Leu Val Asp Val Pro Gly Phe
375 380 385

ctc cca ggc gca ggc cag gag tac ggt ggc att ctg cgt cgt ggc gca 1315
Leu Pro Gly Ala Gly Gln Glu Tyr Gly Gly Ile Leu Arg Arg Gly Ala
390 395 400 405

aag ctg ctc tac gca tac ggc gaa gca acc gtt cca aag atc acc gtc 1363

```
Lys Leu Leu Tyr Ala Tyr Gly Glu Ala Thr Val Pro Lys Ile Thr Val
                410                 415                 420

acc atg cgt aag gct tac ggc gga gcg tac tgc gtg atg ggt tcc aag    1411
Thr Met Arg Lys Ala Tyr Gly Gly Ala Tyr Cys Val Met Gly Ser Lys
            425                 430                 435

ggc ttg ggc tct gac atc aac ctt gca tgg cca acc gca cag atc gcc    1459
Gly Leu Gly Ser Asp Ile Asn Leu Ala Trp Pro Thr Ala Gln Ile Ala
        440                 445                 450

gtc atg ggc gct gct ggc gca gtt gga ttc atc tac cgc aag gag ctc    1507
Val Met Gly Ala Ala Gly Ala Val Gly Phe Ile Tyr Arg Lys Glu Leu
    455                 460                 465

atg gca gct gat gcc aag ggc ctc gat acc gta gct ctg gct aag tcc    1555
Met Ala Ala Asp Ala Lys Gly Leu Asp Thr Val Ala Leu Ala Lys Ser
470                 475                 480                 485

ttc gag cgc gag tat gaa gac cac atg ctc aac ccg tac cac gct gca    1603
Phe Glu Arg Glu Tyr Glu Asp His Met Leu Asn Pro Tyr His Ala Ala
                490                 495                 500

gaa cgt ggc ctg atc gac gcc gtg atc ctg cca agc gaa acc cgc gga    1651
Glu Arg Gly Leu Ile Asp Ala Val Ile Leu Pro Ser Glu Thr Arg Gly
            505                 510                 515

cag att tcc cgc aac ctt cgc ctg ctc aag cac aag aac gtc act cgc    1699
Gln Ile Ser Arg Asn Leu Arg Leu Leu Lys His Lys Asn Val Thr Arg
        520                 525                 530

cct gct cgc aag cac ggc aac atg cca ctg taaatcggcg aatccataaa      1749
Pro Ala Arg Lys His Gly Asn Met Pro Leu
    535                 540

ggt                                                                1752


<210> 212
<211> 543
<212> PRT
<213> Corynebacterium glutamicum

<400> 212
Met Thr Ile Ser Ser Pro Leu Ile Asp Val Ala Asn Leu Pro Asp Ile
  1               5                  10                  15

Asn Thr Thr Ala Gly Lys Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu
             20                  25                  30

Ala His Phe Pro Met Gly Glu Lys Ala Val Glu Lys Val His Ala Ala
         35                  40                  45

Gly Arg Leu Thr Ala Arg Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly
     50                  55                  60

Ser Phe Ile Glu Thr Asp Gln Leu Ala Arg His Arg Thr Thr Ala Phe
 65                  70                  75                  80

Cys Leu Gly Ala Lys Arg Pro Ala Thr Asp Gly Ile Val Thr Gly Trp
                 85                  90                  95
```

```
Gly Thr Ile Asp Gly Arg Glu Val Cys Ile Phe Ser Gln Asp Gly Thr
            100                 105                 110

Val Phe Gly Gly Ala Leu Gly Glu Val Tyr Gly Glu Lys Met Ile Lys
        115                 120                 125

Ile Met Glu Leu Ala Ile Asp Thr Gly Arg Pro Leu Ile Gly Leu Tyr
    130                 135                 140

Glu Gly Ala Gly Ala Arg Ile Gln Asp Gly Ala Val Ser Leu Asp Phe
145                 150                 155                 160

Ile Ser Gln Thr Phe Tyr Gln Asn Ile Gln Ala Ser Gly Val Ile Pro
                165                 170                 175

Gln Ile Ser Val Ile Met Gly Ala Cys Ala Gly Gly Asn Ala Tyr Gly
            180                 185                 190

Pro Ala Leu Thr Asp Phe Val Val Met Val Asp Lys Thr Ser Lys Met
        195                 200                 205

Phe Val Thr Gly Pro Asp Val Ile Lys Thr Val Thr Gly Glu Glu Ile
    210                 215                 220

Thr Gln Glu Glu Leu Gly Gly Ala Thr Thr His Met Val Thr Ala Gly
225                 230                 235                 240

Asn Ser His Tyr Thr Ala Ala Thr Asp Glu Glu Ala Leu Asp Trp Val
                245                 250                 255

Gln Asp Leu Val Ser Phe Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro
            260                 265                 270

Met Glu Asp Phe Asp Glu Glu Glu Gly Gly Val Glu Glu Asn Ile Thr
        275                 280                 285

Ala Asp Asp Leu Lys Leu Asp Glu Ile Ile Pro Asp Ser Ala Thr Val
    290                 295                 300

Pro Tyr Asp Val Arg Asp Val Ile Glu Cys Leu Thr Asp Asp Gly Glu
305                 310                 315                 320

Tyr Leu Glu Ile Gln Ala Asp Arg Ala Glu Asn Val Val Ile Ala Phe
                325                 330                 335

Gly Arg Ile Glu Gly Gln Ser Val Gly Phe Val Ala Asn Gln Pro Thr
            340                 345                 350

Gln Phe Ala Gly Cys Leu Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg
        355                 360                 365

Phe Val Arg Thr Cys Asp Ala Phe Asn Ile Pro Ile Val Met Leu Val
    370                 375                 380

Asp Val Pro Gly Phe Leu Pro Gly Ala Gly Gln Glu Tyr Gly Gly Ile
385                 390                 395                 400

Leu Arg Arg Gly Ala Lys Leu Leu Tyr Ala Tyr Gly Glu Ala Thr Val
                405                 410                 415
```

```
Pro Lys Ile Thr Val Thr Met Arg Lys Ala Tyr Gly Gly Ala Tyr Cys
            420                 425                 430

Val Met Gly Ser Lys Gly Leu Gly Ser Asp Ile Asn Leu Ala Trp Pro
        435                 440                 445

Thr Ala Gln Ile Ala Val Met Gly Ala Ala Gly Ala Val Gly Phe Ile
    450                 455                 460

Tyr Arg Lys Glu Leu Met Ala Ala Asp Ala Lys Gly Leu Asp Thr Val
465                 470                 475                 480

Ala Leu Ala Lys Ser Phe Glu Arg Glu Tyr Glu Asp His Met Leu Asn
                485                 490                 495

Pro Tyr His Ala Ala Glu Arg Gly Leu Ile Asp Ala Val Ile Leu Pro
            500                 505                 510

Ser Glu Thr Arg Gly Gln Ile Ser Arg Asn Leu Arg Leu Leu Lys His
        515                 520                 525

Lys Asn Val Thr Arg Pro Ala Arg Lys His Gly Asn Met Pro Leu
    530                 535                 540


<210> 213
<211> 467
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(444)
<223> FRXA02321

<400> 213
gag tac ggt ggc att ctg cgt cgt ggc gca aag ctg ctc tac gca tcg      48
Glu Tyr Gly Gly Ile Leu Arg Arg Gly Ala Lys Leu Leu Tyr Ala Ser
  1               5                  10                  15

gnn gaa gca ccg gtt cca aag atc acc gtc acc atg cgt aag gct tac      96
Xaa Glu Ala Pro Val Pro Lys Ile Thr Val Thr Met Arg Lys Ala Tyr
             20                  25                  30

ggc gga gcg tac tgc gtg atg ggt tcc aag ggc ttg ggc tct gac atc     144
Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Gly Leu Gly Ser Asp Ile
         35                  40                  45

aac ctt gca tgg cca acc gca cag atc gcc gtc atg ggc gct gct ggc     192
Asn Leu Ala Trp Pro Thr Ala Gln Ile Ala Val Met Gly Ala Ala Gly
     50                  55                  60

gca gtt gga ttc atc tac cgc aag gag ctc atg gca gct gat gcc aag     240
Ala Val Gly Phe Ile Tyr Arg Lys Glu Leu Met Ala Ala Asp Ala Lys
 65                  70                  75                  80

ggc ctc gat acc gta gct ctg gct aag tcc ttc gag cgc gag tat gaa     288
Gly Leu Asp Thr Val Ala Leu Ala Lys Ser Phe Glu Arg Glu Tyr Glu
                 85                  90                  95

gac cac atg ctc aac ccg tac cac gct gca gaa cgt ggc ctg atc gac     336
```

```
Asp His Met Leu Asn Pro Tyr His Ala Ala Glu Arg Gly Leu Ile Asp
            100                 105                 110

gcc gtg atc ctg cca agc gaa acc cgc gga cag att tcc cgc aac ctt     384
Ala Val Ile Leu Pro Ser Glu Thr Arg Gly Gln Ile Ser Arg Asn Leu
        115                 120                 125

cgc ctg ctc aag cac aag aac gtc act cgc cct gct cgc aag cac ggc     432
Arg Leu Leu Lys His Lys Asn Val Thr Arg Pro Ala Arg Lys His Gly
    130                 135                 140

aac atg cca ctg taaatcggcg aatccataaa ggt                           467
Asn Met Pro Leu
145


<210> 214
<211> 148
<212> PRT
<213> Corynebacterium glutamicum

<400> 214
Glu Tyr Gly Gly Ile Leu Arg Arg Gly Ala Lys Leu Leu Tyr Ala Ser
  1               5                  10                  15

Xaa Glu Ala Pro Val Pro Lys Ile Thr Val Thr Met Arg Lys Ala Tyr
             20                  25                  30

Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Gly Leu Gly Ser Asp Ile
         35                  40                  45

Asn Leu Ala Trp Pro Thr Ala Gln Ile Ala Val Met Gly Ala Ala Gly
     50                  55                  60

Ala Val Gly Phe Ile Tyr Arg Lys Glu Leu Met Ala Ala Asp Ala Lys
 65                  70                  75                  80

Gly Leu Asp Thr Val Ala Leu Ala Lys Ser Phe Glu Arg Glu Tyr Glu
                 85                  90                  95

Asp His Met Leu Asn Pro Tyr His Ala Ala Glu Arg Gly Leu Ile Asp
            100                 105                 110

Ala Val Ile Leu Pro Ser Glu Thr Arg Gly Gln Ile Ser Arg Asn Leu
        115                 120                 125

Arg Leu Leu Lys His Lys Asn Val Thr Arg Pro Ala Arg Lys His Gly
    130                 135                 140

Asn Met Pro Leu
145


<210> 215
<211> 514
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(514)
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<223> FRXA02343

<400> 215
tttaaaaact acccgcacgc agcacgaacc tgttcagtga tgtaaatcac cgcggaaata 60

ttgtggacgt taccccccgcc taccgctacg atttcaaaac atg acc att tcc tca 115
Met Thr Ile Ser Ser
1 5

cct ttg att gac gtc gcc aac ctt cca gac atc aac acc act gcc ggc 163
Pro Leu Ile Asp Val Ala Asn Leu Pro Asp Ile Asn Thr Thr Ala Gly
10 15 20

aag atc gcc gac ctt aag gct cgc cgc gcg gaa gcc cat ttc ccc atg 211
Lys Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu Ala His Phe Pro Met
25 30 35

ggt gaa aag gca gta gag aag gtc cac gct gct gga cgc ctc act gcc 259
Gly Glu Lys Ala Val Glu Lys Val His Ala Ala Gly Arg Leu Thr Ala
40 45 50

cgt gag cgc ttg gat tac tta ctc gat gag ggc tcc ttc atc gag acc 307
Arg Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly Ser Phe Ile Glu Thr
55 60 65

gat cag ctg gct cgc cac cgc acc acc gct ttc tgc ctg ggc gct aag 355
Asp Gln Leu Ala Arg His Arg Thr Thr Ala Phe Cys Leu Gly Ala Lys
70 75 80 85

cgt cct gca acc gac ggc atc gtg acc ggc tgg ggc acc att gat gga 403
Arg Pro Ala Thr Asp Gly Ile Val Thr Gly Trp Gly Thr Ile Asp Gly
90 95 100

cgc gaa gtc tgc atc ttc tcg cag gac ggc acc gta ttc ggt ggc gcg 451
Arg Glu Val Cys Ile Phe Ser Gln Asp Gly Thr Val Phe Gly Gly Ala
105 110 115

ctt ggt gag gtg tac ggc gaa aag atg atc aag atc atg gag ctg gca 499
Leu Gly Glu Val Tyr Gly Glu Lys Met Ile Lys Ile Met Glu Leu Ala
120 125 130

atc gac acc ggc cgc 514
Ile Asp Thr Gly Arg
135

<210> 216
<211> 138
<212> PRT
<213> Corynebacterium glutamicum

<400> 216
Met Thr Ile Ser Ser Pro Leu Ile Asp Val Ala Asn Leu Pro Asp Ile
1 5 10 15

Asn Thr Thr Ala Gly Lys Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu
20 25 30

Ala His Phe Pro Met Gly Glu Lys Ala Val Glu Lys Val His Ala Ala
35 40 45

```
Gly Arg Leu Thr Ala Arg Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly
    50                  55                  60

Ser Phe Ile Glu Thr Asp Gln Leu Ala Arg His Arg Thr Thr Ala Phe
 65                  70                  75                  80

Cys Leu Gly Ala Lys Arg Pro Ala Thr Asp Gly Ile Val Thr Gly Trp
                85                  90                  95

Gly Thr Ile Asp Gly Arg Glu Val Cys Ile Phe Ser Gln Asp Gly Thr
            100                 105                 110

Val Phe Gly Gly Ala Leu Gly Glu Val Tyr Gly Glu Lys Met Ile Lys
        115                 120                 125

Ile Met Glu Leu Ala Ile Asp Thr Gly Arg
    130                 135


<210> 217
<211> 492
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(492)
<223> FRXA02850

<400> 217
gaa gag ctt ggc gga gca acc acc cac atg gtg acc gct ggt aac tcc      48
Glu Glu Leu Gly Gly Ala Thr Thr His Met Val Thr Ala Gly Asn Ser
  1               5                  10                  15

cac tac acc gct gcg acc gat gag gaa gca ctg gat tgg gta cag gac      96
His Tyr Thr Ala Ala Thr Asp Glu Glu Ala Leu Asp Trp Val Gln Asp
             20                  25                  30

ctg gtg tcc ttc ctc cca tcc aac aat cgc tcc tac gca ccg atg gaa     144
Leu Val Ser Phe Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro Met Glu
         35                  40                  45

gac ttc gac gag gaa gaa ggc ggc gtt gaa gaa aac atc acc gct gac     192
Asp Phe Asp Glu Glu Glu Gly Gly Val Glu Glu Asn Ile Thr Ala Asp
     50                  55                  60

gat ctg aag ctc gac gag atc atc cca gat tcc gcg acc gtt cct tac     240
Asp Leu Lys Leu Asp Glu Ile Ile Pro Asp Ser Ala Thr Val Pro Tyr
 65                  70                  75                  80

gac gtc cgc gat gtc atn gaa tgc ctc acc gac gat ggc gaa tac ctg     288
Asp Val Arg Asp Val Xaa Glu Cys Leu Thr Asp Asp Gly Glu Tyr Leu
                 85                  90                  95

gaa atc cag gca gnc cgc gca gaa aac gtt gtt att gca ttc ggc cgc     336
Glu Ile Gln Ala Xaa Arg Ala Glu Asn Val Val Ile Ala Phe Gly Arg
            100                 105                 110

atc gaa ggc cag tcc gtt ggc ttt gtt gcc aac cag cca acc cag ttc     384
Ile Glu Gly Gln Ser Val Gly Phe Val Ala Asn Gln Pro Thr Gln Phe
        115                 120                 125
```

```
gct ggc tgc ctg gac atc gac tcc tct gag aag gca gct cgc ttc gtc    432
Ala Gly Cys Leu Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg Phe Val
    130                 135                 140

cgc acc tgc gac gcg ttc aac atc cca atc gtc atg ctt gtg gac gtc    480
Arg Thr Cys Asp Ala Phe Asn Ile Pro Ile Val Met Leu Val Asp Val
145                 150                 155                 160

ccc ggc ttc ctc                                                    492
Pro Gly Phe Leu
```

<210> 218
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 218

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Glu Glu Leu Gly Gly Ala Thr Thr His Met Val Thr Ala Gly Asn Ser
  1               5                  10                  15

His Tyr Thr Ala Ala Thr Asp Glu Glu Ala Leu Asp Trp Val Gln Asp
             20                  25                  30

Leu Val Ser Phe Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro Met Glu
         35                  40                  45

Asp Phe Asp Glu Glu Glu Gly Gly Val Glu Glu Asn Ile Thr Ala Asp
    50                  55                  60

Asp Leu Lys Leu Asp Glu Ile Ile Pro Asp Ser Ala Thr Val Pro Tyr
65                  70                  75                  80

Asp Val Arg Asp Val Xaa Glu Cys Leu Thr Asp Asp Gly Glu Tyr Leu
                85                  90                  95

Glu Ile Gln Ala Xaa Arg Ala Glu Asn Val Val Ile Ala Phe Gly Arg
            100                 105                 110

Ile Glu Gly Gln Ser Val Gly Phe Val Ala Asn Gln Pro Thr Gln Phe
        115                 120                 125

Ala Gly Cys Leu Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg Phe Val
    130                 135                 140

Arg Thr Cys Asp Ala Phe Asn Ile Pro Ile Val Met Leu Val Asp Val
145                 150                 155                 160

Pro Gly Phe Leu
```

<210> 219
<211> 1671
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(1648)
<223> RXA02583

<400> 219
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cagttgtcga tgaaccagaa atcggcacag tcggagctca tttgagtcgc cgcattgatg 60

agatttctcg gaagaattag taacggagag ctgacggaag ttg agt aac acc act   115
                                            Leu Ser Asn Thr Thr
                                            1               5

act gca gag aag cta gcg gat ctg cgc gca cgc ctg gag att gcc aaa   163
Thr Ala Glu Lys Leu Ala Asp Leu Arg Ala Arg Leu Glu Ile Ala Lys
                10                  15                  20

gac cca ggt agt gaa cgc gca cgt aaa aag cgc gac gag gaa ggc cga   211
Asp Pro Gly Ser Glu Arg Ala Arg Lys Lys Arg Asp Glu Glu Gly Arg
            25                  30                  35

acc acc cct cgt cag cgt att gat gct ctg ctt gat gcc gga tcc ttt   259
Thr Thr Pro Arg Gln Arg Ile Asp Ala Leu Leu Asp Ala Gly Ser Phe
        40                  45                  50

gtg gag atc ggc gca cta ggc cgt acc ccg gat gaa ccc gat gcg cct   307
Val Glu Ile Gly Ala Leu Gly Arg Thr Pro Asp Glu Pro Asp Ala Pro
    55                  60                  65

tac tct gac ggt gtg gtg act ggt tat ggt cgc atc gat ggt cgc cca   355
Tyr Ser Asp Gly Val Val Thr Gly Tyr Gly Arg Ile Asp Gly Arg Pro
70                  75                  80                  85

gtg gcc atc tac gcc cat gac aag acc gtt tac ggt ggt tcc gtg ggc   403
Val Ala Ile Tyr Ala His Asp Lys Thr Val Tyr Gly Gly Ser Val Gly
                90                  95                  100

atg act ttc gga cgt aaa gtc agc gaa gtc atg gac atg gct atc cgc   451
Met Thr Phe Gly Arg Lys Val Ser Glu Val Met Asp Met Ala Ile Arg
            105                 110                 115

att ggt tgc cca gtt atc ggt att cag gat tcc ggc gga gcc cgc att   499
Ile Gly Cys Pro Val Ile Gly Ile Gln Asp Ser Gly Gly Ala Arg Ile
        120                 125                 130

cag gat gcg gtg acc tcc ttg gcg atg tac tca gag atc gcg cgt cgt   547
Gln Asp Ala Val Thr Ser Leu Ala Met Tyr Ser Glu Ile Ala Arg Arg
    135                 140                 145

cag ctt ccg ctg tct ggc cgc agc cct cag att tcc atc atg ctg ggt   595
Gln Leu Pro Leu Ser Gly Arg Ser Pro Gln Ile Ser Ile Met Leu Gly
150                 155                 160                 165

aaa tcg gca ggt ggc gca gtg tat gca cct gtg acc act gac ttt gtt   643
Lys Ser Ala Gly Gly Ala Val Tyr Ala Pro Val Thr Thr Asp Phe Val
                170                 175                 180

atc ggc gtt gat ggt gaa aca gaa atg tat gtc acc ggc cca gcc gtg   691
Ile Gly Val Asp Gly Glu Thr Glu Met Tyr Val Thr Gly Pro Ala Val
            185                 190                 195

atc aag gaa gtc acc ggc gag cag atc act tcc gca gac ctc ggt ggc   739
Ile Lys Glu Val Thr Gly Glu Gln Ile Thr Ser Ala Asp Leu Gly Gly
        200                 205                 210
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```
ggt gcg cag cag atg caa aac ggc aac att tcc tat ttg gcg tcc tct    787
Gly Ala Gln Gln Met Gln Asn Gly Asn Ile Ser Tyr Leu Ala Ser Ser
    215                 220                 225

gaa gaa gag gcc ctg aat atg gtc aag gat ttg ctc gac ttc ctg cct    835
Glu Glu Glu Ala Leu Asn Met Val Lys Asp Leu Leu Asp Phe Leu Pro
230                 235                 240                 245

ttg acc tgc aat gat cca gcc cct gtg ttt gca gca cca acg gat gaa    883
Leu Thr Cys Asn Asp Pro Ala Pro Val Phe Ala Ala Pro Thr Asp Glu
                250                 255                 260

gag atc gcc tac gac gaa gct ctg aac tcg ttc atg cct gac gac act    931
Glu Ile Ala Tyr Asp Glu Ala Leu Asn Ser Phe Met Pro Asp Asp Thr
            265                 270                 275

aac cag ggc tac gac atg cat gac ctg ctg gac aag ctt ttc gac gac    979
Asn Gln Gly Tyr Asp Met His Asp Leu Leu Asp Lys Leu Phe Asp Asp
        280                 285                 290

gcc aac ctg ctg gaa atc caa gag gag tac gcc ccc aac ctg atc act    1027
Ala Asn Leu Leu Glu Ile Gln Glu Glu Tyr Ala Pro Asn Leu Ile Thr
    295                 300                 305

acc ttc gcc cgc gtt gat ggc aag gca gtc ggt gtg gtg gcc aac caa    1075
Thr Phe Ala Arg Val Asp Gly Lys Ala Val Gly Val Val Ala Asn Gln
310                 315                 320                 325

cca atg gat aag gca ggc tgc atc gac gct gac gcc gcc gac aag ggc    1123
Pro Met Asp Lys Ala Gly Cys Ile Asp Ala Asp Ala Ala Asp Lys Gly
                330                 335                 340

gcc cgc ttc atc cgt atc tgc gac gcc tac aac atc ccg atc atc ttc    1171
Ala Arg Phe Ile Arg Ile Cys Asp Ala Tyr Asn Ile Pro Ile Ile Phe
            345                 350                 355

gtc gtg gac acc cct ggc tac ctg cct ggc gtg gac caa gag aag gtc    1219
Val Val Asp Thr Pro Gly Tyr Leu Pro Gly Val Asp Gln Glu Lys Val
        360                 365                 370

ggt ttg att cac cgt ggc gca aag cta gcc ttc gca gtg gtg gaa tcg    1267
Gly Leu Ile His Arg Gly Ala Lys Leu Ala Phe Ala Val Val Glu Ser
    375                 380                 385

acc gtc cct aag att tcc ttg atc gtg cgc aag gcc tac ggc gga gca    1315
Thr Val Pro Lys Ile Ser Leu Ile Val Arg Lys Ala Tyr Gly Gly Ala
390                 395                 400                 405

tat gcc gtg atg ggt tcc aag aac ctc acc ggt gac ctc aac ttc gca    1363
Tyr Ala Val Met Gly Ser Lys Asn Leu Thr Gly Asp Leu Asn Phe Ala
                410                 415                 420

tgg cca acc gca cag atc gcc gtg atg ggc gca gcc gca gct gtc gtg    1411
Trp Pro Thr Ala Gln Ile Ala Val Met Gly Ala Ala Ala Ala Val Val
            425                 430                 435

atg atc cag ggc aag cag ctc gaa gcc gcc cca cct gag cag cgt gaa    1459
Met Ile Gln Gly Lys Gln Leu Glu Ala Ala Pro Pro Glu Gln Arg Glu
        440                 445                 450
```

tac atg aag aaa ctg ttc atg gac ttc tac gat gag aac atg acc agc 1507
Tyr Met Lys Lys Leu Phe Met Asp Phe Tyr Asp Glu Asn Met Thr Ser
455 460 465

cca tat gtg gcc gcc gag cgt ggt tac atc gac gcc atg atc gaa cct 1555
Pro Tyr Val Ala Ala Glu Arg Gly Tyr Ile Asp Ala Met Ile Glu Pro
470 475 480 485

gca gag acc cgt ttg gtg ctt cgc cga gca gtc cgc cag ctg gaa acc 1603
Ala Glu Thr Arg Leu Val Leu Arg Arg Ala Val Arg Gln Leu Glu Thr
490 495 500

aag gct gtg cga gac ctc gac aag aag cac acg atc atg ccg atg 1648
Lys Ala Val Arg Asp Leu Asp Lys Lys His Thr Ile Met Pro Met
505 510 515

taacgtccaa agaattatcc aga 1671

<210> 220
<211> 516
<212> PRT
<213> Corynebacterium glutamicum

<400> 220
Leu Ser Asn Thr Thr Thr Ala Glu Lys Leu Ala Asp Leu Arg Ala Arg
1 5 10 15

Leu Glu Ile Ala Lys Asp Pro Gly Ser Glu Arg Ala Arg Lys Lys Arg
20 25 30

Asp Glu Glu Gly Arg Thr Thr Pro Arg Gln Arg Ile Asp Ala Leu Leu
35 40 45

Asp Ala Gly Ser Phe Val Glu Ile Gly Ala Leu Gly Arg Thr Pro Asp
50 55 60

Glu Pro Asp Ala Pro Tyr Ser Asp Gly Val Val Thr Gly Tyr Gly Arg
65 70 75 80

Ile Asp Gly Arg Pro Val Ala Ile Tyr Ala His Asp Lys Thr Val Tyr
85 90 95

Gly Gly Ser Val Gly Met Thr Phe Gly Arg Lys Val Ser Glu Val Met
100 105 110

Asp Met Ala Ile Arg Ile Gly Cys Pro Val Ile Gly Ile Gln Asp Ser
115 120 125

Gly Gly Ala Arg Ile Gln Asp Ala Val Thr Ser Leu Ala Met Tyr Ser
130 135 140

Glu Ile Ala Arg Arg Gln Leu Pro Leu Ser Gly Arg Ser Pro Gln Ile
145 150 155 160

Ser Ile Met Leu Gly Lys Ser Ala Gly Gly Ala Val Tyr Ala Pro Val
165 170 175

Thr Thr Asp Phe Val Ile Gly Val Asp Gly Glu Thr Glu Met Tyr Val
180 185 190

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Thr Gly Pro Ala Val Ile Lys Glu Val Thr Gly Glu Gln Ile Thr Ser
        195                 200                 205

Ala Asp Leu Gly Gly Gly Ala Gln Gln Met Gln Asn Gly Asn Ile Ser
    210                 215                 220

Tyr Leu Ala Ser Ser Glu Glu Glu Ala Leu Asn Met Val Lys Asp Leu
225                 230                 235                 240

Leu Asp Phe Leu Pro Leu Thr Cys Asn Asp Pro Ala Pro Val Phe Ala
                245                 250                 255

Ala Pro Thr Asp Glu Glu Ile Ala Tyr Asp Glu Ala Leu Asn Ser Phe
            260                 265                 270

Met Pro Asp Asp Thr Asn Gln Gly Tyr Asp Met His Asp Leu Leu Asp
        275                 280                 285

Lys Leu Phe Asp Asp Ala Asn Leu Leu Glu Ile Gln Glu Glu Tyr Ala
    290                 295                 300

Pro Asn Leu Ile Thr Thr Phe Ala Arg Val Asp Gly Lys Ala Val Gly
305                 310                 315                 320

Val Val Ala Asn Gln Pro Met Asp Lys Ala Gly Cys Ile Asp Ala Asp
                325                 330                 335

Ala Ala Asp Lys Gly Ala Arg Phe Ile Arg Ile Cys Asp Ala Tyr Asn
            340                 345                 350

Ile Pro Ile Ile Phe Val Val Asp Thr Pro Gly Tyr Leu Pro Gly Val
        355                 360                 365

Asp Gln Glu Lys Val Gly Leu Ile His Arg Gly Ala Lys Leu Ala Phe
    370                 375                 380

Ala Val Val Glu Ser Thr Val Pro Lys Ile Ser Leu Ile Val Arg Lys
385                 390                 395                 400

Ala Tyr Gly Gly Ala Tyr Ala Val Met Gly Ser Lys Asn Leu Thr Gly
                405                 410                 415

Asp Leu Asn Phe Ala Trp Pro Thr Ala Gln Ile Ala Val Met Gly Ala
            420                 425                 430

Ala Ala Ala Val Val Met Ile Gln Gly Lys Gln Leu Glu Ala Ala Pro
        435                 440                 445

Pro Glu Gln Arg Glu Tyr Met Lys Lys Leu Phe Met Asp Phe Tyr Asp
    450                 455                 460

Glu Asn Met Thr Ser Pro Tyr Val Ala Ala Glu Arg Gly Tyr Ile Asp
465                 470                 475                 480

Ala Met Ile Glu Pro Ala Glu Thr Arg Leu Val Leu Arg Arg Ala Val
                485                 490                 495

Arg Gln Leu Glu Thr Lys Ala Val Arg Asp Leu Asp Lys Lys His Thr
            500                 505                 510

Ile Met Pro Met
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515

<210> 221
<211> 1635
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1612)
<223> RXA00870

<400> 221
caagacggcg atgtcgccgc cgctgttgat accgcagcgc gacttgttca cacagatatt 60

caacaattca cttcgcagag catttaagga atttacacac atg tct gaa cca caa 115
Met Ser Glu Pro Gln
1 5

acc atc tcg cac tgg att gac ggc gcg att tcc cca tcc act tcc ggc 163
Thr Ile Ser His Trp Ile Asp Gly Ala Ile Ser Pro Ser Thr Ser Gly
10 15 20

aag acc gct cct gtc tac aat cct gca act ggc cag gtc acc gcc aat 211
Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly Gln Val Thr Ala Asn
25 30 35

gtt gcg ctg gct agc cag gaa gag atc gat gcc acc atc gct tct gcc 259
Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala Thr Ile Ala Ser Ala
40 45 50

acc aag gct gct aag acg tgg ggc aac ctg tct atc gct aag cgc caa 307
Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser Ile Ala Lys Arg Gln
55 60 65

gct gtg ctt ttc aac ttc cgt gag ctg ctg aat gct cgc aag ggt gag 355
Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn Ala Arg Lys Gly Glu
70 75 80 85

ctg gcg gag atc atc act gca gag cac ggc aag gtc ttg tcc gat gcc 403
Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys Val Leu Ser Asp Ala
90 95 100

atg ggt gaa atc ctg cgc ggc cag gaa gtc gtg gag ctt gct acc ggt 451
Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val Glu Leu Ala Thr Gly
105 110 115

ttc cca cac ctg ctt aaa ggt gcg ttc aac gag aac gtc tcc acc ggc 499
Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu Asn Val Ser Thr Gly
120 125 130

att gat gtg tat tcc ttg aag cag cca ctg ggt gtt gtc ggt atc atc 547
Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly Val Val Gly Ile Ile
135 140 145

agc ccg ttc aac ttc cct gcg atg gtg ccg atg tgg ttt ttc cca atc 595
Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met Trp Phe Phe Pro Ile
150 155 160 165

gca atc gct gca ggc aac gca gtt att ttg aag cct tca gag aag gat 643

Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys Pro Ser Glu Lys Asp
170 175 180

cct tcg gca gcg ctg tgg atg gct cag atc tgg aag gaa gct ggt ctt 691
Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp Lys Glu Ala Gly Leu
185 190 195

cca gac ggc gta ttc aac gtg ctc cag ggc gac aag ctg gct gtt gat 739
Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp Lys Leu Ala Val Asp
200 205 210

ggt ttg ctg aac agc cct gat gtc tct gcg att tcc ttc gtg ggt tcc 787
Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile Ser Phe Val Gly Ser
215 220 225

acc cca atc gca aag tac atc tac gag act tcc gcg aag aac ggc aag 835
Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser Ala Lys Asn Gly Lys
230 235 240 245

cgc gtc cag gcg ttg ggc ggc gcg aag aac cac atg ctg gtg ctg cca 883
Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His Met Leu Val Leu Pro
250 255 260

gat gct gat ctg gat ctg gtt gcc gat cag gca atc aac gca ggt tac 931
Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala Ile Asn Ala Gly Tyr
265 270 275

ggc gct gcc ggt gag cgt tgc atg gct gtt tct gtg gtc ttg gct att 979
Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser Val Val Leu Ala Ile
280 285 290

gaa tct gtt gcc gac gag ctc att gag aag atc aag gag cgc atc gac 1027
Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile Lys Glu Arg Ile Asp
295 300 305

acc ctg cgc atc ggc aac ggt gcc ggc gac gag cag ggc gag ccg cac 1075
Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu Gln Gly Glu Pro His
310 315 320 325

ctg ggc cca cta atc acc gac gtc cac cgc gac aag gtc gct tct tat 1123
Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp Lys Val Ala Ser Tyr
330 335 340

gtc gac atc gct gag gcc gac ggc gcc aag atc atc gtg gac ggg cgt 1171
Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile Ile Val Asp Gly Arg
345 350 355

aac tgc gcc gta gac ggg cac gag gag ggc ttc ttc ttc ggc cct acg 1219
Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe Phe Phe Gly Pro Thr
360 365 370

ctt atc gac gac atc cca ctc acg ttc cgc gcc tac acc gaa gaa atc 1267
Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala Tyr Thr Glu Glu Ile
375 380 385

ttc ggc ccg gtc ctc tct gtc gtt cgt gtc gca tcc ttc gac gag gca 1315
Phe Gly Pro Val Leu Ser Val Val Arg Val Ala Ser Phe Asp Glu Ala
390 395 400 405

att gag ctg atc aac tcc ggt gaa ttc ggc aac gga acc gca atc ttc 1363
Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn Gly Thr Ala Ile Phe

410 415 420

acc aac gat ggt gga gcg gca cgc cgc ttc cag cat gag atc gaa gtg 1411
Thr Asn Asp Gly Gly Ala Ala Arg Arg Phe Gln His Glu Ile Glu Val
425 430 435

ggc atg atc ggc atc aac gta cca atc cca gtg cct gtt gcg tac cac 1459
Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val Pro Val Ala Tyr His
440 445 450

tcc ttc ggt ggt tgg aag aac tcc ctc ttc ggt gac gcc aag gca tat 1507
Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly Asp Ala Lys Ala Tyr
455 460 465

ggc act caa ggt ttt gat ttc ttc acc agg gaa aag gcg atc acc agc 1555
Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu Lys Ala Ile Thr Ser
470 475 480 485

cgt tgg ctc gac cca gca acc cac ggt ggc att aac ctc ggt ttc cca 1603
Arg Trp Leu Asp Pro Ala Thr His Gly Gly Ile Asn Leu Gly Phe Pro
490 495 500

cag aac gat taattgaagg agagcacagg act 1635
Gln Asn Asp

<210> 222
<211> 504
<212> PRT
<213> Corynebacterium glutamicum

<400> 222
Met Ser Glu Pro Gln Thr Ile Ser His Trp Ile Asp Gly Ala Ile Ser
1 5 10 15

Pro Ser Thr Ser Gly Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly
20 25 30

Gln Val Thr Ala Asn Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala
35 40 45

Thr Ile Ala Ser Ala Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser
50 55 60

Ile Ala Lys Arg Gln Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn
65 70 75 80

Ala Arg Lys Gly Glu Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys
85 90 95

Val Leu Ser Asp Ala Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val
100 105 110

Glu Leu Ala Thr Gly Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu
115 120 125

Asn Val Ser Thr Gly Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly
130 135 140

Val Val Gly Ile Ile Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met

145 150 155 160

Trp Phe Phe Pro Ile Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys
165 170 175

Pro Ser Glu Lys Asp Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp
180 185 190

Lys Glu Ala Gly Leu Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp
195 200 205

Lys Leu Ala Val Asp Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile
210 215 220

Ser Phe Val Gly Ser Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser
225 230 235 240

Ala Lys Asn Gly Lys Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His
245 250 255

Met Leu Val Leu Pro Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala
260 265 270

Ile Asn Ala Gly Tyr Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser
275 280 285

Val Val Leu Ala Ile Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile
290 295 300

Lys Glu Arg Ile Asp Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu
305 310 315 320

Gln Gly Glu Pro His Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp
325 330 335

Lys Val Ala Ser Tyr Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile
340 345 350

Ile Val Asp Gly Arg Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe
355 360 365

Phe Phe Gly Pro Thr Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala
370 375 380

Tyr Thr Glu Glu Ile Phe Gly Pro Val Leu Ser Val Val Arg Val Ala
385 390 395 400

Ser Phe Asp Glu Ala Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn
405 410 415

Gly Thr Ala Ile Phe Thr Asn Asp Gly Gly Ala Ala Arg Arg Phe Gln
420 425 430

His Glu Ile Glu Val Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val
435 440 445

Pro Val Ala Tyr His Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly
450 455 460

Asp Ala Lys Ala Tyr Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu
465 470 475 480

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Lys Ala Ile Thr Ser Arg Trp Leu Asp Pro Ala Thr His Gly Gly Ile
                485                 490                 495

Asn Leu Gly Phe Pro Gln Asn Asp
            500


<210> 223
<211> 1305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1282)
<223> RXA01260

<400> 223
ctaaacgtgg gctgcattcc ttccaaagtc tctgatcaaa aacgctgaag ttgcccatac 60

ctttacccat gagaagaaga ccttcggcat caatggcgaa gtg acc ttc aac tat   115
                                           Val Thr Phe Asn Tyr
                                           1               5

gag gat gct cac aag cgt tcc cgt ggc gtt tcc gac aag atc gtt gga   163
Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly
                10                  15                  20

ggc gtt cat tac ttg atg aag aag aac aag atc atc gaa att cat ggt   211
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Glu Ile His Gly
            25                  30                  35

ctt gga aac ttc aag gat gct aag act ctt gag gtc acc gac ggt aag   259
Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys
        40                  45                  50

gat gct ggc aag acc atc acc ttt gat gac tgc atc atc gca acc ggt   307
Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
    55                  60                  65

tcg gta gtc aac acc ctc cgt ggc gtt gac ttc tca gag aac gtt gtg   355
Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe Ser Glu Asn Val Val
70                  75                  80                  85

tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc   403
Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val
                90                  95                  100

att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt   451
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly
            105                 110                 115

aac tac ggt gta gat gta acc gtc atc gag ttc atg gat cgt gtg ctt   499
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu
        120                 125                 130

cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag   547
Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys
    135                 140                 145
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aag atg ggc gtt aag ctt ctt cct ggc cat gca acc act gct gtt cgg    595
Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
150                 155                 160                 165

gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac    643
Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp
                170                 175                 180

aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc    691
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe
            185                 190                 195

cgt cca cgc gtt gag gga ttt ggt ctt gaa aac act ggc gtt aag ctc    739
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu
        200                 205                 210

acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc    787
Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val
    215                 220                 225

gat ggc att tac gcc atc ggt gac gtg acc gcc aag ctt cag ctt gct    835
Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala
230                 235                 240                 245

cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt    883
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly
                250                 255                 260

gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc    931
Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr
            265                 270                 275

ttc tgc aac cca cag gtt tct tcc ttt ggt tac acc gaa gag cag gcc    979
Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala
        280                 285                 290

aag gag aag tgg cca gat cgt gag atc aag gtt gct tcc ttc cca ttc    1027
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe
    295                 300                 305

tct gca aac ggt aaa gca gtt ggc ctg gca gaa act gat ggt ttc gca    1075
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala
310                 315                 320                 325

aag atc gtt gct gat gca gaa ttc ggt gag ctg ctc ggt gca cac ctg    1123
Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Ala His Leu
                330                 335                 340

gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag    1171
Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln
            345                 350                 355

aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac    1219
Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His
        360                 365                 370

cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga    1267
Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly
    375                 380                 385

cac atg atc aac ttc tagaatccac ctcgttggcc ctg                      1305
```

His Met Ile Asn Phe
390

<210> 224
<211> 394
<212> PRT
<213> Corynebacterium glutamicum

<400> 224
Val Thr Phe Asn Tyr Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser
1   5   10   15

Asp Lys Ile Val Gly Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile
            20   25   30

Ile Glu Ile His Gly Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu
        35   40   45

Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys
    50   55   60

Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe
65   70   75   80

Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala
                85   90   95

Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe
            100   105   110

Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe
        115   120   125

Met Asp Arg Val Leu Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile
    130   135   140

Ala Lys Ala Tyr Lys Lys Met Gly Val Lys Leu Leu Pro Gly His Ala
145   150   155   160

Thr Thr Ala Val Arg Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln
                165   170   175

Lys Lys Gly Ser Asp Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met
            180   185   190

Val Ser Val Gly Phe Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn
        195   200   205

Thr Gly Val Lys Leu Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr
    210   215   220

Met Arg Thr Asn Val Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala
225   230   235   240

Lys Leu Gln Leu Ala His Val Ala Glu Ala Gln Gly Ile Val Ala Ala
                245   250   255

Glu Thr Ile Ala Gly Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met
            260   265   270

```
Met Pro Arg Ala Thr Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr
        275                 280                 285

Thr Glu Glu Gln Ala Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val
    290                 295                 300

Ala Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu
305                 310                 315                 320

Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu
                325                 330                 335

Leu Gly Ala His Leu Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu
            340                 345                 350

Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg
        355                 360                 365

Ser Val His Ile His Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala
    370                 375                 380

His Gly Ile Ser Gly His Met Ile Asn Phe
385                 390


&lt;210&gt; 225
&lt;211&gt; 294
&lt;212&gt; DNA
&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (101)..(271)
&lt;223&gt; RXA01261

&lt;400&gt; 225
gtgggtgttt ttcattttct tccactctaa aattaagtat ggaaaaccaa ccgcacccgg 60

atgcacgaca atgacccact aaacacgtat ccttgaatgc gtg act gaa cat tat   115
                                           Val Thr Glu His Tyr
                                           1               5

gac gta gta gta ctc gga gcc ggc ccc ggt ggc tat gtc tcc gcc atc   163
Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile
                10                  15                  20

cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac   211
Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr
            25                  30                  35

tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct   259
Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser
        40                  45                  50

gat caa aaa cgc tgaagttgcc catacсttta ccc                         294
Asp Gln Lys Arg
    55


&lt;210&gt; 226
&lt;211&gt; 57
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<212> PRT
<213> Corynebacterium glutamicum

<400> 226
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Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
1               5                   10                  15

Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
            20                  25                  30

Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
        35                  40                  45

Pro Ser Lys Val Ser Asp Gln Lys Arg
    50                  55
```

<210> 227
<211> 555
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(532)
<223> RXA01136

<400> 227
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ccctcgcaac accgacggta gcctcttgga aatggcgcgc atcgtgcgtg agctttcccg 60

ctaggacctg tctactgcct tcactttgtg cgaacaccgc atg acc ttg gat tac   115
                                           Met Thr Leu Asp Tyr
                                           1               5

ttc aag gca tcc ggc act gac tat gct ttg gga ttg gct gca gag tcg   163
Phe Lys Ala Ser Gly Thr Asp Tyr Ala Leu Gly Leu Ala Ala Glu Ser
                10                  15                  20

gaa ggg gca cga cgc act ggt atc acc ggc atg gcg agt gca ttc aag   211
Glu Gly Ala Arg Arg Thr Gly Ile Thr Gly Met Ala Ser Ala Phe Lys
            25                  30                  35

gag ttt gct ggt tgt ggt gag atc gac ctt gaa gca acc agg gta gaa   259
Glu Phe Ala Gly Cys Gly Glu Ile Asp Leu Glu Ala Thr Arg Val Glu
        40                  45                  50

ggt ggc ctc aaa gtt agt gga aag ctt cgt tgg gct tcc aac ttg tgc   307
Gly Gly Leu Lys Val Ser Gly Lys Leu Arg Trp Ala Ser Asn Leu Cys
    55                  60                  65

gaa gat cca gtg att gtg cct gct gca aag acc gca gag ggc tta caa   355
Glu Asp Pro Val Ile Val Pro Ala Ala Lys Thr Ala Glu Gly Leu Gln
70                  75                  80                  85

cta ctg ttc gca ttg ggc gca gaa acc gaa ggt gtc acc ctc ggt tct   403
Leu Leu Phe Ala Leu Gly Ala Glu Thr Glu Gly Val Thr Leu Gly Ser
                90                  95                  100

tca ctt gct cta ctc ggt ttg aac gca act gct tgc gct tgg gtg agc   451
Ser Leu Ala Leu Leu Gly Leu Asn Ala Thr Ala Cys Ala Trp Val Ser
            105                 110                 115
```

```
ttt gag gat gtc ttc att cct ggg gct cag att cta agc cac gat ttc   499
Phe Glu Asp Val Phe Ile Pro Gly Ala Gln Ile Leu Ser His Asp Phe
        120                 125                 130

ctt acc ttg tgg cat cgg tgc gcc caa cct tcg tgatcctacg gatctccgaa 552
Leu Thr Leu Trp His Arg Cys Ala Gln Pro Ser
    135                 140

tac                                                               555


<210> 228
<211> 144
<212> PRT
<213> Corynebacterium glutamicum

<400> 228
Met Thr Leu Asp Tyr Phe Lys Ala Ser Gly Thr Asp Tyr Ala Leu Gly
  1               5                  10                  15

Leu Ala Ala Glu Ser Glu Gly Ala Arg Arg Thr Gly Ile Thr Gly Met
             20                  25                  30

Ala Ser Ala Phe Lys Glu Phe Ala Gly Cys Gly Glu Ile Asp Leu Glu
         35                  40                  45

Ala Thr Arg Val Glu Gly Gly Leu Lys Val Ser Gly Lys Leu Arg Trp
     50                  55                  60

Ala Ser Asn Leu Cys Glu Asp Pro Val Ile Val Pro Ala Ala Lys Thr
 65                  70                  75                  80

Ala Glu Gly Leu Gln Leu Leu Phe Ala Leu Gly Ala Glu Thr Glu Gly
                 85                  90                  95

Val Thr Leu Gly Ser Ser Leu Ala Leu Leu Gly Leu Asn Ala Thr Ala
            100                 105                 110

Cys Ala Trp Val Ser Phe Glu Asp Val Phe Ile Pro Gly Ala Gln Ile
        115                 120                 125

Leu Ser His Asp Phe Leu Thr Leu Trp His Arg Cys Ala Gln Pro Ser
    130                 135                 140




<210> 229
<211> 1140
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<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1117)
<223> RXN00559

<400> 229
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catgaagcat cagcctagta cgaaccgtta aagtgtccat atg tct gat aat ccg    115
                                            Met Ser Asp Asn Pro
                                             1               5

cat gag aat ccc cgt gag aat cca cac cgc tcc cca gaa gtc gtc ctt    163
His Glu Asn Pro Arg Glu Asn Pro His Arg Ser Pro Glu Val Val Leu
                 10                  15                  20

cgt ttc atg gct gcc cct act gac gtt ttg atg gct ggt agc cat ggc    211
Arg Phe Met Ala Ala Pro Thr Asp Val Leu Met Ala Gly Ser His Gly
             25                  30                  35

gtt ggc ggt ggc cga gtc ctg gaa tgg atc gat aag gct gct tat gct    259
Val Gly Gly Gly Arg Val Leu Glu Trp Ile Asp Lys Ala Ala Tyr Ala
         40                  45                  50

tgt gct acc cag tgg tct gga acc tac tgt gtc act gct tat gtt ggt    307
Cys Ala Thr Gln Trp Ser Gly Thr Tyr Cys Val Thr Ala Tyr Val Gly
     55                  60                  65

cac att cac ttc act cgc cct att ccc tct ggc cac atg gtc gag gtg    355
His Ile His Phe Thr Arg Pro Ile Pro Ser Gly His Met Val Glu Val
 70                  75                  80                  85

cgt tcc cgc att gcg atg act ggc cgt tcc tcc atg cac atc gtg aat    403
Arg Ser Arg Ile Ala Met Thr Gly Arg Ser Ser Met His Ile Val Asn
                 90                  95                 100

gag gtg ctt tct gcg gat cct cgc gat ggc aac tac acc cgt gcg tgt    451
Glu Val Leu Ser Ala Asp Pro Arg Asp Gly Asn Tyr Thr Arg Ala Cys
            105                 110                 115

gac tgc ttg gtt att ttc gtg gcg aag gac acc gca act ggt cgc gct    499
Asp Cys Leu Val Ile Phe Val Ala Lys Asp Thr Ala Thr Gly Arg Ala
        120                 125                 130

acc cca gtt cct tca ttt acc cct aag aat gaa gaa gag cag cgc gtg    547
Thr Pro Val Pro Ser Phe Thr Pro Lys Asn Glu Glu Glu Gln Arg Val
    135                 140                 145

ttg gaa gct gct aac tcc cgc atc ggg ctg cgc aag gct att gaa gcg    595
Leu Glu Ala Ala Asn Ser Arg Ile Gly Leu Arg Lys Ala Ile Glu Ala
150                 155                 160                 165

gag atg gaa aag cag acg tac aac gga cct tct gag gcc cct cgt ttg    643
Glu Met Glu Lys Gln Thr Tyr Asn Gly Pro Ser Glu Ala Pro Arg Leu
                170                 175                 180

att acc cgc ttc ttg gct aag cca aca gat atc aac tgg ggt ggc aag    691
Ile Thr Arg Phe Leu Ala Lys Pro Thr Asp Ile Asn Trp Gly Gly Lys
            185                 190                 195

gtc cac ggt ggc act gcc atg gaa tgg atc gat gag gcg ggt gct gcg    739
Val His Gly Gly Thr Ala Met Glu Trp Ile Asp Glu Ala Gly Ala Ala
        200                 205                 210

tgc acc atg gag tgg tct ggt aac cac acc gtt gcg gtt tat gct ggt    787
Cys Thr Met Glu Trp Ser Gly Asn His Thr Val Ala Val Tyr Ala Gly
    215                 220                 225
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ggt atc cgc ttc tac cag ccc att cag atc ggt gac ctc att gag gtg    835
Gly Ile Arg Phe Tyr Gln Pro Ile Gln Ile Gly Asp Leu Ile Glu Val
230                 235                 240                 245

gac gcc cgc atg atg cgt acc gat aag cgt tcc atg cag atg tcc atc    883
Asp Ala Arg Met Met Arg Thr Asp Lys Arg Ser Met Gln Met Ser Ile
                250                 255                 260

cac gtc cgt gcc ggt gat gct cac cgt ggc cgt gct gag cta gaa acc    931
His Val Arg Ala Gly Asp Ala His Arg Gly Arg Ala Glu Leu Glu Thr
            265                 270                 275

gct att cac gca acg gtg acc tac tta gga att gat gtc gac gga gag    979
Ala Ile His Ala Thr Val Thr Tyr Leu Gly Ile Asp Val Asp Gly Glu
        280                 285                 290

cct ttg cct gca cca cag ttt gtg cct cgt acc cct gag gat atc cag    1027
Pro Leu Pro Ala Pro Gln Phe Val Pro Arg Thr Pro Glu Asp Ile Gln
    295                 300                 305

ttg gct gag cat gca aac atc ctg agg gat ctg cgt gct gat tac acc    1075
Leu Ala Glu His Ala Asn Ile Leu Arg Asp Leu Arg Ala Asp Tyr Thr
310                 315                 320                 325

cca atg ccg ctg ttc cag cgc agg gtt cca ctg cag atc gac            1117
Pro Met Pro Leu Phe Gln Arg Arg Val Pro Leu Gln Ile Asp
                330                 335

tagttagacc cgaaaaagcc ccc                                          1140


<210> 230
<211> 339
<212> PRT
<213> Corynebacterium glutamicum

<400> 230
Met Ser Asp Asn Pro His Glu Asn Pro Arg Glu Asn Pro His Arg Ser
  1               5                  10                  15

Pro Glu Val Val Leu Arg Phe Met Ala Ala Pro Thr Asp Val Leu Met
             20                  25                  30

Ala Gly Ser His Gly Val Gly Gly Gly Arg Val Leu Glu Trp Ile Asp
         35                  40                  45

Lys Ala Ala Tyr Ala Cys Ala Thr Gln Trp Ser Gly Thr Tyr Cys Val
     50                  55                  60

Thr Ala Tyr Val Gly His Ile His Phe Thr Arg Pro Ile Pro Ser Gly
 65                  70                  75                  80

His Met Val Glu Val Arg Ser Arg Ile Ala Met Thr Gly Arg Ser Ser
                 85                  90                  95

Met His Ile Val Asn Glu Val Leu Ser Ala Asp Pro Arg Asp Gly Asn
            100                 105                 110

Tyr Thr Arg Ala Cys Asp Cys Leu Val Ile Phe Val Ala Lys Asp Thr
        115                 120                 125
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Ala Thr Gly Arg Ala Thr Pro Val Pro Ser Phe Thr Pro Lys Asn Glu
    130   135   140

Glu Glu Gln Arg Val Leu Glu Ala Ala Asn Ser Arg Ile Gly Leu Arg
145   150   155   160

Lys Ala Ile Glu Ala Glu Met Glu Lys Gln Thr Tyr Asn Gly Pro Ser
                165   170   175

Glu Ala Pro Arg Leu Ile Thr Arg Phe Leu Ala Lys Pro Thr Asp Ile
            180   185   190

Asn Trp Gly Gly Lys Val His Gly Gly Thr Ala Met Glu Trp Ile Asp
        195   200   205

Glu Ala Gly Ala Ala Cys Thr Met Glu Trp Ser Gly Asn His Thr Val
    210   215   220

Ala Val Tyr Ala Gly Gly Ile Arg Phe Tyr Gln Pro Ile Gln Ile Gly
225   230   235   240

Asp Leu Ile Glu Val Asp Ala Arg Met Met Arg Thr Asp Lys Arg Ser
                245   250   255

Met Gln Met Ser Ile His Val Arg Ala Gly Asp Ala His Arg Gly Arg
            260   265   270

Ala Glu Leu Glu Thr Ala Ile His Ala Thr Val Thr Tyr Leu Gly Ile
        275   280   285

Asp Val Asp Gly Glu Pro Leu Pro Ala Pro Gln Phe Val Pro Arg Thr
    290   295   300

Pro Glu Asp Ile Gln Leu Ala Glu His Ala Asn Ile Leu Arg Asp Leu
305   310   315   320

Arg Ala Asp Tyr Thr Pro Met Pro Leu Phe Gln Arg Arg Val Pro Leu
                325   330   335

Gln Ile Asp

<210> 231
<211> 313
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> FRXA00559

<400> 231
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catgaagcat cagcctagta cgaaccgtta aagtgtccat atg tct gat aat ccg 115
                                          Met Ser Asp Asn Pro
                                           1   5

cat gag aat ccc cgt gag aat cca cac cgc tcc cca gaa gtc gtc ctt 163

His Glu Asn Pro Arg Glu Asn Pro His Arg Ser Pro Glu Val Val Leu
10 15 20

cgt ttc atg gct gcc cct act gac gtt ttg atg gct ggt agc cat ggc 211
Arg Phe Met Ala Ala Pro Thr Asp Val Leu Met Ala Gly Ser His Gly
25 30 35

gtt ggc ggt ggc cga gtc ctg gaa tgg atc gat aag gct gct tat gct 259
Val Gly Gly Gly Arg Val Leu Glu Trp Ile Asp Lys Ala Ala Tyr Ala
40 45 50

tgt gct acc cac ggg tct gga acc tac tgc gtc act gct tat gtt ggt 307
Cys Ala Thr His Gly Ser Gly Thr Tyr Cys Val Thr Ala Tyr Val Gly
55 60 65

cac att 313
His Ile
70

<210> 232
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 232
Met Ser Asp Asn Pro His Glu Asn Pro Arg Glu Asn Pro His Arg Ser
1 5 10 15

Pro Glu Val Val Leu Arg Phe Met Ala Ala Pro Thr Asp Val Leu Met
20 25 30

Ala Gly Ser His Gly Val Gly Gly Gly Arg Val Leu Glu Trp Ile Asp
35 40 45

Lys Ala Ala Tyr Ala Cys Ala Thr His Gly Ser Gly Thr Tyr Cys Val
50 55 60

Thr Ala Tyr Val Gly His Ile
65 70

<210> 233
<211> 802
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(802)
<223> RXA01580

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tcaactttgc tccctatcct taaaaagccc acagaaaagg atg tat aag aat atg 115
Met Tyr Lys Asn Met
1 5

cac att gtt gcc cat cgc ggt gcg gaa gat ctg cac ctc gaa aac acc 163
His Ile Val Ala His Arg Gly Ala Glu Asp Leu His Leu Glu Asn Thr

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                  10                        15                        20

atg acc gct ttc cag gct gcc gcg ccc gct gac gct ttt gag ctg gat      211
Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp Ala Phe Glu Leu Asp
            25                  30                  35

atc cac gcc acc gct gac aat cag gtc gtc gtt atc cac gac cgc acc      259
Ile His Ala Thr Ala Asp Asn Gln Val Val Val Ile His Asp Arg Thr
        40                  45                  50

gca gcg cgt gtt gcc gcg cca gat tcc ctg cac cgc gac acc ccg gtt      307
Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His Arg Asp Thr Pro Val
    55                  60                  65

gcg cgc tta agc gcc gcg caa atc aag gag ata acg ctt atc gac gga      355
Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile Thr Leu Ile Asp Gly
70                  75                  80                  85

tcc ccc gta cca acc ctg gag gaa gtt cta ctc cag acg agc ctg ccg      403
Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu Gln Thr Ser Leu Pro
                90                  95                  100

atc caa gtg gaa atc aaa tct gcc ggt gca gtt cca gca gcc gca gca      451
Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val Pro Ala Ala Ala Ala
            105                 110                 115

tta ttg cag aaa tac cca gag cac ctg gag cgc ctg ctg ttc atc agt      499
Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg Leu Leu Phe Ile Ser
        120                 125                 130

ttc atc gat gca gca ctg gtg gaa atc gtg gat cga ctg cca gaa gct      547
Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp Arg Leu Pro Glu Ala
    135                 140                 145

cgc gtg gga atc ttg cgc gat gcg tcc atg gat gat ctg cgc att ctt      595
Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp Asp Leu Arg Ile Leu
150                 155                 160                 165

gat tac atc ccg cta aaa aat gtg ggc gcg atc ttg ccc tcg tgg aaa      643
Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile Leu Pro Ser Trp Lys
                170                 175                 180

gca cta aac gtg gcg tca att gct gat cta cat acc aag gga atc aag      691
Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His Thr Lys Gly Ile Lys
            185                 190                 195

gtt ggc tgc tgg aca att cgg gat gaa aat gcg ttt ggg atc gca caa      739
Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala Phe Gly Ile Ala Gln
        200                 205                 210

caa gct ggc gtt gat tac ccc act gtt agc gat ccc tct cgt ttc tcg      787
Gln Ala Gly Val Asp Tyr Pro Thr Val Ser Asp Pro Ser Arg Phe Ser
    215                 220                 225

cgc cct ccc ctg ctg                                                  802
Arg Pro Pro Leu Leu
230
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<210> 234
<211> 234

<212> PRT
<213> Corynebacterium glutamicum

<400> 234
Met Tyr Lys Asn Met His Ile Val Ala His Arg Gly Ala Glu Asp Leu
1 5 10 15

His Leu Glu Asn Thr Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp
20 25 30

Ala Phe Glu Leu Asp Ile His Ala Thr Ala Asp Asn Gln Val Val Val
35 40 45

Ile His Asp Arg Thr Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His
50 55 60

Arg Asp Thr Pro Val Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile
65 70 75 80

Thr Leu Ile Asp Gly Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu
85 90 95

Gln Thr Ser Leu Pro Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val
100 105 110

Pro Ala Ala Ala Ala Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg
115 120 125

Leu Leu Phe Ile Ser Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp
130 135 140

Arg Leu Pro Glu Ala Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp
145 150 155 160

Asp Leu Arg Ile Leu Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile
165 170 175

Leu Pro Ser Trp Lys Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His
180 185 190

Thr Lys Gly Ile Lys Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala
195 200 205

Phe Gly Ile Ala Gln Gln Ala Gly Val Asp Tyr Pro Thr Val Ser Asp
210 215 220

Pro Ser Arg Phe Ser Arg Pro Pro Leu Leu
225 230

<210> 235
<211> 882
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<223> RXA02677

<400> 235

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agtcgatagc aggtatataa aggccaggag agatgggttc atg aaa gtc atc gcg   115
                                            Met Lys Val Ile Ala
                                             1               5

cac cga ggt tta tcg tct cgc ttt ccc gaa tta aca gag tct gcg ttt   163
His Arg Gly Leu Ser Ser Arg Phe Pro Glu Leu Thr Glu Ser Ala Phe
                10                  15                  20

cgg gcg gct cta gag cta ccg att cat gga att gaa act gat gtc cgg   211
Arg Ala Ala Leu Glu Leu Pro Ile His Gly Ile Glu Thr Asp Val Arg
            25                  30                  35

ctg act aaa tgt ggc gaa gtg gtt aac gtc cat gac ccc att gtg gat   259
Leu Thr Lys Cys Gly Glu Val Val Asn Val His Asp Pro Ile Val Asp
        40                  45                  50

cgc gtg tcg aat ggt cgc ggt cgg gtg tcg cgt ttg gac ttg gaa tcc   307
Arg Val Ser Asn Gly Arg Gly Arg Val Ser Arg Leu Asp Leu Glu Ser
    55                  60                  65

ttg ctg agc ttg aac ttt gga acc aaa gaa acc cca gaa aaa gtg ctt   355
Leu Leu Ser Leu Asn Phe Gly Thr Lys Glu Thr Pro Glu Lys Val Leu
70                  75                  80                  85

act tta aac aat cta tta gat att ttt gag gat tat cca gat aag cac   403
Thr Leu Asn Asn Leu Leu Asp Ile Phe Glu Asp Tyr Pro Asp Lys His
                90                  95                  100

ctt tat ata gaa acc aag cac cca atg cgc tac gcg gtc atg ctg gaa   451
Leu Tyr Ile Glu Thr Lys His Pro Met Arg Tyr Ala Val Met Leu Glu
            105                 110                 115

gaa gaa atc aca aaa atc tta aaa tat cgt ggg ctg acg gaa gac cca   499
Glu Glu Ile Thr Lys Ile Leu Lys Tyr Arg Gly Leu Thr Glu Asp Pro
        120                 125                 130

cgc atc cac atc att tct ttt gca ctt ccc gcg atg tat cgc atg gct   547
Arg Ile His Ile Ile Ser Phe Ala Leu Pro Ala Met Tyr Arg Met Ala
    135                 140                 145

cgc ctt gct cca cag ctt gat cgc att cat ctg cgc agg tcg tgg gag   595
Arg Leu Ala Pro Gln Leu Asp Arg Ile His Leu Arg Arg Ser Trp Glu
150                 155                 160                 165

cgt tgg ggt aat ccg cgc gat gtg cgc tgc ggt gta ccc acc ggt ttg   643
Arg Trp Gly Asn Pro Arg Asp Val Arg Cys Gly Val Pro Thr Gly Leu
                170                 175                 180

ggg ttg tcg ctg gag cgg gcg aag atg gat cca agg atg att ggg gcg   691
Gly Leu Ser Leu Glu Arg Ala Lys Met Asp Pro Arg Met Ile Gly Ala
            185                 190                 195

aaa ggg tta ccc acc tat ctt ttc acc gtc gat aag caa aaa gac atg   739
Lys Gly Leu Pro Thr Tyr Leu Phe Thr Val Asp Lys Gln Lys Asp Met
        200                 205                 210

ctg tgg gcg cgc gaa cag ggc gtc gac atg ctc gcc acc aat tat ccg   787
Leu Trp Ala Arg Glu Gln Gly Val Asp Met Leu Ala Thr Asn Tyr Pro
    215                 220                 225
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